

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
21 March 2002 (21.03.2002)

PCT

(10) International Publication Number
WO 02/22675 A2

(51) International Patent Classification⁷: **C07K 14/415**

(21) International Application Number: **PCT/US01/28506**

(22) International Filing Date:
14 September 2001 (14.09.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/232,778 15 September 2000 (15.09.2000) US
60/300,183 22 June 2001 (22.06.2001) US

(71) Applicants (for all designated States except US): **SYNGENTA PARTICIPATIONS AG** [CH/CH]; Schwarzwald-
dalle 215, CH-4058 Basel (CH). **UNIVERSITY OF
NORTH CAROLINA AT CHAPEL HILL** [US/US];
300 Bynum Hall, Campus Box 4100, Chapel Hill, NC
27599-4100 (US).

(71) Applicants and

(72) Inventors: **GLAZE BROOK, Jane** [US/US]; 4503 Ocean
Valley Lane, San Diego, CA 92130 (US). **WANG, Xun**

[—/US]; 12524 Caminito Vista Soledad, San Diego, CA
92121 (US). **DANGL, Jeffrey, L.** [US/US]; 601 Jones
Ferry Road, Apt. B, Carrboro, NC 27510 (US). **EUL-
GEM, Thomas** [US/US]; 605 Jones Ferry Road, Apt.
VV1, Carrboro, NC 27510 (US). **ZHU, Tong** [—/US];
5260 Caminito Exquisito, San Diego, CA 92130 (US).

(74) Agent: **VIKSINS, Ann, S.**; Schwegman, Lunberg,
Woessner & Kluth, P.O. Box 2938, Minneapolis, MN
55402 (US).

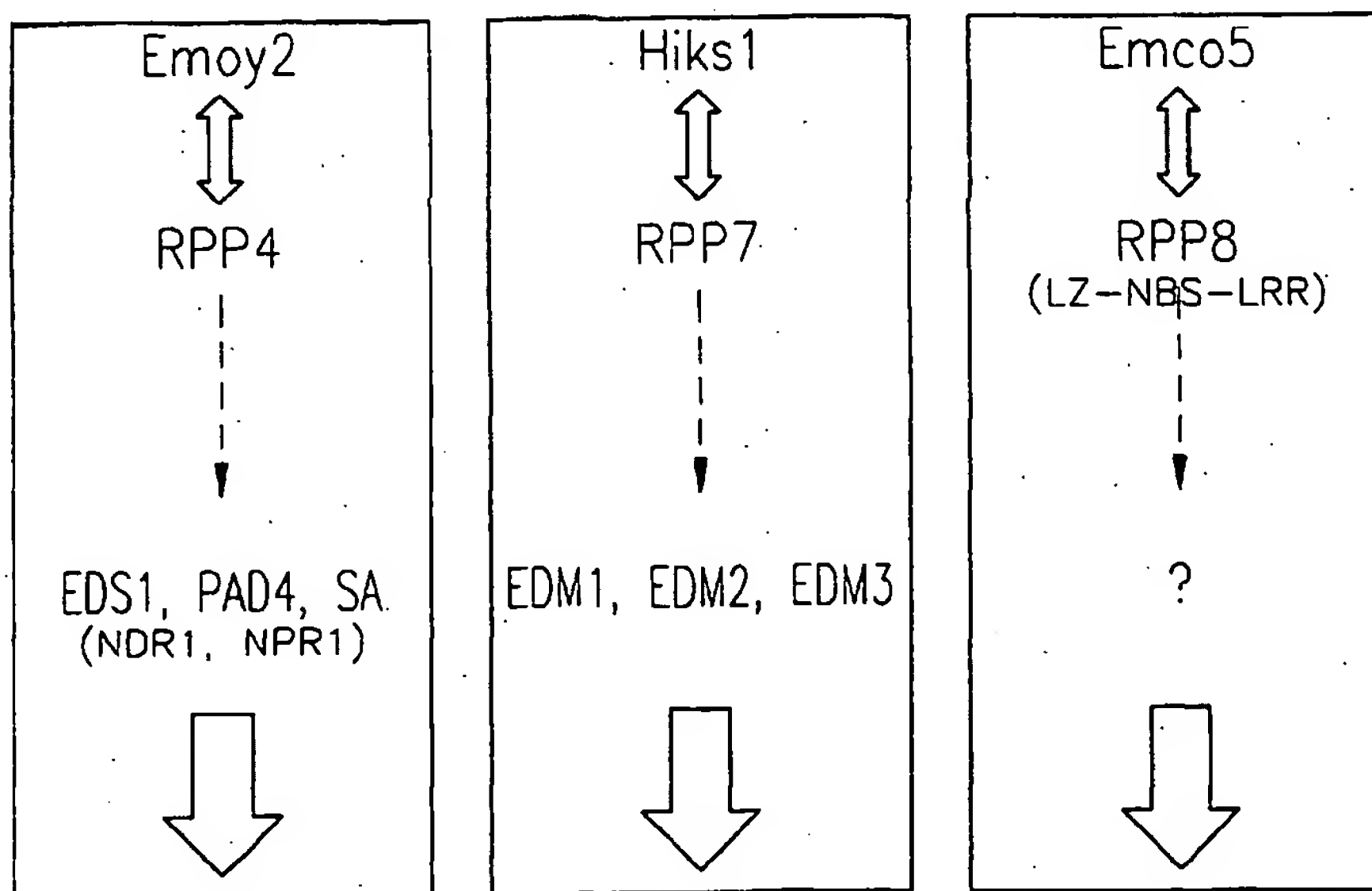
(81) Designated States (national): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,
CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI,
SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU,
ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,

[Continued on next page]

(54) Title: **PLANT GENES, THE EXPRESSION OF WHICH ARE ALTERED BY PATHOGEN INFECTION**

RPP-DEPENDENT DEFENSE PATHWAYS



R E S I S T A N C E

(57) Abstract: Methods to identify genes, the expression of which is altered in response to pathogen infection, are provided, as well as the genes identified thereby.

BEST AVAILABLE COPY

WO 02/22675 A2



CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

— with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

PLANT GENES, THE EXPRESSION OF WHICH ARE ALTERED BY PATHOGEN INFECTION

5

Cross-Reference to Related Applications

This application is a continuation-in-part application of U.S. application Serial No. 60/232,778, filed on September 15, 2000, and of U.S. application Serial No. 60/300,183, filed on June 22, 2001, the disclosures of which are
10 incorporated by reference herein.

Field of the Invention

The present invention generally relates to the field of plant molecular biology, and more specifically to the regulation of gene expression in plants in response to stress, e.g., to pathogen exposure.

15

Background of the Invention

Plants are capable of activating a large array of defense mechanisms in response to pathogen attack. A crucial factor determining the success of these mechanisms is the speed of their activation. Consequently, there is considerable
20 interest in understanding how plants recognize pathogen attack and control expression of defense mechanisms.

Some potential pathogens trigger a very rapid resistance response called gene-for-gene resistance. This occurs when the pathogen carries an avirulence (*avr*) gene that triggers specific recognition by a corresponding host resistance
25 (*R*) gene. *R* gene specificity is generally quite narrow, in most cases only pathogens carrying a particular *avr* gene are recognized. Recognition is thought to be mediated by ligand-receptor binding. *R* genes have been studied extensively in recent years. For a review of *R* genes, see Ellis et al. (1998); Jones et al. (1997); and Ronald (1998).

30 One of the defense mechanisms triggered by gene-for-gene resistance is programmed cell death at the infection site. This is called the hypersensitive response, or HR. Pathogens that induce the HR, or cause cell death by other means, activate a systemic resistance response called systemic acquired resistance (SAR). During SAR, levels of salicylic acid (SA) rise throughout the
35 plant, defense genes such as pathogenesis related (PR) genes are expressed, and the plant becomes more resistant to pathogen attack. SA is a crucial component

of this response. Plants that cannot accumulate SA due to the presence of a transgene that encodes an SA-degrading enzyme (*nahG*), develop a HR in response to challenge by avirulent pathogens, but do not exhibit systemic expression of defense genes and do not develop resistance to subsequent pathogen attack (Ryals et al., 1996). The nature of the systemic signal that triggers SAR is a subject of debate (Shulaev et al., 1995; Vernooji et al., 1994). SA clearly moves from the site of the HR to other parts of the plant, but if this is the signal, it must be effective at extremely low concentration (Willits et al., 1998).

SAR is quite similar to some reactions that occur locally in response to attack by virulent (those that cause disease) or avirulent (those that trigger gene-for-gene resistance) pathogens. In general, activation of defense gene expression occurs more slowly in response to virulent pathogens than in response to avirulent pathogens. Some pathogens trigger expression of defense genes through a different signaling pathway that requires components of the jasmonic acid (JA) and ethylene signaling pathways (Creelman et al., 1997).

One approach to understanding the signal transduction networks that control defense mechanisms is to use genetic methods to identify signaling components and determine their roles within the network. Considerable progress has been made using this approach in *Arabidopsis*-pathogen model systems.

R gene signal transduction

Genes such as *NDR1* and *EDS1*, as well as *DND1* and the lesion-mimic genes, likely act in signal transduction pathways downstream from *R-avr* recognition. *NDR1* and *EDS1* are required for gene-for-gene mediated resistance to avirulent strains of the bacterial pathogen *Pseudomonas syringae* and the oomycete pathogen *Peronospora parasitica*. Curiously, *ndr1* mutants are susceptible to one set of avirulent pathogens, whereas *eds1* mutants are susceptible to a non-overlapping set (Aarts et al., 1998). The five cloned *R* genes that require *EDS1* all belong to the subset of the nucleotide binding site-leucine rich repeat (NBS-LRR) class of *R* genes that contain sequences similar to the cytoplasmic domains of *Drosophila* Toll and mammalian interleukin 1 transmembrane receptors (TIR-NBS-LRR). The two genes that require *NDR1* belong to the leucine-zipper (LZ-NBS-LRR) subclass of NBS-LRR genes. There is another LZ-NBS-LRR gene, *RPP8*, that does not require *EDS1* or *NDR1*, so

the correlation between *R* gene structure and requirement for *EDS1* or *NDR1* is not perfect. Nevertheless, these results show that *R* genes differ in their requirements for downstream factors and that these differences are correlated with *R* gene structural type.

5 *NDR1* encodes a protein with two predicted transmembrane domains (Century et al. 1997). RPM1, which requires *NDR1* to mediate resistance, is membrane-associated, despite the fact that its primary sequence does not include any likely membrane-integral stretches (Boyes et al., 1998). It is possible that part of the function of *NDR1* is to hold *R* proteins close to the membrane. *EDS1*
10 encodes a protein with blocks of homology to triacyl glycerol lipases (Falk et al., 1999). The significance of this homology is not known, but it is tempting to speculate that *EDS1* is involved in synthesis or degradation of a signal molecule. *EDS1* expression is inducible by SA and pathogen infection, suggesting that *EDS1* may be involved in signal amplification (Falk et al., 1999).

15 It has been extremely difficult to isolate mutations in genes other than the *R* genes that are required for gene-for-gene resistance. A selection procedure was devised (McNellis et al., 1998) on the basis of precisely controlled inducible expression of the *avr* gene *avrRpt2* in plants carrying the corresponding resistance gene *RPS2*. Expression of *avrRpt2* in this background is lethal, as it
20 triggers a systemic HR. It is now possible to select for mutants with subtle defects in gene-for-gene signaling by requiring growth on a concentration of inducer slightly higher than the lethal dose.

Putative plant receptor proteins encoded by *RPP* genes (recognition of *P. parasitica*) mediate specific recognition of *Peronospora* isolates and trigger
25 defense reactions. Recently, McDowell et al. (2000) reported that two members of this class, *RPP7* and *RPP8* (the latter of which encodes a LZ-NBS-LRR type R protein) were not significantly suppressed by mutations in either *EDS1* or *NDR1*, and that *RPP7* resistance was also not compromised by mutations in *EIN2*, *JAR1* or *COI1*, which affect ethylene or jasmonic acid signaling, or in
30 *coil/npr1* or *coil/NahG* backgrounds. The authors suggested that *RPP7* initiates resistance through a novel signaling pathway that is independent of salicylic acid accumulation or jasmonic acid response components.

SA-dependent signaling

SA levels increase locally in response to pathogen attack, and systemically in response to the SAR-inducing signal. SA is necessary and sufficient for activation of *PR* gene expression and enhanced disease resistance.

5 Physiological analyses and characterization of certain lesion-mimic mutants strongly suggest that there is a positive autoregulatory loop affecting SA concentrations (Shirasu et al., 1997; Hunt et al., 1997; Weymann et al., 1995). Several mutants with defects in SA signaling have been characterized. These include *npr1*, in which expression of *PR* genes in response to SA is blocked;
10 *cpr1*, *cpr5*, and *cpr6*, which constitutively express *PR* genes; the *npr1* suppressor *ssil*; *pad4*, which has a defect in SA accumulation; and *eds5*, which has a defect in *PR1* expression.

Expression of the defense genes *PR1*, *BG2*, and *PR5* in response to SA treatment requires a gene called *NPR1* or *NIM1*. Mutations in *npr1* abolish
15 SAR, and cause enhanced susceptibility to infection by various pathogens (Cao et al., 1994; Delaney et al., 1995; Glazebrook et al., 1996; Shah et al., 1997). *NPR1* appears to be a positive regulator of *PR* gene expression that acts downstream from SA. *NPR1* encodes a novel protein that contains ankyrin repeats (which are often involved in protein-protein interactions (Cao et al.,
20 1997; Ryals et al., 1997), and that is localized to the nucleus in the presence of SA (Dong et al., 1998). Consequently, it is unlikely that *NPR1* acts as a transcription factor to directly control *PR* gene expression, but its nuclear localization suggests that it may interact with such transcription factors.

PAD4 appears to act upstream from SA. In *pad4* plants infected with a
25 virulent *P. syringae* strain, SA levels, synthesis of the antimicrobial compound camalexin, and *PR1* expression are all reduced (Zhou et al., 1998). SA is necessary, but not sufficient, for activation of camalexin synthesis (Zhou et al., 1998; Zhao et al., 1996). The camalexin defect in *pad4* plants is reversible by exogenous SA (Zhou et al., 1998). Mutations in *pad4* do not affect SA levels,
30 camalexin synthesis, or *PR1* when plants are infected with an avirulent *P. syringae* strain (Zhou et al., 1998). Taken together, these results suggest that *PAD4* is required for signal amplification to activate the SA pathway in response to pathogens that do not elicit a strong defense response (Zhou et al., 1998).

JA-dependent signaling

JA signaling affects diverse processes including fruit ripening, pollen development, root growth, and response to wounding (Creelman et al., 1997). The *jar1* and *coi1* mutants fail to respond to JA (Feys et al., 1994; Staswick et al., 1992). *COI1* has been cloned, and found to encode protein containing leucine-rich repeats and a degenerate F-box motif (Xie et al., 1998). These features are characteristic of proteins that function in complexes that ubiquitinate protein targeted for degradation.

In the past few years it has become apparent that JA plays an important role in regulation of pathogen defenses. For example, the induction of the defensin gene *PDF1.2* after inoculation of *Arabidopsis* with the avirulent pathogen *Alternaria brassicicola* does not require SA or NPR1, but does require ethylene and JA signaling (Penninck et al., 1996).

SA signaling and JA signaling pathways are interconnected in complicated ways. Studies in other systems have shown that SA signaling and JA signaling are mutually inhibitory (Creelman et al., 1997; Harms et al., 1998). However, synthesis of camalexin in response to *P. syringae* infection is blocked in *nahG* (Zhou et al., 1998; Zhao et al., 1996) and *coi1* (Glazebrook, 1999) plants, strongly suggesting that camalexin synthesis requires both SA and JA signaling.

Induced systemic resistance (ISR)

Some rhizosphere-associated bacteria promote disease resistance (van Loon et al., 1998). This phenomenon, called ISR, has been studied using *Pseudomonas fluorescens* strain WCS417r to colonize *Arabidopsis* roots (Pieterse et al., 1996). Colonized plants are more resistant to infection by the fungal pathogen *Fusarium oxysporum* f sp *raphani* and *P. syringae* (Pieterse et al., 1996). ISR occurs in *nahG* plants, indicating that it is not a SA-dependent phenomenon (Pieterse et al., 1996). Rather, ISR appears to be JA- and ethylene-dependent. The observation that ethylene can induce ISR in *jar1* mutants led to the hypothesis that ISR requires a JA signal followed by an ethylene signal (Pieterse et al., 1998). No changes in gene expression associated with ISR have been detected (Pieterse et al., 1998), suggesting that it is different from activation of *PDF1.2* expression by *A. brassicicola*.

Curiously, ISR requires *NPR1* (Pieterse et al., 1996). This was unexpected in light of the fact that *NPR1* was previously known to be involved only in SA-dependent processes and ISR is SA-independent. If the SA-dependent signal is received, *NPR1* mediates a resistance response characterized by *PR1* expression, whereas if the ISR signal is received, *NPR1* mediates a different resistance response. It is difficult to imagine how this could occur, unless *NPR1* is interacting with different 'adapter' molecules to mediate the different signals. The ankyrin repeats found in *NPR1* could function in protein-protein interactions between *NPR1* and adapter proteins. Identification of proteins that interact with *NPR1*, and characterization of plants with loss-of-function mutations affecting those proteins, would be very helpful for understanding how *NPR1* acts in each pathway. It would also be worthwhile to determine if the *ssi1* or *cpr6* mutations suppress the ISR defect of *npr1* mutants.

Relevance to disease resistance

Characterization of the effects of various mutations on resistance to different pathogens has revealed that there is considerable variation in the extent to which pathogens are affected by defense mechanisms. SAR is known to confer resistance to a wide array of pathogens, including bacteria, fungi, oomycetes, and viruses. JA signaling is important for limiting the growth of certain fungal pathogens. In *Arabidopsis*, the SA pathway mutants *npr1* and *pad4* show enhanced susceptibility to *P. syringae* and *P. parasitica* (Cao et al., 1994; Delaney et al., 1995; Shah et al., 1997; Zhou et al., 1998; Glazebrook et al., 1997).

Overexpression of rate-limiting defense response regulators may cause the signaling network to respond faster or more strongly to pathogen attack, thereby improving resistance. For example, overexpression of *NPR1* caused increased resistance to *P. syringae* and *P. parasitica* in a dosage dependent manner (Cao et al., 1998). Moreover, *NPR1*-overexpression had no obvious deleterious effects on plant growth, in contrast to mutations that lead to constitutive overexpression of defense responses, which generally cause dwarfism.

Thus, what is needed is the systematic identification of genes useful to confer resistance to pathogens.

Summary of the Invention

The invention provides an isolated nucleic acid molecule (polynucleotide), e.g., DNA, comprising a plant or fungal nucleotide sequence, the expression of which is altered in response to stress, e.g., pathogen infection.

5 For example, the invention provides a nucleic acid molecule comprising a plant or fungal nucleotide sequence comprising at least a portion of a key effector gene(s) responsible for host resistance to particular pathogens. To provide resistance or tolerance to a pathogen in a plant, this sequence may be overexpressed individually, in the sense or antisense orientation, or in

10 combination with other sequences, to confer improved disease resistance or tolerance to a plant relative to a plant that does not comprise and/or express the sequence. The overexpression may be constitutive, or it may be preferable to express the effector gene(s) from an inducible promoter including a promoter which is responsive to external stimuli, such as chemical application, or to

15 pathogen infection, e.g., so as to avoid possible deleterious effects on plant growth. In one embodiment of the invention, the promoter employed to express the nucleotide sequence of the invention may be one that mediates rapid and transient transcription after pathogen infection. Thus, the invention also provides an isolated nucleic acid molecule comprising a plant nucleotide

20 sequence which alters, e.g., increases or decreases, the transcription of plant genes, e.g., open reading frames, in response to stress, e.g., pathogen infection.

As described herein, *Arabidopsis* plants of differing genotypes were infected with different strains of an oomycete, *P. parasitica*. RNA was isolated from each plant/pathogen pair and employed to prepare probes which were hybridized to a gene

25 chip having nucleic acid sequences (probe sets) corresponding to approximately 8,200 *Arabidopsis* genes. Genes were then identified that were upregulated or downregulated in response to infection, including genes that were dependent on *RPP7* or *RPP8*, which act via unconventional signaling cascades and are not dependent on defense regulators such as EDS1, NDR1, PAD4, NPR1, RAR1, PBS3 or salicylic acid (SA). Among the

30 genes showing strong *Peronospora*-induced expression changes, clusters of genes were identified that were specifically upregulated by *RPP7* or *RPP8*, or both. In particular in one analysis, the expression of 184 genes (SEQ ID NOs:1-211 and 792) related to 217 probe sets was upregulated by either *RPP7* or *RPP8*, or both, while in another analysis the expression of genes related to 194 probe sets (SEQ ID NOs:212-399 and 793) was

upregulated by either *RPP7* or *RPP8*, or both. Further, as described below, promoters of genes that were rapidly and transiently transcribed after *P. parasitica* infection and were *RPP7/8*-dependent were significantly enriched with both novel sequence motifs and potential binding sites of known transcription factors. Specifically, the promoters were significantly enriched with two novel sequence motifs (referred to as "motif 1" and "motif 2"), one of which was similar to binding sites for Myb transcription factors, sequence motifs related to WRKY binding sites, and two other novel sequence motifs ("motif 3" and "motif 4"). Moreover, comparisons between expression signatures of wild type plants as well as the *RPP7* loss of function mutants, and *edm1*, *edm2* and *edm3* mutants, allow for predictions regarding the *RPP7* pathway hierarchy.

In addition, more than 200 genes (SEQ ID NOs:75, 214, 228, 301, 339, 400-684, 792-795) were identified that were specifically controlled by the *RPP4*-dependent pathway, which mediates resistance of the *Arabidopsis* ecotype Col-0 to the *Peronospora* isolate Emoy2. According to their response to SA, an important mediator of local and systemic defense responses, and the protein biosynthesis inhibitor cycloheximide (CHX), these genes were further subcategorized into immediate early and secondary response genes. A set of immediate early SA responsive genes (SEQ ID NOs:150, 159, 117, 126, 208, 428, 426, 436, 430, 434, 478, 641, 609, 615, and 526) was found to consist exclusively of regulatory genes. Such genes are likely controlled by transcription factors acting closely downstream of SA. One highly conserved motif in the promoters of these immediate early genes was similar to binding sites of WRKY transcription factors (SEQ ID NOs:757-765). Other conserved promoter motifs appeared to be novel and may facilitate the cloning of their cognate transcription factors. A cluster of SA/CHX super-induced genes was found to show elevated expression ground states in the *npr1* mutant (SEQ ID NOs:214, 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447 and 551) suggesting an NPR1-dependent de-repression mechanism in the control of some SA responsive immediate early genes.

Thus, the invention provides an isolated nucleic acid molecule comprising a plant or fungal nucleotide sequence encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising an open reading frame, the expression of which is altered in response to a pathogen that induces a response mediated by *R* genes, including pathogens such as bacteria, fungi, oomycetes, viruses, nematodes and insects, e.g., aphids (see Hammond-Kosack and Jones (1997), which is specifically incorporated by

reference herein). For example, the plant or fungal nucleotide sequence encodes a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising an open reading frame, the expression of which is altered in response to infection by an oomycete such as *Peronospora*, and is *RPP4*-,
5 *RPP7*-, and/or *RPP8*-dependent. These sequences can be identified by employing an array of nucleic acid samples, e.g., a plurality of oligonucleotides, each plurality corresponding to a different plant gene, on a solid substrate, e.g., a DNA chip, and probes corresponding to nucleic acid from pathogen-infected (e.g., wild-type) plant cells and to nucleic acid from uninfected plant cells or
10 plant cells having a mutation which alters the response to pathogen infection. Thus, genes, the expression of which are altered by pathogen infection, can be systematically identified. Preferably, the nucleotide sequence is from plant DNA, either a dicot or a monocot, which encodes a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by an open reading
15 frame comprising any one of SEQ ID NOs:1-684 and 792-795, or the complement thereof. More preferably, the nucleotide sequence is from plant DNA that is substantially similar to an *Arabidopsis* nucleic acid segment having any one of SEQ ID NOs: 1-684 and 792-795, or the complement thereof. The term "substantially similar", when used herein with respect to a polypeptide
20 means a polypeptide corresponding to a reference polypeptide, wherein the polypeptide has substantially the same structure and function as the reference polypeptide, e.g., where only changes in amino acid sequence are those which do not affect the polypeptide function. When used for a polypeptide or an amino acid sequence, the percentage of identity between the substantially similar and
25 the reference polypeptide or amino acid sequence is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, up to at least 99%, where the reference polypeptide is an *Arabidopsis* polypeptide encoded by an open reading
30 frame comprising any one of SEQ ID NOs:1-684 and 792-795, or the complement thereof. However, the percent of identity between the substantially similar and the reference polypeptide may be less than 65% as long as the two polypeptides have the same or similar function, e.g., catalyze the same or similar reaction. Another indication that two polypeptides are substantially similar to

each other is that an agent, e.g., an antibody, which specifically binds to one of the polypeptides, specifically binds to the other.

In its broadest sense, the term "substantially similar", when used herein with respect to a nucleotide sequence, means a nucleotide sequence

5 corresponding to a reference nucleotide sequence, wherein the corresponding sequence is from a gene that encodes a polypeptide having substantially the same structure and function as the polypeptide encoded by a gene comprising the reference nucleotide sequence. The term "substantially similar" is specifically intended to include nucleotide sequences wherein the sequence has been

10 modified to optimize expression in particular cells. The percentage of identity between the substantially similar nucleotide sequence and the reference nucleotide sequence is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%,

15 96%, 97%, 98%, up to at least 99%, wherein the reference sequence is preferably any one of SEQ ID NOs: 1-684 and 792-795, or the complement thereof. Sequence comparisons may be carried out using a Smith-Waterman sequence alignment algorithm (see e.g., Waterman (1995) or [http://www](http://www.hto.usc.edu/software/seqaln/index.html)

20 [hto.usc.edu/software/seqaln/index.html](http://www.hto.usc.edu/software/seqaln/index.html)). The localS program, version 1.16, is preferably used with following parameters: match: 1, mismatch penalty: 0.33, open-gap penalty: 2, extended-gap penalty: 2. Further, a nucleotide sequence that is "substantially similar" to a reference nucleotide sequence hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C,

25 more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC,

30 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

Hence, the isolated nucleic acid molecules of the invention also include the orthologs of the *Arabidopsis* sequences disclosed herein, i.e., the corresponding nucleic acid molecules in organisms other than *Arabidopsis*,

including, but not limited to, plants other than *Arabidopsis*, preferably cereal plants, e.g., corn, wheat or rice, as well as rye, turfgrass, sorghum, millet, sugarcane, soybean, barley, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugarbeet, and in fungi. An ortholog is a gene from a different species that
5 encodes a product having the same function as the product encoded by a gene from a reference organism. The encoded ortholog products likely have at least 70% amino acid sequence identity to each other. Hence, the invention includes an isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide having at least 70% identity to a polypeptide encoded by one or
10 more of the *Arabidopsis* sequences, although it is also envisioned that orthologous genes to those disclosed herein may encode a polypeptide with less than 70%, e.g., less than 65% amino acid sequence identity, but which polypeptide has the same or similar function. Databases such GenBank or one found at <http://bioserver.myongji.ac.kr/rjce.html> (for rice) may be employed to
15 identify sequences related to the *Arabidopsis* sequences, e.g., orthologs in cereal crops such as rice. Alternatively, recombinant DNA techniques such as hybridization or PCR may be employed to identify sequences related to the *Arabidopsis* sequences.

Thus, the invention preferably includes an isolated nucleic acid molecule
20 comprising a plant or fungal nucleotide sequence that encodes a polypeptide that has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and at least 99%, amino acid sequence identity to an *Arabidopsis* polypeptide encoded by an open reading
25 frame comprising any one of SEQ ID NOs: 1-684 and 792-795, or a fragment (portion) thereof which encodes a polypeptide having substantially the same activity as a polypeptide encoded by an open reading frame comprising a corresponding sequence listed in SEQ ID NOs: 1-684 and 792-795. In one embodiment, the isolated nucleic acid molecule is not SEQ ID NOs: 1-684 and
30 792-795. The invention also provides anti-sense nucleic acid molecules corresponding to the open reading frames or genes identified as responsive to pathogen infection. Also provided are expression cassettes, e.g., recombinant vectors, and host cells, comprising the nucleic acid molecule of the invention in either sense or antisense orientation.

Also provided is an isolated nucleic acid molecule comprising a plant or fungal nucleotide sequence comprising a nucleic acid sequence having at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and at least 99%, nucleic acid sequence similarity to an *Arabidopsis* open reading frame comprising any one of SEQ ID NOs: 1-684 and 792-795, the complement thereof, or a fragment (portion) thereof which encodes a polypeptide having substantially the same activity as a polypeptide encoded by an open reading frame comprising a corresponding sequence listed in SEQ ID NOs: 1-684 and 792-795.

The nucleic acid molecules of the invention, their encoded polypeptides and compositions thereof, are useful to provide resistance to pathogens and as a diagnostic for the presence or absence of the pathogen by correlating the expression level or pattern of expression of one or more of the nucleic acid molecules of the invention or one or more of the polypeptides encoded thereby. As one embodiment of the invention includes isolated nucleic acid molecules that have increased expression in response to pathogen infection, the invention further provides compositions and methods for enhancing resistance to pathogen infection. The compositions of the invention include plant or fungal nucleotide sequences and the amino acid sequences for the polypeptides or partial-length polypeptides encoded thereby which are useful to provide tolerance or resistance to a plant to a pathogen, preferably by preventing or inhibiting pathogen infection. The resistance or tolerance may be accomplished by decreasing or eliminating expression of a plant gene necessary for pathogen infection and/or replication or by overexpressing a gene product that inhibits pathogen infection and/or replication. Methods of the invention involve stably transforming a plant with one or more of at least a portion of these nucleotide sequences which confer tolerance or resistance operably linked to a promoter capable of driving expression of that nucleotide sequence in a plant cell. By "portion" or "fragment", as it relates to a nucleic acid molecule, sequence or segment of the invention, when it is linked to other sequences for expression, is meant a sequence having at least 80 nucleotides, more preferably at least 150 nucleotides, and still more preferably at least 400 nucleotides. If not employed for expressing, a "portion" or "fragment" means at least 9, preferably 12, more

preferably 15, even more preferably at least 20, consecutive nucleotides, e.g., probes and primers (oligonucleotides), corresponding to the nucleotide sequence of the nucleic acid molecules of the invention. By "resistant" is meant a plant which exhibits substantially no phenotypic changes as a consequence of infection with the pathogen. By "tolerant" is meant a plant which, although it may exhibit some phenotypic changes as a consequence of infection, does not have a substantially decreased reproductive capacity or substantially altered metabolism. Thus, some of the isolated nucleic acid molecules of the invention are useful in a method of combating a pathogen in an agricultural crop. The method comprises introducing to a plant, plant cell, or plant tissue an expression cassette comprising a nucleic acid molecule of the invention so as to yield a transformed differentiated plant, transformed cell or transformed tissue. Transformed cells or tissue can be regenerated to provide a transformed differentiated plant. The transformed differentiated plant preferably expresses the nucleic acid molecule in an amount that confers resistance to the transformed plant to pathogen infection relative to a corresponding nontransformed plant. The present invention also provides a transformed plant prepared by the method, progeny and seed thereof.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields under conditions of pathogen infection and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and probes.

The invention also includes recombinant nucleic acid molecules which have been modified so as to comprise codons other than those present in the unmodified sequence. The recombinant nucleic acid molecules of the invention include those in which the modified codons specify amino acids that are the same as those specified by the codons in the unmodified sequence, as well as those that specify different amino acids, i.e., they encode a variant polypeptide having one or more amino acid substitutions relative to the polypeptide encoded by the unmodified sequence.

The invention further includes a nucleotide sequence which is complementary to one (hereinafter "test" sequence) which hybridizes under stringent conditions with the nucleic acid molecules of the invention as well as RNA which is encoded by the nucleic acid molecule. When the hybridization is performed under stringent conditions, either the test or nucleic acid molecule of invention is preferably supported, e.g., on a membrane or DNA chip. Thus, either a denatured test or nucleic acid molecule of the invention is preferably first bound to a support and hybridization is effected for a specified period of time at a temperature of, e.g., between 55 and 70°C, in double strength citrate buffered saline (SC) containing 0.1% SDS followed by rinsing of the support at the same temperature but with a buffer having a reduced SC concentration. Depending upon the degree of stringency required such reduced concentration buffers are typically single strength SC containing 0.1% SDS, half strength SC containing 0.1% SDS and one-tenth strength SC containing 0.1% SDS.

The present invention also provides a method to identify a gene, the expression of which is altered in response to an external stimulus, e.g., pathogen infection. The method comprises contacting a plurality of samples comprising portions or fragments of isolated nucleic acid molecules with a probe which corresponds to a population of a nucleic acid sequences, the expression of which is altered in response to an external stimulus, so as to form a binary complex. Each sample corresponds to a different gene. Then complex formation is detected or determined. The method may be employed with nucleic acid samples and probes from any organism, e.g., any prokaryotic or eukaryotic organism. Preferably, the nucleic acid sample and probes are from a plant, such as a dicot or monocot. For example, the method comprises contacting a solid substrate comprising a plurality of samples comprising portions or fragments of isolated plant nucleic acid with a probe comprising plant nucleic acid corresponding to at least a portion of RNA from a pathogen infected plant so as to form a complex. Preferred pathogens are those which induce an *R*-gene dependent resistance response. Each individual sample comprises one or more nucleic acid sequences corresponding to a plant gene, e.g., a pool of oligonucleotides corresponding to the same gene or a portion of that gene. The plurality of samples is provided on a DNA chip. A second plurality of samples on a solid substrate, i.e., a DNA chip, each comprising a plurality of samples comprising portions or fragments of

isolated plant nucleic acid is contacted with a probe comprising plant nucleic acid corresponding to at least a portion of RNA from an uninfected or mutant plant or plant cells so as to form a complex. Then complex formation with nucleic acid from infected cells and from uninfected or mutant cells is compared.

5 The invention also provides a method for identifying a plant cell infected with a pathogen, e.g., one that induces a *RPP4*-, *RPP7*- and/or *RPP8*-dependent resistance response. The method comprises contacting nucleic acid obtained from a plant cell suspected of being infected with the pathogen with at least one, preferably at least two, oligonucleotides under conditions effective to amplify at
10 least a portion of a nucleotide sequence in the isolated plant nucleic acid which is substantially similar to at least one of SEQ ID NOs: 1-684 and 792-795, so as to yield an amplified product. Then the presence of the amplified product is detected or determined. The presence of the amplified product, e.g., in an amount that is different than the amount of the corresponding amplified product
15 from an uninfected or mutant plant, corresponding to one or more of SEQ ID NOs: 1-684 and 792-795 or an ortholog thereof, is indicative of pathogen infection.

 The invention provides an additional method for identifying a plant cell infected with a pathogen. The method comprises hybridizing a probe selected
20 from SEQ ID NOs: 1-684 and 792-795 to nucleic acid obtained from a plant cell suspected of being infected with a pathogen. The amount of the probe hybridized to nucleic acid obtained from a cell suspected of being infected with a pathogen is compared to hybridization of the probe to nucleic acid isolated from an uninfected or mutant cell. A change in the amount of the hybridized probe in
25 nucleic acid isolated from a cell suspected of being infected by a pathogen relative to the amount of hybridized probe in nucleic acid isolated from an uninfected or mutant cell is indicative of infection.

 Also provided is an isolated nucleic acid molecule comprising a nucleotide sequence that directs transcription, e.g., a promoter, of a linked
30 nucleic acid segment in a host cell, such as a plant cell, wherein transcription is altered, e.g., increased, in response to a pathogen infection. Preferably, the pathogen is *R*-dependent, and more preferably, one that triggers a response that is dependent on *RPP4*, *RPP7* and/or *RPP8*, such as an oomycete (for example, *Peronospora*). It is preferred that the nucleotide sequence is from plant genomic

DNA which has at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, nucleotide sequence identity to a sequence of a promoter from an
5 *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-684 and 792-795, e.g., SEQ ID NOs:774-788, or comprising motifs such as one of SEQ ID NOs:685-773. Thus, the invention also includes orthologs of *Arabidopsis* promoters. Preferably, the nucleotide sequence includes the promoter region from a gene corresponding to SEQ ID NOs: 1-770 and 792-795, which region preferably
10 includes at least one copy of at least one of the following, e.g., a nucleic acid sequence comprising one of SEQ ID NOs:685-697 ("motif 1"), SEQ ID NOs:698-709 ("motif 2"), GGT/CCCA ("motif 3"), GNCCAAA ("motif 4"), or SEQ ID NOs:710-713, 714-756, or 757-773. The promoter sequence is preferably about 25 to 2000, e.g., 50 to 500 or 100 to 1400, nucleotides in length.

15 In one embodiment of the invention, the isolated nucleic acid molecule comprises a plant nucleotide sequence which is the promoter region for any one of SEQ ID NOs: 1-684 and 792-795, or is structurally related to the promoter for SEQ ID NOs: 1-684 and 792-795, i.e., is an orthologous promoter, and is linked to a plant structural gene or open reading frame. Hence, the present invention
20 further provides an expression cassette or a recombinant vector containing the nucleic acid molecule, and the vector may be a plasmid. Such cassettes or vectors, when present in a plant, plant cell or plant tissue result in transcription of the linked nucleic acid segment in the plant, plant tissue or plant cell. Transcription of the linked segment is altered in response to pathogen infection,
25 including *Peronospora* infection. For promoters with motif 1, transcription of linked segments may be altered in response to agents or other stimuli that induce Myb-like transcription factors.

Generally, the promoters of the invention may be employed to express a nucleic acid segment that is operably linked to the promoter, for example, an
30 open reading frame or a portion thereof, an anti-sense construct or a transgene. The open reading frame may be obtained from an insect resistance gene, a bacterial disease resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a nematode disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a

mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a positive selectable marker, a gene affecting plant agronomic characteristics, i.e., yield, standability and the like, or an environment or stress resistance gene, i.e., one or more genes
5 that confer herbicide resistance or tolerance, insect resistance or tolerance, disease resistance or tolerance (viral, bacterial, fungal, oomycete, or nematode), stress tolerance or resistance (as exemplified by resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, salt stress, or oxidative stress), increased yields, food content and makeup, physical appearance, male
10 sterility, drydown, standability, prolificacy, starch properties or quantity, oil quantity and quality, amino acid or protein composition, and the like.

Preferably, the promoters of the invention include a consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743,
15 250 to about 743, 400 to about 743, 600 to about 743, of the promoter sequences from genes comprising any one of SEQ ID NOs:685-788, 714-756, and 757-773, or the promoter orthologs thereof, which include the minimal promoter region.

In a particular embodiment of the invention said consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743,
20 250 to about 743, 400 to about 743, 600 to about 743, has at least 75%, preferably 80%, more preferably 90% and most preferably 95% sequence identity with a corresponding consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40
25 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, of any one of SEQ ID NOs:685-788, 714-756, and 757-773, or the promoter orthologs thereof, which include the minimal promoter region.

The expression cassettes or vectors of the invention may optionally
30 include other regulatory sequences, e.g., transcription terminator sequences, introns and/or enhancers, and may be contained in a host cell. The expression cassette or vector may augment the genome of a transformed plant or may be maintained extrachromosomally. The expression cassette or vector may further have a Ti plasmid and be contained in an *Agrobacterium tumefaciens* cell; it may

be carried on a microparticle, wherein the microparticle is suitable for ballistic transformation of a plant cell; or it may be contained in a plant cell protoplast. Further, the expression cassette can be contained in a plant, plant cell or plant tissue from a dicot or a monocot. In particular, the plant may be a cereal plant.

5 The present invention further provides a method of augmenting a plant genome by contacting plant cells with an expression cassette or vector of the invention, i.e., one having a nucleotide sequence that directs transcription of a linked nucleic acid segment in a plant cell, wherein transcription of the linked segment is altered in response to a pathogen such as an oomycete, e.g.,
10 *Peronospora*, infection, and wherein the nucleic sequence is from plant DNA that has at least 65%, and more preferably at least 70%, identity to the sequence of a promoter from an *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-684 and 792-795, so as to yield transformed plant cells; and regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the
15 differentiated transformed plant expresses the linked fragment in the cells of the plant in response to infection. The present invention also provides a plant prepared by the method, progeny and seed thereof.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in
20 which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and
25 probes.

The invention also provides a method of plant breeding, e.g., to prepare a crossed fertile transgenic plant. The method comprises crossing a fertile transgenic plant comprising a particular nucleic acid molecule of the invention with itself or with a second plant, e.g., one lacking the particular nucleic acid
30 molecule, to prepare the seed of a crossed fertile transgenic plant comprising the particular nucleic acid molecule. The seed is then planted to obtain a crossed fertile transgenic plant. The plant may be a monocot or a dicot. In a particular embodiment, the plant is a cereal plant.

The crossed fertile transgenic plant may have the particular nucleic acid molecule inherited through a female parent or through a male parent. The second plant may be an inbred plant. The crossed fertile transgenic may be a hybrid. Also included within the present invention are seeds of any of these
5 crossed fertile transgenic plants.

The present invention also provides a method to identify a nucleotide sequence that directs transcription of nucleic acid in the genome of a plant cell in response to pathogen exposure, by contacting a probe comprising plant nucleic acid, e.g., cRNA, isolated from tissues of a plant contacted with the pathogen
10 with a plurality of isolated nucleic acid samples on a plurality of solid substrates, wherein each sample is a plurality of oligonucleotides corresponding to at least a portion of a plant gene, so as to form a complex between at least a portion of the probe and a nucleic acid sample(s) having sequences that are structurally related to the sequences in the probe. Then complex formation is determined or
15 detected to determine which samples represent genes comprising promoters that are responsive to infection with the pathogen. The probe and/or samples may be nucleic acid from a dicot or from a monocot.

A method to shuffle the nucleic acid molecules of the invention is provided. This method involves fragmentation of a (parent) nucleic acid
20 molecule corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-684 and 792-795, the ortholog thereof, or the corresponding gene thereof, followed by religation. This method allows for the production of polypeptides having altered activity relative to the polypeptide encoded by the parent nucleic acid molecule. Accordingly, the invention provides cells and transgenic plants
25 containing nucleotide sequences produced through shuffling that encode polypeptides having altered activity relative to the polypeptide encoded by the parent nucleic acid molecule.

A computer readable medium containing the nucleic acid sequences of the invention as well as methods of use for the computer readable medium are
30 provided. This medium allows a nucleic acid molecule corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-399, 685-756 and 774-793 or 71, 78, 80, 117, 126, 150, 159, 168, 208, 214, 264-265, 355, 400-657, 659-684, 792-795 to be used as a reference sequence to search against databases. This medium also allows for computer-based manipulation of a nucleic acid sequence

corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-399, 685-756 and 774-793 or 71, 78, 80, 117, 126, 150, 159, 168, 208, 214, 264-265, 355, 400-657, 659-684, 792-795, and the corresponding gene or polypeptide encoded by the nucleic acid sequence.

5

Brief Description of the Figures

Figure 1 depicts *RPP*-dependent defense pathways.

Figure 2 depicts nucleotide sequences including the promoter region and motifs therein for genes, the expression of which is altered in response to pathogen infection (SEQ ID NOs: 774-788).

10

Figure 3 is a schematic of the overlap in genes that are induced early after *P. parasitica* infection and in a *RPP8*-specific manner, genes that are induced late after infection and in a *RPP8*-specific manner, and genes induced early and late after infection in a *RPP7*-specific manner.

15

Figure 4 shows a schematic of *RPP4*-pathway, *RPP7*-pathway and *RPP8*-upregulated transcription factor genes.

Detailed Description of the Invention

Definitions

20

The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, composed of monomers (nucleotides) containing a sugar, phosphate and a base which is either a purine or pyrimidine. Unless specifically limited, the term encompasses nucleic acids containing known analogs of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences as well as the sequence explicitly indicated.

25

30

Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzner et al., 1991; Ohtsuka et al., 1985; Rossolini et al., 1994). A "nucleic acid fragment" is a fraction of a given nucleic acid molecule. In higher plants, deoxyribonucleic

acid (DNA) is the genetic material while ribonucleic acid (RNA) is involved in the transfer of information contained within DNA into proteins. The term "nucleotide sequence" refers to a polymer of DNA or RNA which can be single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases capable of incorporation into DNA or RNA polymers. The terms "nucleic acid", "nucleic acid molecule", "nucleic acid fragment" or "nucleic acid sequence or segment" may also be used interchangeably with gene, cDNA, DNA and RNA encoded by a gene.

The invention encompasses isolated or substantially purified nucleic acid or protein compositions. In the context of the present invention, an "isolated" or "purified" DNA molecule or an "isolated" or "purified" polypeptide is a DNA molecule or polypeptide that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or polypeptide may exist in a purified form or may exist in a non-native environment such as, for example, a transgenic host cell. For example, an "isolated" or "purified" nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. In one embodiment, an "isolated" nucleic acid is free of sequences that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A protein that is substantially free of cellular material includes preparations of protein or polypeptide having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating protein. When the protein of the invention, or biologically active portion thereof, is recombinantly produced, preferably culture medium represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-protein-of-interest chemicals. Fragments and variants of the disclosed nucleotide sequences and proteins or partial-length proteins encoded thereby are also encompassed by the present invention. By "fragment" or "portion" is meant a full length or less than

full length of the nucleotide sequence encoding, or the amino acid sequence of, a polypeptide or protein. Alternatively, fragments or portions of a nucleotide sequence that are useful as hybridization probes generally do not encode fragment proteins retaining biological activity. Thus, fragments or portions of a
5 nucleotide sequence may range from at least about 9 nucleotides, about 12 nucleotides, about 20 nucleotides, about 50 nucleotides, about 100 nucleotides or more.

The term "gene" is used broadly to refer to any segment of nucleic acid associated with a biological function. Thus, genes include coding sequences
10 and/or the regulatory sequences required for their expression. For example, gene refers to a nucleic acid fragment that expresses mRNA, functional RNA, or specific protein, including regulatory sequences. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety of sources, including
15 cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

"Naturally occurring" is used to describe an object that can be found in nature as distinct from being artificially produced by man. For example, a
20 protein or nucleotide sequence present in an organism (including a virus), which can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory, is naturally occurring.

A "marker gene" encodes a selectable or screenable trait.

"Selectable marker" is a gene whose expression in a cell gives the cell a
25 selective advantage. The selective advantage possessed by the cells transformed with the selectable marker gene may be due to their ability to grow in the presence of a negative selective agent, such as an antibiotic or a herbicide, compared to the growth of non-transformed cells. The selective advantage possessed by the transformed cells, compared to non-transformed cells, may also
30 be due to their enhanced or novel capacity to utilize an added compound as a nutrient, growth factor or energy source. Selectable marker gene also refers to a gene or a combination of genes whose expression in a cell gives the cell both a negative and/or a positive selective advantage.

The term "chimeric" refers to any gene or DNA that contains 1) DNA

sequences, including regulatory and coding sequences, that are not found together in nature, or 2) sequences encoding parts of proteins not naturally adjoined, or 3) parts of promoters that are not naturally adjoined. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are
5 derived from different sources, or comprise regulatory sequences and coding sequences derived from the same source, but arranged in a manner different from that found in nature.

A "transgene" refers to a gene that has been introduced into the genome by transformation and is stably maintained. Transgenes may include, for
10 example, DNA that is either heterologous or homologous to the DNA of a particular plant to be transformed. Additionally, transgenes may comprise native genes inserted into a non-native organism, or chimeric genes. The term "endogenous gene" refers to a native gene in its natural location in the genome of an organism. A "foreign" gene refers to a gene not normally found in the host
15 organism but that is introduced by gene transfer.

The terms "protein," "peptide" and "polypeptide" are used interchangeably herein.

By "variants" is intended substantially similar sequences. For nucleotide sequences, variants include those sequences that, because of the degeneracy of
20 the genetic code, encode the identical amino acid sequence of the native protein. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those
25 generated, for example, by using site-directed mutagenesis which encode the native protein, as well as those that encode a polypeptide having amino acid substitutions. Generally, nucleotide sequence variants of the invention will have at least 40, 50, 60, to 70%, e.g., preferably 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, to 79%, generally at least 80%, e.g., 81%-84%, at least 85%, e.g.,
30 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, to 98%, sequence identity to the native (endogenous) nucleotide sequence.

"DNA shuffling" is a method to introduce mutations or rearrangements, preferably randomly, in a DNA molecule or to generate exchanges of DNA sequences between two or more DNA molecules, preferably randomly. The

DNA molecule resulting from DNA shuffling is a shuffled DNA molecule that is a non-naturally occurring DNA molecule derived from at least one template DNA molecule. The shuffled DNA preferably encodes a variant polypeptide modified with respect to the polypeptide encoded by the template DNA, and may
5 have an altered biological activity with respect to the polypeptide encoded by the template DNA.

The nucleic acid molecules of the invention can be optimized for enhanced expression in plants of interest. See, for example, EPA035472; WO91/16432; Perlak et al., 1991; and Murray et al., 1989. In this manner, the
10 genes or gene fragments can be synthesized utilizing plant-preferred codons. See, for example, Campbell and Gowri, 1990 for a discussion of host-preferred codon usage. Thus, the nucleotide sequences can be optimized for expression in any plant. It is recognized that all or any part of the gene sequence may be optimized or synthetic. That is, synthetic or partially optimized sequences may
15 also be used. Variant nucleotide sequences and proteins also encompass sequences and protein derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different coding sequences can be manipulated to create a new polypeptide possessing the desired properties. In this manner, libraries of recombinant polynucleotides are
20 generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer, 1994; Stemmer, 1994; Cramer et al., 1997; Moore et al., 1997; Zhang et al., 1997; Cramer et al., 1998; and
25 U.S. Patent Nos. 5,605,793 and 5,837,458.

"Conservatively modified variations" of a particular nucleic acid sequence refers to those nucleic acid sequences that encode identical or essentially identical amino acid sequences, or where the nucleic acid sequence does not encode an amino acid sequence, to essentially identical sequences.
30 Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given polypeptide. For instance the codons CGT, CGC, CGA, CGG, AGA, and AGG all encode the amino acid arginine. Thus, at every position where an arginine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the

encoded protein. Such nucleic acid variations are "silent variations" which are one species of "conservatively modified variations." Every nucleic acid sequence described herein which encodes a polypeptide also describes every possible silent variation, except where otherwise noted. One of skill will
5 recognize that each codon in a nucleic acid (except ATG, which is ordinarily the only codon for methionine) can be modified to yield a functionally identical molecule by standard techniques. Accordingly, each "silent variation" of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

"Recombinant DNA molecule" is a combination of DNA sequences that
10 are joined together using recombinant DNA technology and procedures used to join together DNA sequences as described, for example, in Sambrook et al., Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press (1989).

The terms "heterologous DNA sequence," "exogenous DNA segment" or "heterologous nucleic acid," each refer to a sequence that originates from a
15 source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the
20 terms refer to a DNA segment that is foreign or heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides.

A "homologous" DNA sequence is a DNA sequence that is naturally
25 associated with a host cell into which it is introduced.

"Wild-type" refers to the normal gene, or organism found in nature without any known mutation.

"Genome" refers to the complete genetic material of an organism.

"Vector" is defined to include, inter alia, any plasmid, cosmid, phage or
30 *Agrobacterium* binary vector in double or single stranded linear or circular form which may or may not be self transmissible or mobilizable, and which can transform prokaryotic or eukaryotic host either by integration into the cellular genome or exist extrachromosomally (e.g. autonomous replicating plasmid with an origin of replication).

Specifically included are shuttle vectors by which is meant a DNA vehicle capable, naturally or by design, of replication in two different host organisms, which may be selected from actinomycetes and related species, bacteria and eukaryotic (e.g. higher plant, mammalian, yeast or fungal cells).

5 "Cloning vectors" typically contain one or a small number of restriction endonuclease recognition sites at which foreign DNA sequences can be inserted in a determinable fashion without loss of essential biological function of the vector, as well as a marker gene that is suitable for use in the identification and selection of cells transformed with the cloning vector. Marker genes typically
10 include genes that provide tetracycline resistance, hygromycin resistance or ampicillin resistance.

"Expression cassette" as used herein means a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operably linked to the nucleotide sequence of
15 interest which is operably linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the
20 nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. The expression of the nucleotide sequence in the expression cassette may be under
25 the control of a constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, the promoter can also be specific to a particular tissue or organ or stage of development.

Such expression cassettes will comprise the transcriptional initiation
30 region of the invention linked to a nucleotide sequence of interest. Such an expression cassette is provided with a plurality of restriction sites for insertion of the gene of interest to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes.

The transcriptional cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of interest, and a transcriptional and translational termination region functional in plants. The termination region may be native with the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also, Guerineau et al., 1991; Proudfoot, 1991; Sanfacon et al., 1991; Mogen et al., 1990; Munroe et al., 1990; Ballas et al., 1989; Joshi et al., 1987.

An oligonucleotide corresponding to a nucleic acid molecule of the invention may be about 30 or fewer nucleotides in length (e.g., 9, 12, 15, 18, 20, 21 or 24, or any number between 9 and 30). Generally specific primers are upwards of 14 nucleotides in length. For optimum specificity and cost effectiveness, primers of 16-24 nucleotides in length may be preferred. Those skilled in the art are well versed in the design of primers for use processes such as PCR. If required, probing can be done with entire restriction fragments of the gene disclosed herein which may be 100's or even 1000's of nucleotides in length.

"Coding sequence" refers to a DNA or RNA sequence that codes for a specific amino acid sequence and excludes the non-coding sequences. It may constitute an "uninterrupted coding sequence", i.e., lacking an intron, such as in a cDNA or it may include one or more introns bounded by appropriate splice junctions. An "intron" is a sequence of RNA which is contained in the primary transcript but which is removed through cleavage and re-ligation of the RNA within the cell to create the mature mRNA that can be translated into a protein.

The terms "open reading frame" and "ORF" refer to the amino acid sequence encoded between translation initiation and termination codons of a coding sequence. The terms "initiation codon" and "termination codon" refer to a unit of three adjacent nucleotides ('codon') in a coding sequence that specifies initiation and chain termination, respectively, of protein synthesis (mRNA translation).

A "functional RNA" refers to an antisense RNA, ribozyme, or other RNA that is not translated.

The term "RNA transcript" refers to the product resulting from RNA polymerase catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from posttranscriptional processing of the primary transcript and is referred to as the mature RNA. "Messenger RNA" (mRNA) refers to the RNA that is without introns and that can be translated into protein by the cell. "cDNA" refers to a single- or a double-stranded DNA that is complementary to and derived from mRNA.

"Regulatory sequences" and "suitable regulatory sequences" each refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences include enhancers, promoters, translation leader sequences, introns, and polyadenylation signal sequences. They include natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. As is noted above, the term "suitable regulatory sequences" is not limited to promoters. However, some suitable regulatory sequences useful in the present invention will include, but are not limited to constitutive plant promoters, plant tissue-specific promoters, plant development specific promoters, inducible plant promoters and viral promoters.

"5' non-coding sequence" refers to a nucleotide sequence located 5' (upstream) to the coding sequence. It is present in the fully processed mRNA upstream of the initiation codon and may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency (Turner et al., 1995).

"3' non-coding sequence" refers to nucleotide sequences located 3' (downstream) to a coding sequence and include polyadenylation signal sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by Ingelbrecht et al., 1989.

The term "translation leader sequence" refers to that DNA sequence portion of a gene between the promoter and coding sequence that is transcribed into RNA and is present in the fully processed mRNA upstream (5') of the translation start codon. The translation leader sequence may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency.

The term "mature" protein refers to a post-translationally processed polypeptide without its signal peptide. "Precursor" protein refers to the primary product of translation of an mRNA. "Signal peptide" refers to the amino terminal extension of a polypeptide, which is translated in conjunction with the polypeptide forming a precursor peptide and which is required for its entrance into the secretory pathway. The term "signal sequence" refers to a nucleotide sequence that encodes the signal peptide.

The term "intracellular localization sequence" or "signal sequence" refers to a nucleotide sequence that encodes an intracellular targeting signal. An "intracellular targeting signal" is an amino acid sequence that is translated in conjunction with a protein and directs it to a particular sub-cellular compartment. "Endoplasmic reticulum (ER) stop transit signal" refers to a carboxy-terminal extension of a polypeptide, which is translated in conjunction with the polypeptide and causes a protein that enters the secretory pathway to be retained in the ER. "ER stop transit sequence" refers to a nucleotide sequence that encodes the ER targeting signal. Other intracellular targeting sequences encode targeting signals active in seeds and/or leaves and vacuolar targeting signals.

"Promoter" refers to a nucleotide sequence, usually upstream (5') to its coding sequence, which controls the expression of the coding sequence by providing the recognition for RNA polymerase and other factors required for proper transcription. "Promoter" includes a minimal promoter that is a short DNA sequence comprised of a TATA-box and other sequences that serve to specify the site of transcription initiation, to which regulatory elements are added for control of expression. "Promoter" also refers to a nucleotide sequence that includes a minimal promoter plus regulatory elements that is capable of controlling the expression of a coding sequence or functional RNA. This type of promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an "enhancer" is a DNA sequence which can stimulate promoter activity and may be an innate

element of the promoter or a heterologous element inserted to enhance the level or tissue specificity of a promoter. It is capable of operating in both orientations (normal or flipped), and is capable of functioning even when moved either upstream or downstream from the promoter. Both enhancers and other upstream promoter elements bind sequence-specific DNA-binding proteins that mediate their effects. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even be comprised of synthetic DNA segments. A promoter may also contain DNA sequences that are involved in the binding of protein factors which control the effectiveness of transcription initiation in response to physiological or developmental conditions.

The "initiation site" is the position surrounding the first nucleotide that is part of the transcribed sequence, which is also defined as position +1. With respect to this site all other sequences of the gene and its controlling regions are numbered. Downstream sequences (i.e. further protein encoding sequences in the 3' direction) are denominated positive, while upstream sequences (mostly of the controlling regions in the 5' direction) are denominated negative.

Promoter elements, particularly a TATA element, that are inactive or that have greatly reduced promoter activity in the absence of upstream activation are referred to as "minimal or core promoters." In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription. A "minimal or core promoter" thus consists only of all basal elements needed for transcription initiation, e.g., a TATA box and/or an initiator.

"Constitutive expression" refers to expression using a constitutive or regulated promoter. "Conditional" and "regulated expression" refer to expression controlled by a regulated promoter.

"Constitutive promoter" refers to a promoter that is able to express the gene that it controls in all or nearly all of the plant tissues during all or nearly all developmental stages of the plant. Each of the transcription-activating elements do not exhibit an absolute tissue-specificity, but mediate transcriptional activation in most plant parts at a level of $\geq 1\%$ of the level reached in the part of the plant in which transcription is most active.

"Regulated promoter" refers to promoters that direct gene expression not constitutively, but in a temporally- and/or spatially-regulated manner, and

include both tissue-specific and inducible promoters. It includes natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. Different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. New promoters of various types useful in plant cells are constantly being discovered, numerous examples may be found in the compilation by Okamuro et al., 1989. Since in most cases the exact boundaries of regulatory sequences have not been completely defined, DNA fragments of different lengths may have identical promoter activity.

Typical regulated promoters useful in plants include but are not limited to safener-inducible promoters, promoters derived from the tetracycline-inducible system, promoters derived from salicylate-inducible systems, promoters derived from alcohol-inducible systems, promoters derived from glucocorticoid-inducible system, promoters derived from pathogen-inducible systems, and promoters derived from ecdysone-inducible systems.

"Tissue-specific promoter" refers to regulated promoters that are not expressed in all plant cells but only in one or more cell types in specific organs (such as leaves or seeds), specific tissues (such as embryo or cotyledon), or specific cell types (such as leaf parenchyma or seed storage cells). These also include promoters that are temporally regulated, such as in early or late embryogenesis, during fruit ripening in developing seeds or fruit, in fully differentiated leaf, or at the onset of senescence.

"Inducible promoter" refers to those regulated promoters that can be turned on in one or more cell types by an external stimulus, such as a chemical, light, hormone, stress, or a pathogen.

"Operably-linked" refers to the association of nucleic acid sequences on single nucleic acid fragment so that the function of one is affected by the other. For example, a regulatory DNA sequence is said to be "operably linked to" or "associated with" a DNA sequence that codes for an RNA or a polypeptide if the two sequences are situated such that the regulatory DNA sequence affects expression of the coding DNA sequence (i.e., that the coding sequence or functional RNA is under the transcriptional control of the promoter). Coding sequences can be operably-linked to regulatory sequences in sense or antisense orientation.

"Expression" refers to the transcription and/or translation of an endogenous gene or a transgene in plants. For example, in the case of antisense constructs, expression may refer to the transcription of the antisense DNA only. In addition, expression refers to the transcription and stable accumulation of sense (mRNA) or functional RNA. Expression may also refer to the production of protein.

"Altered levels" refers to the level of expression in transgenic cells or organisms that differs from that of normal or untransformed cells or organisms.

"Overexpression" refers to the level of expression in transgenic cells or organisms that exceeds levels of expression in normal or untransformed cells or organisms.

"Antisense inhibition" refers to the production of antisense RNA transcripts capable of suppressing the expression of protein from an endogenous gene or a transgene.

"Co-suppression" and "transwitch" each refer to the production of sense RNA transcripts capable of suppressing the expression of identical or substantially similar transgene or endogenous genes (U.S. Patent No. 5,231,020).

"Gene silencing" refers to homology-dependent suppression of viral genes, transgenes, or endogenous nuclear genes. Gene silencing may be transcriptional, when the suppression is due to decreased transcription of the affected genes, or post-transcriptional, when the suppression is due to increased turnover (degradation) of RNA species homologous to the affected genes. (English et al., 1996). Gene silencing includes virus-induced gene silencing (Ruiz et al., 1998).

"Silencing suppressor" gene refers to a gene whose expression leads to counteracting gene silencing and enhanced expression of silenced genes. Silencing suppressor genes may be of plant, non-plant, or viral origin. Examples include, but are not limited to HC-Pro, P1-HC-Pro, and 2b proteins. Other examples include one or more genes in TGMV-B genome.

"Transcription stop fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as polyadenylation signal sequences, capable of terminating transcription. Examples include the 3' non-regulatory regions of genes encoding nopaline synthase and the small subunit of ribulose biphosphate carboxylase.

"Translation stop fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as one or more termination codons in all three frames, capable of terminating translation. Insertion of a translation stop fragment adjacent to or near the initiation codon at the 5' end of the coding sequence will result in no translation or improper translation. Excision of the translation stop fragment by site-specific recombination will leave a site-specific sequence in the coding sequence that does not interfere with proper translation using the initiation codon.

The terms "*cis*-acting sequence" and "*cis*-acting element" refer to DNA or RNA sequences whose functions require them to be on the same molecule. An example of a *cis*-acting sequence on the replicon is the viral replication origin.

The terms "*trans*-acting sequence" and "*trans*-acting element" refer to DNA or RNA sequences whose function does not require them to be on the same molecule.

"Chromosomally-integrated" refers to the integration of a foreign gene or DNA construct into the host DNA by covalent bonds. Where genes are not "chromosomally integrated" they may be "transiently expressed." Transient expression of a gene refers to the expression of a gene that is not integrated into the host chromosome but functions independently, either as part of an autonomously replicating plasmid or expression cassette, for example, or as part of another biological system such as a virus.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full length cDNA or gene sequence, or the complete cDNA or gene sequence.

(b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences.

Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm. Preferred, non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller, 1988; the local homology algorithm of Smith et al., 1981; the homology alignment algorithm of Needleman and Wunsch, 1970; the search-for-similarity-method of Pearson and Lipman, 1988; the algorithm of Karlin and Altschul, 1990, modified as in Karlin and Altschul, 1993.

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575 Science Drive, Madison, Wisconsin, USA).

Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins et al., 1988; Higgins et al., 1989; Corpet et al., 1988; Huang et al., 1992; and Pearson et al., 1994. The ALIGN program is based on the algorithm of Myers and Miller, *supra*. The BLAST programs of Altschul et al., 1990, are based on the algorithm of Karlin and Altschul *supra*.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., 1990). These initial neighborhood word hits act as seeds for initiating searches to find

longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul et al., 1997. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul et al., *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g. BLASTN for nucleotide sequences, BLASTX for proteins) can be used. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, $M=5$, $N=-4$, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989). See <http://www.ncbi.nlm.nih.gov>. Alignment may also be performed manually by inspection.

For purposes of the present invention, comparison of nucleotide sequences for determination of percent sequence identity to the promoter sequences disclosed herein is preferably made using the BlastN program (version 1.4.7 or later) with its default parameters or any equivalent program. By

5 "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the preferred program.

(c) As used herein, "sequence identity" or "identity" in the context of two
10 nucleic acid or polypeptide sequences makes reference to a specified percentage of residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window, as measured by sequence comparison algorithms or by visual inspection. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions
15 which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted
20 upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity." Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity.
25 Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).

30 (d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal

alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or 79%, preferably at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, and most preferably at least 95%, 96%, 97%, 98%, or 99% sequence identity, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 70%, more preferably at least 80%, 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions (see below). Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C, depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

(e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70%, 71%, 72%, 73%, 74%,

75%, 76%, 77%, 78%, or 79%, preferably 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, or even more preferably, 95%, 96%, 97%, 98% or 99%, sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch, 1970. An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

As noted above, another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions. The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA. "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern hybridizations are sequence dependent, and are different under different environmental parameters. Longer sequences hybridize specifically at higher temperatures. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Specificity is typically the function of post-

hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, 1984; $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, 5 %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with 10 >90% identity are sought, the T_m can be decreased 10°C . Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point (T_m); moderately stringent 15 conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T , those of ordinary skill will understand that variations in the 20 stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, 1993. Generally, highly 25 stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.

An example of highly stringent wash conditions is 0.15 M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2X SSC 30 wash at 65°C for 15 minutes (see, Sambrook, *infra*, for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, e.g., more than 100 nucleotides, is 1X SSC at 45°C for 15 minutes.

An example low stringency wash for a duplex of, e.g., more than 100 nucleotides, is 4-6X SSC at 40°C for 15 minutes. For short probes (e.g., about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.5 M, more preferably about 0.01 to 1.0 M, Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C and at least about 60°C for long robes (e.g., >50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2X (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or Northern blot is 50% formamide, e.g., hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C.

The following are examples of sets of hybridization/wash conditions that may be used to clone orthologous nucleotide sequences that are substantially identical to reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5

M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with
5 washing in 0.1X SSC, 0.1% SDS at 65°C.

By "variant" polypeptide is intended a polypeptide derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native
10 protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may result from, for example, genetic polymorphism or from human manipulation. Methods for such manipulations are generally known in the art.

Thus, the polypeptides of the invention may be altered in various ways
15 including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the polypeptides can be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel, 1985; Kunkel et al., 1987; U.
20 S. Patent No. 4,873,192; Walker and Gaastra, 1983, and the references cited therein. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff et al., 1978, herein incorporated by reference. Conservative substitutions, such as exchanging one amino acid with another having similar
25 properties, are preferred.

Thus, the genes and nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant forms. Likewise, the polypeptides of the invention encompass both naturally occurring proteins as well as variations and modified forms thereof. Such variants will continue to
30 possess the desired activity. The deletions, insertions, and substitutions of the polypeptide sequence encompassed herein are not expected to produce radical changes in the characteristics of the polypeptide. However, when it is difficult to predict the exact effect of the substitution, deletion, or insertion in advance of

doing so, one skilled in the art will appreciate that the effect will be evaluated by routine screening assays.

Individual substitutions deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids (typically less than 5%,
5 more typically less than 1%) in an encoded sequence are "conservatively modified variations," where the alterations result in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following five groups each contain amino acids that are conservative
10 substitutions for one another: Aliphatic: Glycine (G), Alanine (A), Valine (V), Leucine (L), Isoleucine (I); Aromatic: Phenylalanine (F), Tyrosine (Y), Tryptophan (W); Sulfur-containing: Methionine (M), Cysteine (C); Basic: Arginine (R), Lysine (K), Histidine (H); Acidic: Aspartic acid (D), Glutamic acid (E), Asparagine (N), Glutamine (Q). See also, Creighton, 1984. In addition,
15 individual substitutions, deletions or additions which alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence are also "conservatively modified variations."

"Production tissue" refers to mature, harvestable tissue consisting of non-dividing, terminally-differentiated cells. It excludes young, growing tissue
20 consisting of germline, meristematic, and not-fully-differentiated cells.

"Germline cells" refer to cells that are destined to be gametes and whose genetic material is heritable.

The word "plant" refers to any plant, particularly to seed plant, and "plant cell" is a structural and physiological unit of the plant, which comprises a cell
25 wall but may also refer to a protoplast. The plant cell may be in form of an isolated single cell or a cultured cell, or as a part of higher organized unit such as, for example, a plant tissue, or a plant organ.

"Plant tissue" includes differentiated and undifferentiated tissues or plants, including but not limited to roots, stems, shoots, leaves, pollen, seeds,
30 tumor tissue and various forms of cells and culture such as single cells, protoplast, embryos, and callus tissue. The plant tissue may be in plants or in organ, tissue or cell culture.

The term "altered plant trait" means any phenotypic or genotypic change in a transgenic plant relative to the wild-type or non-transgenic plant host.

The term "transformation" refers to the transfer of a nucleic acid fragment into the genome of a host cell, resulting in genetically stable inheritance. Host cells containing the transformed nucleic acid fragments are referred to as "transgenic" cells, and organisms comprising transgenic cells are referred to as "transgenic organisms". Examples of methods of transformation of plants and plant cells include *Agrobacterium*-mediated transformation (De Blaere et al., 1987) and particle bombardment technology (Klein et al., 1987; U.S. Patent No. 4,945,050). Whole plants may be regenerated from transgenic cells by methods well known to the skilled artisan (see, for example, Fromm et al., 1990).

"Transformed," "transgenic," and "recombinant" refer to a host cell or organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome generally known in the art and are disclosed in Sambrook et al., 1989. See also Innis et al., 1995; and Gelfand, 1995; and Innis and Gelfand, 1999. Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially mismatched primers, and the like. For example, "transformed," "transformant," and "transgenic" plants or calli have been through the transformation process and contain a foreign gene integrated into their chromosome. The term "untransformed" refers to normal plants that have not been through the transformation process.

A "transgenic plant" is a plant having one or more plant cells that contain an expression vector.

"Transiently transformed" refers to cells in which transgenes and foreign DNA have been introduced (for example, by such methods as *Agrobacterium*-mediated transformation or biolistic bombardment), but not selected for stable maintenance.

"Stably transformed" refers to cells that have been selected and regenerated on a selection media following transformation.

"Transient expression" refers to transgene expression in cells, e.g., after transformation with recombinant virus or by such methods as *Agrobacterium*-mediated transformation, electroporation, or biolistic bombardment, but not selected for its stable maintenance.

"Genetically stable" and "heritable" refer to chromosomally-integrated genetic elements that are stably maintained in the plant and stably inherited by progeny through successive generations.

5 "Primary transformant" and "T0 generation" refer to transgenic plants that are of the same genetic generation as the tissue which was initially transformed (i.e., not having gone through meiosis and fertilization since transformation).

"Secondary transformants" and the "T1, T2, T3, etc. generations" refer to transgenic plants derived from primary transformants through one or more meiotic and fertilization cycles. They may be derived by self-fertilization of
10 primary or secondary transformants or crosses of primary or secondary transformants with other transformed or untransformed plants.

"Significant increase" is an increase that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater.

15 "Significantly less" means that the decrease is larger than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or greater.

I. The Nucleic Acid Molecules of the Invention and Polypeptide Encoded

20 Thereby

This invention relates to isolated plant, e.g., *Arabidopsis* and rice, nucleic acid molecules, sequences and segments (fragments), the expression of which is altered in response to pathogen infection, as well as the endogenous plant promoters for those expressed molecules, sequences or segments. However, the
25 expression of these genes may also be altered in response to non-pathogens, e.g., in response to environmental stimuli. The nucleic acid molecules can be used in pathogen control strategies, e.g., by overexpressing nucleic acid molecules which can confer tolerance to a cell, or by altering the expression of host genes which are required for pathogen infection, e.g., by "knocking out" the expression of at
30 least one genomic copy of the gene. Plants having genetic disruptions in host genes may be less susceptible to infection, e.g., due to a decrease or absence of a host protein needed for infection, or, alternatively, hypersusceptible to infection. Plants that are hypersusceptible to infection may be useful to prepare transgenic

plants as the expression of the gene(s) which was disrupted may be related to gene silencing.

Preferred sources for the nucleic acid molecules of the invention include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Wolffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wolffella* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*, *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*).

Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt, Biosystematic Investigation on the Family of Duckweeds: The family of

Lemnaceae - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, *Lotus*, e.g., trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula,

Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia.

Other vegetable sources (and databases to identify orthologs of the invention) for the nucleic acid sequences of the invention include those are shown in Table 1.

Table 1

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Cucurbitaceae	<i>Cucumis sativus</i>	Cucumber		http://www.cucurbit.org/
	<i>Cucumis melo</i>	Melon		http://genome.cornell.edu/cgc/
	<i>Citrullus lanatus</i>	Watermelon		
	<i>Cucurbita pepo</i>	Squash – summer		
	<i>Cucurbita maxima</i>	Squash - winter		
	<i>Cucurbita moschata</i>	Pumpkin /butternut		
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Solanaceae	<i>Lycopersicon esculentum</i>	Tomato	<ul style="list-style-type: none"> • 15x BAC on variety Heinz 1706 order from Clemson Genome center (www.genome.clemson.edu) • 11.6x BAC of <i>L. cheesmanii</i> (originates from J. Giovannoni) available from Clemson genome center (www.genome.clemson.edu) • EST collection 	genome.cornell.edu/solgenes http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=solgenes http://genome.cornell.edu/tgc/ http://tgrc.ucdavis.edu/

			<p>from TIGR (www.tigr.org/tigrdb/lgi/index.html)</p> <ul style="list-style-type: none"> • EST collection from Clemson Genome Center (www.genome.clemson.edu) • TAG 99:254-271, 1999 (esculentum x pennelli) • TAG 89:1007-1013, 1994 (peruvianum) • Plant Cell Reports 12:293-297, 1993 (RAPDs) • Genetics 132:1141-1160, 1992 (potato x tomato) • Genetics 120:1095-1105, 1988 (RFLP potato and tomato) • Genetics 115:387-393, 1986 (esculentum x pennelli isozyme and cDNAs) 	
	<i>Capsicum annuum</i>	Pepper		http://neptune.netimages.com/~chile/science.html
	<i>Capsicum frutescens</i>	Chile pepper		
	<i>Solanum melongena</i>	Eggplant		
	(<i>Nicotiana tabacum</i>)	(Tobacco)		
	(<i>Solanum tuberosum</i>)	(Potato)		
	(<i>Petunia x hybrida hort. ex E. Vilm.</i>)	(Petunia)	4x BAC of <i>Petunia hybrida</i> 7984 available from	

			Clemson genome center (www.genome.clemson.edu)	
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Brassicaceae	<i>Brassica oleracea</i> L. var. <i>italica</i>	Broccoli		http://res.agr.ca/ecorc/cwmt/crucifer/traits/index.htm http://geneous.cit.cornell.edu/cabbage/aboutcab.html
	<i>Brassica oleracea</i> L. var. <i>capitata</i>	Cabbage		
	<i>Brassica rapa</i>	Chinese Cabbage		
	<i>Brassica oleracea</i> L. var. <i>botrytis</i>	Cauliflower		
	<i>Raphanus sativus</i> var. <i>niger</i>	Daikon		
	(<i>Brassica napus</i>)	(Oilseed rape)		http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=brassicadb
		Arabidopsis	12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=agr
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Umbelliferae	<i>Daucus carota</i>	Carrot		
Compositae	<i>Lactuca sativa</i>	Lettuce		
	<i>Helianthus annuus</i>	(Sunflower)		
Total				
Chenopodiaceae	<i>Spinacia oleracea</i>	Spinach		
	(<i>Beta vulgaris</i>)	(Sugar Beet)		
Total				

Leguminosae	<i>Phaseolus vulgaris</i>	Bean	4.3x BAC available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=beangenes
	<i>Pisum sativum</i>	Pea		
	(<i>Glycine max</i>)	(Soybean)	7.5x and 7.9x BACs available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase
Total			http://www.nal.usda.gov/pgdic/Map_projects/	
Gramineae	<i>Zea mays</i>	Sweet Corn	Novartis BACs for Mo17 and B73 have been donated to Clemson Genome Center (www.genome.clemson.edu)	
	(<i>Zea mays</i>)	(Field Corn)		http://www.agron.missouri.edu/mnl/
Total			http://www.nal.usda.gov/pgdic/Map_projects/	
Liliaceae	<i>Allium cepa</i>	Onion		
		Leek		
		(Garlic)		
		(Asparagus)		
Total			http://www.nal.usda.gov/pgdic/Map_projects/	

Preferred forage and turf grass nucleic acid sources for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop. Preferably, the nucleic acid sources are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.), and even more preferably corn and soybean.

According to one embodiment, the present invention is directed to a nucleic acid molecule comprising a nucleotide sequence obtained or obtainable

from any plant gene which encodes a polypeptide having at least 70% amino acid sequence identity to a polypeptide encoded by SEQ ID NOs. 1-684 or 789-795, or a promoter for said gene. Thus, based on the *Arabidopsis* nucleic acid sequences of the present invention, orthologs of those sequences may be

5 identified or isolated from the genome of any desired organism, preferably from another plant, according to well known techniques based on their sequence similarity to the *Arabidopsis* coding sequences, e.g., hybridization, PCR or computer generated sequence comparisons. For example, all or a portion of a particular *Arabidopsis* sequence is used as a probe that selectively hybridizes to

10 other gene sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen source organism. Further, suitable genomic and cDNA libraries may be prepared from any cell or tissue of an organism. Such techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, e.g.,

15 Sambrook et al., 1989) and amplification by PCR using oligonucleotide primers preferably corresponding to sequence domains conserved among related polypeptide or subsequences of the nucleotide sequences provided herein (see, e.g., Innis et al., 1990). These methods are particularly well suited to the isolation of gene sequences from organisms closely related to the organism from

20 which the probe sequence is derived. The application of these methods using the *Arabidopsis* coding sequences as probes is well suited for the isolation of gene sequences from any source organism, preferably other plant species. In a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted

25 from any plant of interest. Methods for designing PCR primers and PCR cloning are generally known in the art as discussed hereinabove.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA

30 fragments (i.e., genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P , or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the

sequence of the invention. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook et al., 1989. In general, sequences that hybridize to the sequences disclosed herein will have at least 40% to 50%, about 5 60% to 70% and even about 80% 85%, 90%, 95% to 98% or more identity with the disclosed sequences. That is, the sequence similarity of sequences may range, sharing at least about 40% to 50%, about 60% to 70%, and even about 80%, 85%, 90%, 95% to 98% sequence similarity:

The nucleic acid molecules of the invention can also be identified by, for 10 example, a search of known databases for genes encoding polypeptides having a specified amino acid sequence identity. Methods of alignment of sequences for comparison are well known in the art and are described hereinabove.

II. Expression Cassettes of the Invention

15 The present invention also encompasses expression cassettes, preferably in the form of a recombinant vectors comprising the nucleic acid sequences of the invention. In such vectors, the expression cassette comprises regulatory elements for expression of the nucleotide sequences in a host cell capable of expressing the nucleotide sequences. Such regulatory elements usually comprise 20 promoter and termination signals and preferably also comprise elements allowing efficient translation of polypeptides encoded by the nucleic acid sequences of the present invention. For efficient initiation of translation, sequences adjacent to the initiating methionine may require modification. For example, they can be modified by the inclusion of sequences known to be 25 effective in plants. Joshi (1987) has suggested an appropriate consensus for plants and Clontech suggests a further consensus translation initiator (1993/1994 catalog, page 210). These consensus are suitable for use with the nucleotide sequences of this invention. The sequences are incorporated into constructions comprising the nucleotide sequences, up to and including the ATG (whilst 30 leaving the second amino acid unmodified), or alternatively up to and including the GTC subsequent to the ATG (with the possibility of modifying the second amino acid of the transgene).

Vectors comprising the nucleic acid sequences are usually capable of replication in particular host cells, e.g., as extrachromosomal molecules, and are

therefore used to amplify the nucleic acid sequences of this invention in the host cells. In a preferred embodiment, host cells for such vectors are plant cells.

A. Promoters and Enhancers

Expression of the nucleotide sequences in transgenic plants is driven by
5 promoters shown to be functional in plants. The choice of promoter will vary depending on the temporal and spatial requirements for expression, and also depending on the target species. In many cases, expression in multiple tissues is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and *vice versa*, ideally dicotyledonous promoters
10 are selected for expression in dicotyledons, and monocotyledonous promoters for expression in monocotyledons. However, there is no restriction to the provenance of selected promoters; it is sufficient that they are operational in driving the expression of the nucleotide sequences in the desired cell.

These promoters include, but are not limited to, constitutive, inducible,
15 temporally regulated, developmentally regulated, chemically regulated, stress-responsive, tissue-preferred and tissue-specific promoters. Promoter sequences are known to be strong or weak. A strong promoter provides for a high level of gene expression, whereas a weak promoter provides for a very low level of gene expression. An inducible promoter is a promoter that provides for the turning on
20 and off of gene expression in response to an exogenously added agent, or to an environmental or developmental stimulus. A bacterial promoter such as the P_{tac} promoter can be induced to varying levels of gene expression depending on the level of isothiopropylgalactoside added to the transformed bacterial cells. An isolated promoter sequence that is a strong promoter for heterologous nucleic
25 acid is advantageous because it provides for a sufficient level of gene expression to allow for easy detection and selection of transformed cells and provides for a high level of gene expression when desired.

Preferred promoters that are expressed constitutively include promoters from genes encoding actin or ubiquitin and the CaMV 35S and 19S promoters.
30 The nucleotide sequences of this invention can also be expressed under the regulation of promoters that are chemically regulated. This enables the nucleic acid sequence or encoded polypeptide to be synthesized only when the crop plants are treated with the inducing chemicals. Preferred technology for chemical induction of gene expression is detailed in the published application EP

0 332 104 (to Ciba-Geigy) and U.S. Patent 5,614,395. A preferred promoter for chemical induction is the tobacco PR-1a promoter.

Tissue-specific or tissue-preferential promoters useful in the present invention. Also useful are promoters which confer seed-specific expression, such as those disclosed by Schernthaner et al., 1988; anther (tapetal) specific promoter B6 (Huffman et al.); and pistil-specific promoters such as a modified S13 promoter (Dzelkalns et al., 1993).

Preferred tissue specific expression patterns include green tissue-specific, root-specific, stem-specific, and flower-specific. Promoters suitable for expression in green tissue include many which regulate genes involved in photosynthesis and many of these have been cloned from both monocotyledons and dicotyledons. A preferred promoter is the maize PEPC promoter from the phosphoenol carboxylase gene (Hudspeth & Grula, 1989). A preferred promoter for root-specific expression is that described by de Framond (1991; EP 0 452 269 to Ciba-Geigy). A preferred stem specific promoter is that described in U.S. Patent No. 5,625,136 (to Ciba-Geigy) and which drives expression of the maize *trpA* gene.

Other promoters which direct specific or enhanced expression in certain plant tissues will be known to those of skill in the art in light of the present disclosure. These include, for example, the *rbcS* promoter, specific for green tissue; the *ocs*, *nos*, and *mas* promoters which have higher activity in roots or wounded leaf tissue; a truncated (-90 to +8) 35S promoter which directs enhanced expression in roots, an tubulin gene that directs expression in roots and promoters derived from zein storage protein genes which direct expression in endosperm. It is particularly contemplated that one may advantageously use the 16 bp *ocs* enhancer element from the octopine synthase (*ocs*) gene (Bonchez et al., 1989), especially when present in multiple copies, to achieve enhanced expression in roots.

Preferred plant promoters include, but are not limited to, a promoter such as the CaMV 35S promoter, an enhanced 35S promoter or others such as CaMV 19S, *nos*, *Adh1*, sucrose synthase, α -tubulin, ubiquitin, actin, *cab*, PEPCase or those associated with the R gene complex. Further suitable promoters include the U2 and U5 snRNA promoters from maize, the promoter from alcohol dehydrogenase, the Z4 promoter from a gene encoding the Z4 22 kD zein

protein, the Z10 promoter from a gene encoding a 10 kD zein protein, a Z27 promoter from a gene encoding a 27 kD zein protein, the A20 promoter from the gene encoding a 19 kD -zein protein, inducible promoters, such as the light inducible promoter derived from the pea *rbcS* gene and the actin promoter from rice; seed specific promoters, such as the phaseolin promoter from beans, may also be used. Other promoters useful in the practice of the invention are known to those of skill in the art.

Examples of tissue specific promoters which have been described include the lectin (Vodkin, 1983; Lindstrom et al., 1990,) corn alcohol dehydrogenase 1 (Vogel et al., 1992; Dennis et al., 1984), corn light harvesting complex (Simpson, 1985; Bansal et al., 1992), corn heat shock protein (Odell et al., 1985; Rochester et al., 1986), pea small subunit RuBP carboxylase (Poulsen et al., 1986; Cashmore et al., 1983), Ti plasmid mannopine synthase (Langridge et al., 1989), Ti plasmid nopaline synthase (Langridge et al., 1989), petunia chalcone isomerase (vanTunen et al., 1988), bean glycine rich protein 1 (Keller et al., 1989), truncated CaMV 35s (Odell et al., 1985), potato patatin (Wenzler et al., 1989), root cell (Yamamoto et al., 1990), maize zein (Reina et al., 1990; Kriz et al., 1987; Wandelt et al., 1989; Langridge et al., 1983; Reina et al., 1990), globulin-1 (Belanger et al., 1991), α -tubulin, cab (Sullivan et al., 1989), PEPCase (Hudspeth & Grula, 1989), R gene complex-associated promoters (Chandler et al., 1989), and chalcone synthase promoters (Franken et al., 1991).

Inducible promoters that have been described include the ABA- and turgor-inducible promoters, the promoter of the auxin-binding protein gene (Schwob et al., 1993), the UDP glucose flavonoid glycosyl-transferase gene promoter (Ralston et al., 1988), the MPI proteinase inhibitor promoter (Cordero et al., 1994), and the glyceraldehyde-3-phosphate dehydrogenase gene promoter (Kohler et al., 1995; Quigley et al., 1989; Martinez et al., 1989).

Several tissue-specific regulated genes and/or promoters have been reported in plants. These include genes encoding the seed storage proteins (such as napin, cruciferin, beta-conglycinin, and phaseolin) zein or oil body proteins (such as oleosin), or genes involved in fatty acid biosynthesis (including acyl carrier protein, stearoyl-ACP desaturase, and fatty acid desaturases (*fad 2-1*)), and other genes expressed during embryo development (such as *Bce4*, see, for example, EP 255378 and Kridl et al., 1991). Particularly useful for seed-specific

expression is the pea vicilin promoter (Czako et al., 1992. (See also U.S. Pat. No. 5,625,136, herein incorporated by reference.) Other useful promoters for expression in mature leaves are those that are switched on at the onset of senescence, such as the SAG promoter from Arabidopsis (Gan et al., 1995, 270
5 (5244), 1986-8).

A class of fruit-specific promoters expressed at or during antithesis through fruit development, at least until the beginning of ripening, is discussed in U.S. 4,943,674, the disclosure of which is hereby incorporated by reference. cDNA clones that are preferentially expressed in cotton fiber have been isolated
10 (John et al., 1992). cDNA clones from tomato displaying differential expression during fruit development have been isolated and characterized (Mansson et al., 1985, Slater et al., 1985). The promoter for polygalacturonase gene is active in fruit ripening. The polygalacturonase gene is described in U.S. Patent No. 4,535,060, U.S. Patent No. 4,769,061, U.S. Patent No. 4,801,590, and U.S.
15 Patent No. 5,107,065, which disclosures are incorporated herein by reference.

Other examples of tissue-specific promoters include those that direct expression in leaf cells following damage to the leaf (for example, from chewing insects), in tubers (for example, patatin gene promoter), and in fiber cells (an example of a developmentally-regulated fiber cell protein is E6 (John et al.,
20 1992). The E6 gene is most active in fiber, although low levels of transcripts are found in leaf, ovule and flower.

The tissue-specificity of some "tissue-specific" promoters may not be absolute and may be tested by one skilled in the art using the diphtheria toxin sequence. One can also achieve tissue-specific expression with "leaky"
25 expression by a combination of different tissue-specific promoters (Beals et al., 1997). Other tissue-specific promoters can be isolated by one skilled in the art (see U.S. 5,589,379). Several inducible promoters ("gene switches") have been reported. Many are described in the review by Gatz (1996 and 1997). These include tetracycline repressor system, *Lac* repressor system, copper-inducible
30 systems, salicylate-inducible systems (such as the PR1a system), glucocorticoid- (Aoyama, 1997) and ecdysone-inducible systems. Also included are the benzene sulphonamide- (U.S. Patent No. 5,364,780) and alcohol- (WO 97/06269 and WO 97/06268) inducible systems and glutathione S-transferase promoters. Other studies have focused on genes inducibly regulated in response to

environmental stress or stimuli such as increased salinity, drought, pathogen and wounding. (Graham et al., 1985; Graham et al., 1985, Smith et al., 1986).

Accumulation of metallocarboxypeptidase-inhibitor protein has been reported in leaves of wounded potato plants (Graham et al., 1981). Other plant genes have
5 been reported to be induced methyl jasmonate, elicitors, heat-shock, anaerobic stress, or herbicide safeners.

Frequently it is desirable to have continuous or inducible expression of a DNA sequence throughout the cells of an organism in a tissue-independent manner. For example, increased resistance of a plant to infection by soil- and air
10 borne pathogens might be accomplished by genetic manipulation of the plant's genome to comprise a continuous promoter operably linked to a heterologous or homologous pathogen-resistance gene such that pathogen-resistance proteins are continuously expressed throughout the plant's tissues.

Alternatively, it might be desirable to inhibit expression of a native DNA
15 sequence within a plant's tissues to achieve a desired phenotype. In this case, such inhibition might be accomplished with transformation of the plant to comprise a constitutive, tissue-independent promoter operably linked to an antisense nucleotide sequence, such that constitutive expression of the antisense sequence produces an RNA transcript that interferes with translation of the
20 mRNA of the native DNA sequence.

Other elements include those that can be regulated by endogenous or exogenous agents, e.g., by DNA binding proteins such as zinc finger proteins, including naturally occurring zinc finger proteins or chimeric zinc finger proteins (see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO
25 98/53060; WO 98/53057; WO 98/53058; WO 00/23464; WO 95/19431; and WO 98/54311) or myb-like transcription factors. For example, a chimeric zinc finger protein may include amino acid sequences which bind to a specific DNA sequence (the zinc finger) and amino acid sequences that activate (e.g., GAL 4 sequences) or repress the transcription of the sequences linked to the specific
30 DNA sequence.

B. 5' and 3' Sequences

In addition to promoters, a variety of 3' transcriptional terminators are also available for use in the present invention. Transcriptional terminators are responsible for the termination of transcription and correct mRNA

polyadenylation. The 3' nontranslated regulatory DNA sequence preferably includes from about 50 to about 1,000, more preferably about 100 to about 1,000, nucleotide base pairs and contains plant transcriptional and translational termination sequences. Appropriate transcriptional terminators and those which are known to function in plants include the CaMV 35S terminator, the tml terminator, the nopaline synthase terminator, the pea rbcS E9⁺ terminator, the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3' end of the protease inhibitor I or II genes from potato or tomato, although other 3' elements known to those of skill in the art can also be employed.

The 5' regulatory region of the expression cassette may also include other enhancing sequences. Numerous sequences have been found to enhance gene expression in transgenic plants. These include sequences which have been shown to enhance expression such as intron sequences (e.g., from *Adhl*, *bronzel* or the sucrose synthase intron) and viral leader sequences (e.g., from TMV, MCMV and AMV). For example, a number of non-translated leader sequences derived from viruses are known to enhance expression. Specifically, leader sequences from Tobacco Mosaic Virus (TMV), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (e.g., Gallie et al., 1987; Skuzeski et al., 1990). Other leaders known in the art include but are not limited to: Picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5 noncoding region) (Elroy-Stein et al., 1989); Potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison et al., 1986); MDMV leader (Maize Dwarf Mosaic Virus); Human immunoglobulin heavy-chain binding protein (BiP) leader, (Macejak et al., 1991); Untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling et al., 1987; Tobacco mosaic virus leader (TMV), (Gallie et al., 1989; and Maize Chlorotic Mottle Virus leader (MCMV) (Lommel et al., 1991. See also, Della-Cioppa et al., 1987.

C. Targeting Sequences

It may be preferable to target expression of the nucleotide sequences of the present invention to different cellular localizations in the plant. In some cases, localization in the cytosol may be desirable, whereas in other cases, localization in some subcellular organelle, e.g., the nucleus, may be preferred. Subcellular

localization of transgene encoded enzymes is undertaken using techniques well known in the art. Typically, the DNA encoding the target peptide from a known organelle-targeted gene product is manipulated and fused upstream of the nucleotide sequence. Many such target sequences are known for the chloroplast and their functioning in heterologous constructions has been shown. The expression of the nucleotide sequences of the present invention is also targeted to the endoplasmic reticulum or to the vacuoles of the host cells. Techniques to achieve this are well-known in the art.

D. Marker Genes

10 In order to improve the ability to identify transformants, one may desire to employ a selectable or screenable marker gene as, or in addition to, the preselected nucleic acid sequence or segment. "Marker genes" are genes that impart a distinct phenotype to cells expressing the marker gene and thus allow such transformed cells to be distinguished from cells that do not have the marker.

15 Such genes may encode either a selectable or screenable marker, depending on whether the marker confers a trait which one can 'select' for by chemical means, i.e., through the use of a selective agent (e.g., a herbicide, antibiotic, or the like), or whether it is simply a trait that one can identify through observation or testing, i.e., by 'screening' (e.g., the R-locus trait). Of course, many examples of suitable

20 marker genes are known to the art and can be employed in the practice of the invention.

Included within the terms selectable or screenable marker genes are also genes which encode a "secretable marker" whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include

25 markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected by their catalytic activity. Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, e.g., by ELISA; small active enzymes detectable in extracellular solution (e.g., α -amylase, β -lactamase, phosphinothricin

30 acetyltransferase); and proteins that are inserted or trapped in the cell wall (e.g., proteins that include a leader sequence such as that found in the expression unit of extensin or tobacco PR-S).

With regard to selectable secretable markers, the use of a gene that encodes a polypeptide that becomes sequestered in the cell wall, and which polypeptide

includes a unique epitope is considered to be particularly advantageous. Such a secreted antigen marker would ideally employ an epitope sequence that would provide low background in plant tissue, a promoter-leader sequence that would impart efficient expression and targeting across the plasma membrane, and
5 would produce protein that is bound in the cell wall and yet accessible to antibodies. A normally secreted wall protein modified to include a unique epitope would satisfy all such requirements.

Elements of the present disclosure are exemplified in detail through the use of particular marker genes. However in light of this disclosure, numerous other
10 possible selectable and/or screenable marker genes will be apparent to those of skill in the art in addition to the one set forth herein below. Therefore, it will be understood that the following discussion is exemplary rather than exhaustive. In light of the techniques disclosed herein and the general recombinant techniques which are known in the art, the present invention renders possible the
15 introduction of any gene, including marker genes, into a recipient cell to generate a transformed plant cell, e.g., a monocot cell.

Possible selectable markers for use in connection with the present invention include, but are not limited to, a *neo* gene, which codes for kanamycin resistance and can be selected for using kanamycin, G418, a gene encoding
20 resistance to bleomycin, and the like; a *bar* gene which codes for bialaphos resistance; a gene which encodes an altered EPSP synthase protein thus conferring glyphosate resistance; a nitrilase gene such as *bxn* from *Klebsiella ozaenae* which confers resistance to bromoxynil; a mutant acetolactate synthase gene (ALS) which confers resistance to imidazolinone, sulfonylurea or other
25 ALS-inhibiting chemicals (European Patent Application 154,204, 1985); a methotrexate-resistant DHFR gene; a dalapon dehalogenase gene that confers resistance to the herbicide dalapon; or a mutated anthranilate synthase gene that confers resistance to 5-methyl tryptophan. Where a mutant EPSP synthase gene is employed, additional benefit may be realized through the incorporation of a
30 suitable chloroplast transit peptide, CTP (European Patent Application 0 218 571, 1987).

An illustrative embodiment of a selectable marker gene capable of being used in systems to select transformants is the genes that encode the enzyme phosphinothricin acetyltransferase, such as the *bar* gene from *Streptomyces*

hygroscopicus or the *pat* gene from *Streptomyces viridochromogenes* (U.S. Patent No. 5,550,318). The enzyme phosphinothricin acetyltransferase (PAT) inactivates the active ingredient in the herbicide bialaphos, phosphinothricin (PPT). PPT inhibits glutamine synthetase, causing rapid accumulation of ammonia and cell death. The success in using this selective system in conjunction with monocots was particularly surprising because of the major difficulties which have been reported in transformation of cereals.

Screenable markers that may be employed include, but are not limited to, a β -glucuronidase or *uidA* gene (GUS) which encodes an enzyme for which various chromogenic substrates are known; an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues; a β -lactamase gene, which encodes an enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a *xyIE* gene which encodes a catechol dioxygenase that can convert chromogenic catechols; an α -amylase gene; a tyrosinase gene which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to form the easily detectable compound melanin; a β -galactosidase gene, which encodes an enzyme for which there are chromogenic substrates; a luciferase (*lux*) gene, which allows for bioluminescence detection; or an aequorin gene, which may be employed in calcium-sensitive bioluminescence detection, or a green fluorescent protein.

Genes from the maize R gene complex are contemplated to be particularly useful as screenable markers. The R gene complex in maize encodes a protein that acts to regulate the production of anthocyanin pigments in most seed and plant tissue. Maize strains can have one, or as many as four, R alleles which combine to regulate pigmentation in a developmental and tissue specific manner. A gene from the R gene complex was applied to maize transformation, because the expression of this gene in transformed cells does not harm the cells. Thus, an R gene introduced into such cells will cause the expression of a red pigment and, if stably incorporated, can be visually scored as a red sector. If a maize line carries dominant alleles for genes encoding the enzymatic intermediates in the anthocyanin biosynthetic pathway (C2, A1, A2, Bz1 and Bz2), but carries a recessive allele at the R locus, transformation of any cell from that line with R will result in red pigment formation. Exemplary lines include Wisconsin 22

which contains the rg-Stadler allele and TR112, a K55 derivative which is r-g, b, Pl. Alternatively any genotype of maize can be utilized if the C1 and R alleles are introduced together.

A further screenable marker contemplated for use in the present invention is firefly luciferase, encoded by the *lux* gene. The presence of the *lux* gene in transformed cells may be detected using, for example, X-ray film, scintillation counting, fluorescent spectrophotometry, low-light video cameras, photon counting cameras or multiwell luminometry. It is also envisioned that this system may be developed for populational screening for bioluminescence, such as on tissue culture plates, or even for whole plant screening.

E. Other Sequences

A vector of the invention can also further comprise plasmid DNA. Plasmid vectors include additional DNA sequences that provide for easy selection, amplification, and transformation of the expression cassette in prokaryotic and eukaryotic cells, e.g., pUC-derived vectors such as pUC8, pUC9, pUC18, pUC19, pUC23, pUC119, and pUC120, pSK-derived vectors, pGEM-derived vectors, pSP-derived vectors, or pBS-derived vectors. The additional DNA sequences include origins of replication to provide for autonomous replication of the vector, additional selectable marker genes, preferably encoding antibiotic or herbicide resistance, unique multiple cloning sites providing for multiple sites to insert DNA sequences or genes encoded in the expression cassette, and sequences that enhance transformation of prokaryotic and eukaryotic cells.

Another vector that is useful for expression in both plant and prokaryotic cells is the binary Ti plasmid (as disclosed in Schilperoort et al., U.S. Patent No. 4,940,838) as exemplified by vector pGA582. This binary Ti plasmid vector has been previously characterized by An, cited *supra*. This binary Ti vector can be replicated in prokaryotic bacteria such as *E. coli* and *Agrobacterium*. The *Agrobacterium* plasmid vectors can be used to transfer the expression cassette to dicot plant cells, and under certain conditions to monocot cells, such as rice cells. The binary Ti vectors preferably include the nopaline T DNA right and left borders to provide for efficient plant cell transformation, a selectable marker gene, unique multiple cloning sites in the T border regions, the *colE1* replication of origin and a wide host range replicon. The binary Ti vectors carrying an

expression cassette of the invention can be used to transform both prokaryotic and eukaryotic cells, but is preferably used to transform dicot plant cells.

Virtually any DNA may be used for delivery to recipient cells to ultimately produce fertile transgenic plants in accordance with the present invention. For example, DNA segments in the form of vectors and plasmids, or linear DNA fragments, in some instance containing only the DNA element to be expressed in the plant, and the like, may be employed.

Vectors, plasmids, cosmids, YACs (yeast artificial chromosomes) and DNA segments for use in transforming such cells will, of course, generally comprise the cDNA, gene or genes which one desires to introduce into the cells. These DNA constructs can further include structures such as promoters, enhancers, polylinkers, or even regulatory genes as desired. The DNA segment or gene chosen for cellular introduction will often encode a protein which will be expressed in the resultant recombinant cells, such as will result in a screenable or selectable trait and/or which will impart an improved phenotype to the regenerated plant. However, this may not always be the case, and the present invention also encompasses transgenic plants incorporating non-expressed transgenes.

20 III. Transformation

The expression cassettes of the present invention can be introduced into a host cell, e.g., a plant cell, in a number of art-recognized ways. Those skilled in the art will appreciate that the choice of method might depend on the type of cell, e.g., monocotyledonous or dicotyledonous, targeted for transformation. Vectors which may be used to transform plant tissue with the expression cassettes of the present invention include both *Agrobacterium* vectors and ballistic vectors, as well as vectors suitable for DNA-mediated transformation, e.g., direct uptake or via electroporation. However, cells other than plant cells may be transformed with the expression cassettes of the invention.

30 Suitable methods of transforming plant cells include, but are not limited to, microinjection (Crossway et al., 1986), direct DNA transfer to plant cells by PEG precipitation; liposomes; electroporation (Riggs et al., 1986, *Agrobacterium*-mediated transformation (Hinchey et al., 1988), direct gene transfer (Paszkowski et al., 1984), and ballistic particle acceleration using

devices available from Agracetus, Inc., Madison, Wis. and BioRad, Hercules, Calif. (see, for example, Sanford et al., U.S. Pat. No. 4,945,050; and McCabe et al., 1988). Also see, Weissinger et al., 1988; Sanford et al., 1987 (onion); Christou et al., 1988 (soybean); McCabe et al., 1988 (soybean); Datta et al., 1990 (rice); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Fromm et al., 1990 (maize); and Gordon-Kamm et al., 1990 (maize); Svab et al., 1990 (tobacco chloroplast); Koziel et al., 1993 (maize); Shimamoto et al., 1989 (rice); Christou et al., 1991 (rice); European Patent Application EP 0 332 581 (orchardgrass and other Pooideae); Vasil et al., 1993 (wheat); Weeks et al., 1993 (wheat).

In one embodiment, a nucleotide sequence of the present invention is directly transformed into the plastid genome. Plastid transformation technology is extensively described in U.S. Patent Nos. 5,451,513, 5,545,817, and 5,545,818, in PCT application no. WO 95/16783, and in McBride et al., 1994.

The basic technique for chloroplast transformation involves introducing regions of cloned plastid DNA flanking a selectable marker together with the gene of interest into a suitable target tissue, e.g., using biolistics or protoplast transformation (e.g., calcium chloride or PEG mediated transformation). The 1 to 1.5 kb flanking regions, termed targeting sequences, facilitate orthologous recombination with the plastid genome and thus allow the replacement or modification of specific regions of the plastome. Initially, point mutations in the chloroplast 16S rRNA and *rps12* genes conferring resistance to spectinomycin and/or streptomycin are utilized as selectable markers for transformation (Svab et al., 1990; Staub et al., 1992). This resulted in stable homoplasmic transformants at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub et al., 1993). Substantial increases in transformation frequency are obtained by replacement of the recessive rRNA or r-protein antibiotic resistance genes with a dominant selectable marker, the bacterial *aadA* gene encoding the spectinomycin-detoxifying enzyme aminoglycoside-3'-adenyltransferase (Svab et al., 1993). Other selectable markers useful for plastid transformation are known in the art and encompassed within the scope of the invention. Typically, approximately 15-20 cell division cycles following transformation are required to reach a

homoplastidic state. Plastid expression, in which genes are inserted by orthologous recombination into all of the several thousand copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein. In a preferred embodiment, a nucleotide sequence of the present invention is inserted into a plastid targeting vector and transformed into the plastid genome of a desired plant host. Plants homoplastic for plastid genomes containing a nucleotide sequence of the present invention are obtained, and are preferentially capable of high expression of the nucleotide sequence.

Agrobacterium tumefaciens cells containing a vector comprising an expression cassette of the present invention, wherein the vector comprises a Ti plasmid, are useful in methods of making transformed plants. Plant cells are infected with an *Agrobacterium tumefaciens* as described above to produce a transformed plant cell, and then a plant is regenerated from the transformed plant cell. Numerous *Agrobacterium* vector systems useful in carrying out the present invention are known. For example, U.S. Pat. No. 4,459,355 discloses a method for transforming susceptible plants, including dicots, with an *Agrobacterium* strain containing the Ti plasmid. The transformation of woody plants with an *Agrobacterium* vector is disclosed in U.S. Patent No. 4,795,855. Further, U.S. Patent No. 4,940,838 to Schilperoort et al. discloses a binary *Agrobacterium* vector (i.e., one in which the *Agrobacterium* contains one plasmid having the vir region of a Ti plasmid but no T region, and a second plasmid having a T region but no vir region) useful in carrying out the present invention.

It is particularly preferred to use the binary type vectors of Ti and Ri plasmids of *Agrobacterium spp.* Ti-derived vectors transform a wide variety of higher plants, including monocotyledonous and dicotyledonous plants, such as soybean, cotton, rape, tobacco, and rice (Pacciotti et al., 1985; Byrne et al., 1987; Sukhapinda et al., 1987; Lorz et al., 1985; Potrykus, 1985; Park et al., 1985; Hiei et al., 1994. The use of T-DNA to transform plant cells has received extensive study and is amply described (EP 120516; Hoekema, 1985; Knauf, et al., 1983; and An. et al., 1985. For introduction into plants, the nucleotide sequences of the invention can be inserted into binary vectors as described in the examples.

Transformation of plants can be undertaken with a single DNA molecule or multiple DNA molecules (i.e., co-transformation), and both these techniques are suitable for use with the expression cassettes of the present invention.

Numerous transformation vectors are available for plant transformation, and the
 5 expression cassettes of this invention can be used in conjunction with any such vectors. The selection of vector will depend upon the preferred transformation technique and the target species for transformation.

Preferred plant cells for transformation include, but are not limited to, cells from plant such as corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B.*
 10 *juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus*
 15 *tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa
 20 (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.),
 25 oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L.*
 30 *valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wofieldia* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*, *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*).

Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt,

5 Biosystematic Investigation on the Family of Duckweeds: The family of *Lemnaceae* - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis*

10 such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and

15 chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*);

20 redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils,

25 chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, *Lotus*, e.g., trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula,

30 blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry,

nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, caluliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia. Other vegetables are in Table 1.

10 Preferred forage and turf grass for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop.

Preferably, plants of the present invention are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, 15 barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, and the like), and even more preferably rice, corn and soybean.

In a preferred embodiment, the host cells are monocot or dicot cells, including, but are not limited to, wheat, corn (maize), rice, oat, barley, millet, rye, rape and alfalfa, as well as asparagus, tomato, egg plant, apple, pear, quince, 20 cherry, apricot, pepper, melon, lettuce, cauliflower, *Brassica*, e.g., broccoli, cabbage, brussels sprout, sugar beet, sugar cane, sweetcorn, onion, carrot, leek, cucumber, tobacco, aubergine, beet, broad bean, carrot, celery, chicory, cotton, radish, pumpkin, hemp, buckwheat, orchardgrass, creeping bent top, redtop, ryegrass, tobacco, turfgrass, tall fescue, cow pea, endive, gourd, grape, raspberry, 25 chenopodium, blueberry, pineapple, avocado, mango, banana, groundnut, nectarine, papaya, garlic, pea, peach, peanut, pepper, pineapple, plum, potato, safflower, snap bean, spinach, squashes, strawberry, sunflower, sorghum, sweet potato, turnip, watermelon, legumes such as *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., 30 lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia,

Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. More preferably, the host cells are monocot cells such as maize, rice, wheat, barley, oats, and sorghum, which can be
5 regenerated into a transgenic plant.

Any plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a vector of the present invention. The term "organogenesis," as used herein, means a process by which shoots and roots are developed sequentially from meristematic centers; the
10 term "embryogenesis," as used herein, means a process by which shoots and roots develop together in a concerted fashion (not sequentially), whether from somatic cells or gametes. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen,
15 embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristems, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem).

The choice of plant tissue source for transformation will depend on the nature of the host plant and the transformation protocol. Useful tissue sources
20 include callus, suspension culture cells, protoplasts, leaf segments, stem segments, tassels, pollen, embryos, hypocotyls, tuber segments, meristematic regions, and the like. The tissue source is selected and transformed so that it retains the ability to regenerate whole, fertile plants following transformation, i.e., contains totipotent cells. Type I or Type II embryonic maize callus and
25 immature embryos are preferred *Zea mays* tissue sources. Selection of tissue sources for transformation of monocots is described in detail in U.S. Application Serial No. 08/112,245 and PCT publication WO 95/06128 (incorporated herein by reference).

For certain plant species, different antibiotic or herbicide selection markers
30 may be preferred. Selection markers used routinely in transformation include the nptII gene which confers resistance to kanamycin and related antibiotics (Messing & Vierra, 1982); Bevan et al., 1983), the *bar* gene which confers resistance to the herbicide phosphinothricin (White et al., 1990, Spencer et al., 1990), the *hph* gene which confers resistance to the antibiotic hygromycin

(Blochinger & Diggelmann), and the *dhfr* gene, which confers resistance to methotrexate (Bourouis et al., 1983).

Thus, the present invention also provides a transformed (transgenic) plant cell, *in planta* or *ex planta*, including, but not limited to, a transformed plant cell

5 from plants such as corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet

10 (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos*

15 *nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond

20 (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L.*

25 *miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wofliella* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*,

30 *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*). Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt,

Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (5 *Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), 10 carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga 15 menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, 20 soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., 25 trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, 30 apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, caluliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens,

Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia, as well
 5 as from vegetables including those described in Table 1.

In a preferred embodiment, the transformed cells, include, but are not limited to, transformed wheat, corn (maize), rice, oat, barley, millet, rye, rape and alfalfa, as well as asparagus, tomato, egg plant, apple, pear, quince, cherry, apricot, pepper, melon, lettuce, cauliflower, *Brassica*, e.g., broccoli, cabbage,
 10 brussels sprout, sugar beet, sugar cane, sweetcorn, onion, carrot, leek, cucumber, tobacco, aubergine, beet, broad bean, carrot, celery, chicory, cotton, radish, pumpkin, hemp, buckwheat, orchardgrass, creeping bent top, redtop, ryegrass, tobacco, turfgrass, tall fescue, cow pea, endive, gourd, grape, raspberry, chenopodium, blueberry, pineapple, avocado, mango, banana, groundnut,
 15 nectarine, papaya, garlic, pea, peach, peanut, pepper, pineapple, plum, potato, safflower, snap bean, spinach, squashes, strawberry, sunflower, sorghum, sweet potato, turnip, watermelon, legumes such as *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field
 20 bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia, Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura,
 25 Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. Preferably, the host cells are monocot cells such as maize, rice, wheat, barley, oats, and sorghum, which can be regenerated into a transgenic plant.

30 IV. Identification of Transgenic Plants

To confirm the presence of the preselected nucleic acid segment(s) or "transgene(s)" in the regenerating plants, a variety of assays may be performed. Such assays include, for example, "molecular biological" assays well known to those of skill in the art, such as Southern and Northern blotting, *in situ*

hybridization and nucleic acid-based amplification methods such as PCR or RT-PCR; "biochemical" assays, such as detecting the presence of a protein product, e.g., by immunological means (ELISAs and Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the phenotype of the whole regenerated plant, e.g., for disease or pest resistance.

DNA may be isolated from cell lines or any plant parts to determine the presence of the preselected nucleic acid segment through the use of techniques well known to those skilled in the art. Note that intact sequences will not always be present, presumably due to rearrangement or deletion of sequences in the cell.

The presence of nucleic acid elements introduced through the methods of this invention may be determined by polymerase chain reaction (PCR). Using this technique discrete fragments of nucleic acid are amplified and detected by gel electrophoresis. This type of analysis permits one to determine whether a preselected nucleic acid segment is present in a stable transformant, but does not prove integration of the introduced preselected nucleic acid segment into the host cell genome. In addition, it is not possible using PCR techniques to determine whether transformants have exogenous genes introduced into different sites in the genome, i.e., whether transformants are of independent origin. It is contemplated that using PCR techniques it would be possible to clone fragments of the host genomic DNA adjacent to an introduced preselected DNA segment.

Positive proof of DNA integration into the host genome and the independent identities of transformants may be determined using the technique of Southern hybridization. Using this technique specific DNA sequences that were introduced into the host genome and flanking host DNA sequences can be identified. Hence the Southern hybridization pattern of a given transformant serves as an identifying characteristic of that transformant. In addition it is possible through Southern hybridization to demonstrate the presence of introduced preselected DNA segments in high molecular weight DNA, i.e., confirm that the introduced preselected DNA segment has been integrated into the host cell genome. The technique of Southern hybridization provides information that is obtained using PCR, e.g., the presence of a preselected DNA segment, but also demonstrates integration into the genome and characterizes each individual transformant.

It is contemplated that using the techniques of dot or slot blot hybridization which are modifications of Southern hybridization techniques one could obtain the same information that is derived from PCR, e.g., the presence of a preselected DNA segment.

5 Both PCR and Southern hybridization techniques can be used to demonstrate transmission of a preselected DNA segment to progeny. In most instances the characteristic Southern hybridization pattern for a given transformant will segregate in progeny as one or more Mendelian genes (Spencer et al., 1992); Laursen et al., 1994) indicating stable inheritance of the gene. The
10 nonchimeric nature of the callus and the parental transformants (R_0) was suggested by germline transmission and the identical Southern blot hybridization patterns and intensities of the transforming DNA in callus, R_0 plants and R_1 progeny that segregated for the transformed gene.

Whereas DNA analysis techniques may be conducted using DNA isolated
15 from any part of a plant, RNA may only be expressed in particular cells or tissue types and hence it will be necessary to prepare RNA for analysis from these tissues. PCR techniques may also be used for detection and quantitation of RNA produced from introduced preselected DNA segments. In this application of PCR it is first necessary to reverse transcribe RNA into DNA, using enzymes
20 such as reverse transcriptase, and then through the use of conventional PCR techniques amplify the DNA. In most instances PCR techniques, while useful, will not demonstrate integrity of the RNA product. Further information about the nature of the RNA product may be obtained by Northern blotting. This technique will demonstrate the presence of an RNA species and give information
25 about the integrity of that RNA. The presence or absence of an RNA species can also be determined using dot or slot blot Northern hybridizations. These techniques are modifications of Northern blotting and will only demonstrate the presence or absence of an RNA species.

While Southern blotting and PCR may be used to detect the preselected
30 DNA segment in question, they do not provide information as to whether the preselected DNA segment is being expressed. Expression may be evaluated by specifically identifying the protein products of the introduced preselected DNA segments or evaluating the phenotypic changes brought about by their expression.

Assays for the production and identification of specific proteins may make use of physical-chemical, structural, functional, or other properties of the proteins. Unique physical-chemical or structural properties allow the proteins to be separated and identified by electrophoretic procedures, such as native or
5 denaturing gel electrophoresis or isoelectric focussing, or by chromatographic techniques such as ion exchange or gel exclusion chromatography. The unique structures of individual proteins offer opportunities for use of specific antibodies to detect their presence in formats such as an ELISA assay. Combinations of approaches may be employed with even greater specificity such as Western
10 blotting in which antibodies are used to locate individual gene products that have been separated by electrophoretic techniques. Additional techniques may be employed to absolutely confirm the identity of the product of interest such as evaluation by amino acid sequencing following purification. Although these are among the most commonly employed, other procedures may be additionally
15 used.

Assay procedures may also be used to identify the expression of proteins by their functionality, especially the ability of enzymes to catalyze specific chemical reactions involving specific substrates and products. These reactions may be followed by providing and quantifying the loss of substrates or the
20 generation of products of the reactions by physical or chemical procedures. Examples are as varied as the enzyme to be analyzed.

Very frequently the expression of a gene product is determined by evaluating the phenotypic results of its expression. These assays also may take many forms including but not limited to analyzing changes in the chemical
25 composition, morphology, or physiological properties of the plant. Morphological changes may include greater stature or thicker stalks. Most often changes in response of plants or plant parts to imposed treatments are evaluated under carefully controlled conditions termed bioassays.

30 V. Utility

Once an expression cassette of the invention has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques. Particularly preferred plants of the invention

include the agronomically important crops listed above. The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction and can thus be maintained and propagated in progeny plants. The present invention also relates to a transgenic plant cell, tissue, organ, seed or plant part obtained from the transgenic plant. Also included within the invention are transgenic descendants of the plant as well as transgenic plant cells, tissues, organs, seeds and plant parts obtained from the descendants.

Preferably, the expression cassette in the transgenic plant is sexually transmitted. In one preferred embodiment, the coding sequence is sexually transmitted through a complete normal sexual cycle of the R0 plant to the R1 generation. Additionally preferred, the expression cassette is expressed in the cells, tissues, seeds or plant of a transgenic plant in an amount that is different than the amount in the cells, tissues, seeds or plant of a plant which only differs in that the expression cassette is absent.

The transgenic plants produced herein are thus expected to be useful for a variety of commercial and research purposes. Transgenic plants can be created for use in traditional agriculture to possess traits beneficial to the grower (e.g., agronomic traits such as resistance to water deficit, pest resistance, herbicide resistance or increased yield), beneficial to the consumer of the grain harvested from the plant (e.g., improved nutritive content in human food or animal feed), or beneficial to the food processor (e.g., improved processing traits). In such uses, the plants are generally grown for the use of their grain in human or animal foods. However, other parts of the plants, including stalks, husks, vegetative parts, and the like, may also have utility, including use as part of animal silage or for ornamental purposes. Often, chemical constituents (e.g., oils or starches) of maize and other crops are extracted for foods or industrial use and transgenic plants may be created which have enhanced or modified levels of such components.

Transgenic plants may also find use in the commercial manufacture of proteins or other molecules, where the molecule of interest is extracted or purified from plant parts, seeds, and the like. Cells or tissue from the plants may also be cultured, grown *in vitro*, or fermented to manufacture such molecules.

The transgenic plants may also be used in commercial breeding programs, or may be crossed or bred to plants of related crop species. Improvements

encoded by the expression cassette may be transferred, e.g., from maize cells to cells of other species, e.g., by protoplast fusion.

The transgenic plants may have many uses in research or breeding, including creation of new mutant plants through insertional mutagenesis, in order
5 to identify beneficial mutants that might later be created by traditional mutation and selection. An example would be the introduction of a recombinant DNA sequence encoding a transposable element that may be used for generating genetic variation. The methods of the invention may also be used to create plants having unique "signature sequences" or other marker sequences which can
10 be used to identify proprietary lines or varieties.

Thus, the transgenic plants and seeds according to the invention can be used in plant breeding which aims at the development of plants with improved properties conferred by the expression cassette, such as tolerance of viruses or other pests, or other stresses. The various breeding steps are characterized by
15 well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate descendant plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding,
20 variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain
25 properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines which for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can
30 be obtained which, due to their optimized genetic "equipment", yield harvested product of better quality than products which were not able to tolerate comparable adverse developmental conditions.

VI. A Computer Readable Medium

The invention also provides a computer readable medium having stored thereon a data structure containing nucleic acid sequences having at least 70% sequence identity to a nucleic acid sequence selected from those listed in SEQ ID Nos: 1-795 as well as complementary, ortholog, and variant sequences thereof. Storage and use of nucleic acid sequences on a computer readable medium is well known in the art. (See for example U.S. Patent Nos. 6,023,659; 5,867,402; 5,795,716) Examples of such medium include, but are not limited to, magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory. Accordingly, the nucleic acid sequences contained on the computer readable medium may be compared through use of a module that receives the sequence information and compares it to other sequence information. Examples of other sequences to which the nucleic acid sequences of the invention may be compared include those maintained by the National Center for Biotechnology Information (NCBI)(<http://www.ncbi.nlm.nih.gov/>) and the Swiss Protein Data Bank. A computer is an example of such a module that can read and compare nucleic acid sequence information. Accordingly, the invention also provides the method of comparing a nucleic acid sequence of the invention to another sequence. For example, a sequence of the invention may be submitted to the NCBI for a Blast search as described herein where the sequence is compared to sequence information contained within the NCBI database and a comparison is returned. The invention also provides nucleic acid sequence information in a computer readable medium that allows the encoded polypeptide to be optimized for a desired property. Examples of such properties include, but are not limited to, increased or decreased: thermal stability, chemical stability, hydrophylicity, hydrophobicity, and the like. Methods for the use of computers to model polypeptides and polynucleotides having altered activities are well known in the art and have been reviewed. (Lesyng et al., 1993; Surles et al., 1994; Koehl et al., 1996; Rossi et al., 2001).

The invention will be further described by the following examples which is not intended to limit the scope of the invention.

Example 1**GeneChip Standard Protocol****Quantitation of total RNA**

Total RNA from plant tissue is extracted and quantified.

- 5 1. Quantify total RNA using GeneQuant
 1OD₂₆₀=40 mg RNA/ml; A₂₆₀/A₂₈₀=1.9 to about 2.1
2. Run gel to check the integrity and purity of the extracted RNA

Synthesis of double-stranded cDNA

- 10 Gibco/BRL SuperScript Choice System for cDNA Synthesis (Cat#1B090-019)
 was employed to prepare cDNAs. T7-(dT)₂₄ oligonucleotides were prepared
 and purified by HPLC. (5'-
- 15 GGCCAGTGAATTGTAATACGACTCACTATAGGGAGGCGG-(dT)₂₄-
 3'(SEQ ID NO:800).

Step 1. Primer hybridization:

Incubate at 70°C for 10 minutes

Quick spin and put on ice briefly

- 20 **Step 2. Temperature adjustment:**

I Incubate at 42°C for 2 minutes

Step 3. First strand synthesis:

- DEPC-water- 1 µl
- RNA (10 µg final)-10 µl
- 25 T7=(dT)₂₄ Primer (100 pmol final)-1 µl pmol
- 5X 1st strand cDNA buffer-4 µl
- 0.1M DTT (10 mM final)- 2 µl
- 10 mM dNTP mix (500 µM final)-1 µl
- Superscript II RT 200 U/µl- 1 µl
- 30 Total of 20 µl

Mix well

Incubate at 42°C for 1 hour

Step 4. Second strand synthesis:

Place reactions on ice, quick spin

- DEPC-water- 91 μ l
 5X 2nd strand cDNA buffer- 30 μ l
 mM dNTP mix (250 mM final) - 3 μ l
E. coli DNA ligase (10 U/ μ l)-1 μ l
 5 *E. coli* DNA polymerase 1-10 U/ μ l- 4 μ l
 RnaseH 2U/ μ l -1 μ l
 T4 DNA polymerase 5 U/ μ l-2 μ l
 0.5 M EDTA (0.5 M final)--10 μ l
 Total 162 μ l
 10 Mix/spin down/incubate 16°C for 2 hours

Step 5. Completing the reaction:

Incubate at 16°C for 5 minutes

Purification of double stranded cDNA

- 15 1. Centrifuge PLG (Phase Lock Gel, Eppendorf 5 Prime, Inc., PI-188233)
 at 14,000X, transfer 162 μ l of cDNA to PLG
 2. Add 162 μ l of Phenol:Chloroform:Isoamyl alcohol (pH 8.0), centrifuge
 2 minutes
 3. Transfer the supernatant to a fresh 1.5 ml tube, add
 20 Glycogen (5 mg/ml) 2
 0.5 M NH₄OAc (0.75xVol) 120
 ETOH (2.5xVol, -20 °C) 400
 4. Mix well and centrifuge at 14,000X for 20 minutes
 5. Remove supernatant, add 0.5 ml 80% EtOH (-20°C)
 25 6. Centrifuge for 5 minutes, air dry or by speed vac for 5-10 minutes
 7. Add 44 μ l DEPC H₂O

Analyze of quantity and size distribution of cDNA

Run a gel using 1 μ l of the double-stranded synthesis product

30 Synthesis of biotinylated cRNA

(use Enzo BioArray High Yield RNA Transcript Labeling Kit Cat#900182)

Purified cDNA	22 μ l
10X Hy buffer	4 μ l
10X biotin ribonucleotides	4 μ l

10X DTT	4 μ l
10X Rnase inhibitor mix	4 μ l
20X T7 RNA polymerase	2 μ l
Total	40 μ l

- 5 Centrifuge 5 seconds, and incubate for 4 hours at 37°C
Gently mix every 30-45 minutes

Purification and quantification of cRNA

(use Qiagen Rneasy Mini kit Cat# 74103)

- 10 Determine concentration and dilute to 1 μ g/ μ l concentration

Fragmentation of cRNA

	cRNA (1 μ g/ μ l)	15 μ l
	5X Fragmentation Buffer*	6 μ l
15	DEPC H ₂ O	9 μ l
		30 μ l

*5x Fragmentation Buffer

	1M Tris (pH8.1)	4.0 ml
20	MgOAc	0.64 g
	KOAc	0.98 g
	DEPC H ₂ O	
	Total	20 ml
	Filter Sterilize	

25

Array wash and staining

Stringent Wash Buffer**

Non-Stringent Wash Buffer***

SAPE Stain****

- 30 Antibody Stain*****

Wash on fluidics station using the appropriate antibody amplification protocol

**Stringent Buffer: 12X MES 83.3 ml, 5 M NaCl 5.2 ml, 10% Tween 1.0 ml, H₂O 910 ml,

Filter Sterilize

***Non-Stringent Buffer: 20X SSPE 300 ml, 10% Tween 1.0 ml, H₂O 698 ml,
Filter Sterilize, Antifoam 1.0.

****SAPE stain: 2X Stain Buffer 600 µl, BSA 48 µl, SAPE 12µl, H₂O 540 µl.

5 *****Antibody Stain: 2X Stain Buffer 300 µl, H₂O 266.4 µl, BSA 24 ul, Goat
IgG 6 µl, Biotinylated Ab 3.6 µl

Example 2Identification of *Arabidopsis* Genes Induced by *Peronospora* Infection

10

To define the transcriptional profile for *Peronospora*-induced and/or *RPP7*- and *RPP8*- dependent genes, four *Arabidopsis* lines were infected with one of two different *P. parasitica* isolates (see Table 2). One *Arabidopsis* line was Col-0::*RPP8* which carries the cloned *RPP8* genomic clone (*RPP8* mediates
15 resistance of the ecotype La-er against Emco5; McDowell et al. 1998) and is Emco5 resistant. Wild-type Col-0 plants are Emco5 susceptible. *RPP7* mediates resistance of *Arabidopsis* against the *Peronospora* isolate Hiks1, and occurs naturally in Col-0. Another *Arabidopsis* line had a loss of function *rpp7* mutant
20 allele (Col-0 (*rpp7*)) (McDowell et al., 2000). Finally, three mutants in the signaling pathway for *RPP7*, i.e., they lack a *RPP7*-mediated response, were identified, i.e., *edm1*, *edm2* and *edm3*, and a line with one of the mutant alleles, i.e., *edm1*, was used.

RNA samples were collected from two week old seedlings at three time points, 0, 12 and 24 hours post infection with 100,000 spores/ml. Twelve hours
25 post-inoculation was determined to be an appropriate time point for analysis of both incompatible interactions, based on trypan blue staining of HR sites and *PR-1* and *sen1* induction. Forty-eight hours post-inoculation was determined to be a time point where both compatible interactions exhibit dense hyphal growth and both *PR-1* and *sen1* expression. Three independent sets of RNA were
30 pooled.

Table 2

<u>Plant</u>	<u><i>Peronospora</i> isolate</u>	<u>Time of RNA collection</u>
Col-0 (<i>RPP7</i> , <i>incomp.</i>)	Hiks1	0, 12, 48 hours
35 Col-0 (<i>rpp7</i> , <i>comp.</i>)	Hiks1	0, 12, 48 hours

Col-0 (<i>edm1</i> , <i>comp.</i>)	Hiks1	0, 12, 48 hours
Col-0 (<i>tgRPP8</i> , <i>incomp.</i>)	Emco5	0, 12, 48 hours
Col-0 (<i>rpp8</i> , <i>comp.</i>)	Emco5	0, 12, 48 hours

5 RNAs were labeled as described in Example 1 and hybridized to an Affymetrix Gene Chip having sequences corresponding to about 8,200 *Arabidopsis* genes. The data collected from these chips was employed to determine:

- 1) the difference, if any, between *RPP7* and *RPP8* triggered signaling (and how these profiles compare to other profiles, for example, to the profiles of *RPM1* and *RPS2*);
- 2) which portion of the transcriptional response is *R* dependent;
- 3) which genes are either commonly or uniquely induced during two different compatible interactions;
- 4) which genes are specifically activated during the incompatible interactions (gleaned by comparison with isogenic compatible controls) and, hence, may be important for the plant's defense against *Peronospora*;
- 5) which genes whose expression is a prerequisite for induced defense reactions against *Peronospora*; and
- 6) which genes are specifically repressed during the incompatible interactions, which may be required for successful Oomycete infections.

Results

Genes Expressed Early and Transiently After Infection

The normalized "average difference" (AD) from the chip experiments were processed as follows. All values together with the respective gene identifiers were loaded in EXCEL. Genes having, for a given treatment, AD values of 25 or less were considered as being not expressed. To reduce spurious background fluctuation, this cut off level was elevated to 75 for most of the analyses and normalized all AD values of 75 or less. For all five infection time courses, the AD values were divided by the corresponding 0 hour time point AD value. To visualize differences in gene expression ground states between the four experimental *Arabidopsis* lines, the following ratios were calculated for the 0 hour AD values: Col-0 (from Emco5 series)/Col-0-*RPP8* and *rpp7*/Col-0 (from Hiks1 series) and *edm1*/Col-0 (from Hiks1 series). These ratios indicate whether

a given gene is up- or down-regulated by the *RPP7* or *RPP8* pathway, respectively. The resulting set of 18 expression ratio series was then loaded into CLUSTER (Eisen et al., 1998). The AD values were log transformed (base 2) and filtered to include only genes in the final data set that showed at least a 3-
5 fold expression change (which equals a 1.6-fold change of the log transformed values). These criteria were fulfilled by 464 genes that define the final data set. With this data set Average linkage clustering was performed (uncentered correlation). The resulting clustergram was displayed using TREEVIEW (Eisen et al., 1998). A second clustergram was generated in the same way applying a cut
10 off value of 50 on the normalized AD values. This clustergram includes 619 genes (probe sets).

Based on these clustergrams, gene clusters showing distinct expression behaviors were defined. Cluster cR7/R8 (see Table 3) contained genes that are early and transiently upregulated early and transiently after *P. parasitica*
15 infection of *Arabidopsis* in an *RPP7/8* dependent manner. Upregulation by the *RPP8* pathway was generally stronger. Strong induced expression of cR7/R8 genes was detectable 12 hours after Emco5 infection in Col-0(*tgRPP8*) plants (incompatible interaction), whereas no elevated expression can be observed 48 hours post infection in the same plants (as compared to untreated control plants).
20 Only weakly elevated or no elevated expression was detected at all tested time points in Col-0 plants (compatible interaction). After Hiks1 infection, elevated expression of these genes was only observed in Col-0 plants (incompatible interaction) after 12 hours. At no other time point following Hiks1 infection was substantially elevated expression of these genes observed. The expression ground
25 state of these genes is similar in all four *Arabidopsis* lines.

Table 3

20245 s at	cut off = 75
18716 At	
18022 at	
14609 at	
17014 s at	
17051 s at	
19640 at	
14248 at	
13176_at	

15978 at cut off +50
 17014 s at
 14609 at
 13764 at
 16649 s at Subcluster A
 13215 s at
 17653 at
 17008 at
 15042 at
 12778_r_at

14614 at
 17051 s at
 14248 at Subcluster B
 20245 s at
 19640 at
 18716 at
 18022_at

17500 s at
 13217 s at
 18928 at

The cR7/R8 cluster was originally defined using the clustergram based on a cut off value of 75 and comprised only 9 genes. Applying a cut off value of 50, the cluster became larger, comprising 21 genes, which could be divided into two subclusters (Table 4). Subcluster cR7/R8 A includes genes strongly and transiently upregulated by the *RPP8* pathway, but either not, or only faintly, upregulated by the *RPP7* pathway. Members of subcluster B showed pronounced upregulation by both *RPP* pathways after 12 hours and also elevated expression during compatible Emco5 infections in Col-0.

10

Table 4

Subcluster AGene-identifier (probe set)

15978_at

17014_s_at*

14609_at

16649_s_at+

13215_s_at⁺

17653_at

17008_at

Related to

X68592.6_at

atu05206_s_at

AC002340.147_at

athorf_s_at

CafferoylCoAmethyltrans_s_a
t

AL035679.144_at

AC006585.212_at

15042_at	AL021961.3_at
12778_r_at	AC006577.16_r_at

Subcluster B

<u>Gene-identifier (probe set)</u>	<u>Related to</u>
14614_at	AC004165.66_at
17051_s_at	af098947_s_at
14248_at	PAD3_at
20245_s_at	AC005309.97_s_at
19640_at	AC004561.78_at
18716_at	X91916_at
18022_at	AJ010971_at
17500_s_at [†]	athcallga_s_at
13217_s_at [†]	calmodulinlike_s_at
18928_at	AC002333.181_at

* Genes printed in **bold** were identified using a cut off value of 75; all others were identified using a cut off value of 50.

[†]The probe sets 16649 and 13215 as well as 17500 and 13217 correspond to the same genes.

Thus, the predominant feature of genes of the cR7/R8 cluster is more pronounced expression along with *RPP7* and *RPP8* mediated *Peronospora* resistance in comparison to the corresponding compatible interactions. Expression of these genes peaks in around 12 hours post infection and returns to ground state by 48 hours post infection. Hence, increased transcript levels of these genes coincide with the time window of decision between disease or resistance. Within 48 hours after infection with each tested *Peronospora* isolate, the plant either responds with HR and hinders development of oomycete hyphae or allows successful infection.

Identification of Conserved Sequence Motifs Within cR7/R8 Upstream Regions

To identify potential *cis*-elements involved in the specific regulation of cR7/R8 genes, stretches comprising 1.1 to 1.2 kb localized directly upstream of the translation start sites of coding regions from this cluster were collected from genomic *Arabidopsis* sequences (see Figure 2). Two motif search algorithms were used to recognize conserved motifs: AlignAce (Roth et al., 1998) and MEME (Bailey and Elkan, 1994). A search with AlignAce (default settings) revealed two conserved motifs within a set of 8 promoters comprising 7 from the originally defined cR7R8 using a cut off value of 75 and the promoter of a gene encoding a putative Myb-like transcription factor (Martin & Paz-Ares, 1997)

(probe set 13176, SEQ ID NO:36), which shows a similar expression behavior as cR7/R8. The AlignAce output is shown below in Table 5:

Table 5

Motif 1	MAP Score:	SEQ ID NO.	Corresponding Probe Set
*****	6.87857		
CAACAATTAT	0 36 1	685	17014
CAACTATGTC	0 981 1	686	17014
CAACAATGAC	1 934 0	687	20245
CAACAATGAC	2 271 1	688	14609
AAACAATGAT	2 1184 1	689	14609
CAACATTGAC	3 163 0	690	17051
CAACATTGTT	3 298 0	691	17051
CAACAATGTT	4 613 1	692	19640
CAACTATGAT	4 791 0	693	19640
CAACAATGAT	4 1064 0	694	19640
CAAAAATGAT	7 397 0	695	17008
CAACATTGAT	7 415 1	696	17008
CATATCA/TA/TTGAC (Consensus)		697	N.A.

5

Motif 2	MAP Score:	SEQ ID NO.	Corresponding Probe Set
***** **	2.22382		
TTTGGGCAAAA	1 368 0	698	20245
GTTGGGTCAAA	1 739 0	699	20245
GATGGGCACAA	2 691 0	700	14609
GATGGGCCAAA	3 700 0	701	17051
GATGGGTATAA	4 344 0	702	19640
GATGGGACTAA	5 98 1	703	14248
TTTGGGCCTAA	5 971 1	704	14248
TATGGGCCCAA	5 1012 0	705	14248
CTTGGGACAAA	7 579 1	706	17008
GATGGGTCAAC	7 1009 0	707	17008
CATGGGAATAA	7 1072 1	708	17008
NATTGGGNC/ANAA (Consensus)		709	N.A.

For each motif, examples from cR7/R8 promoters are listed. Nucleotides evaluated by AlignAce as being conserved are indicated by a "*" above the examples. Besides motifs 1 and 2, a variety of additional ones were found by AlignAce, which, however, consisted almost exclusively of Ts and As. These motifs probably do not constitute functional *cis*-elements. Promoter sequences

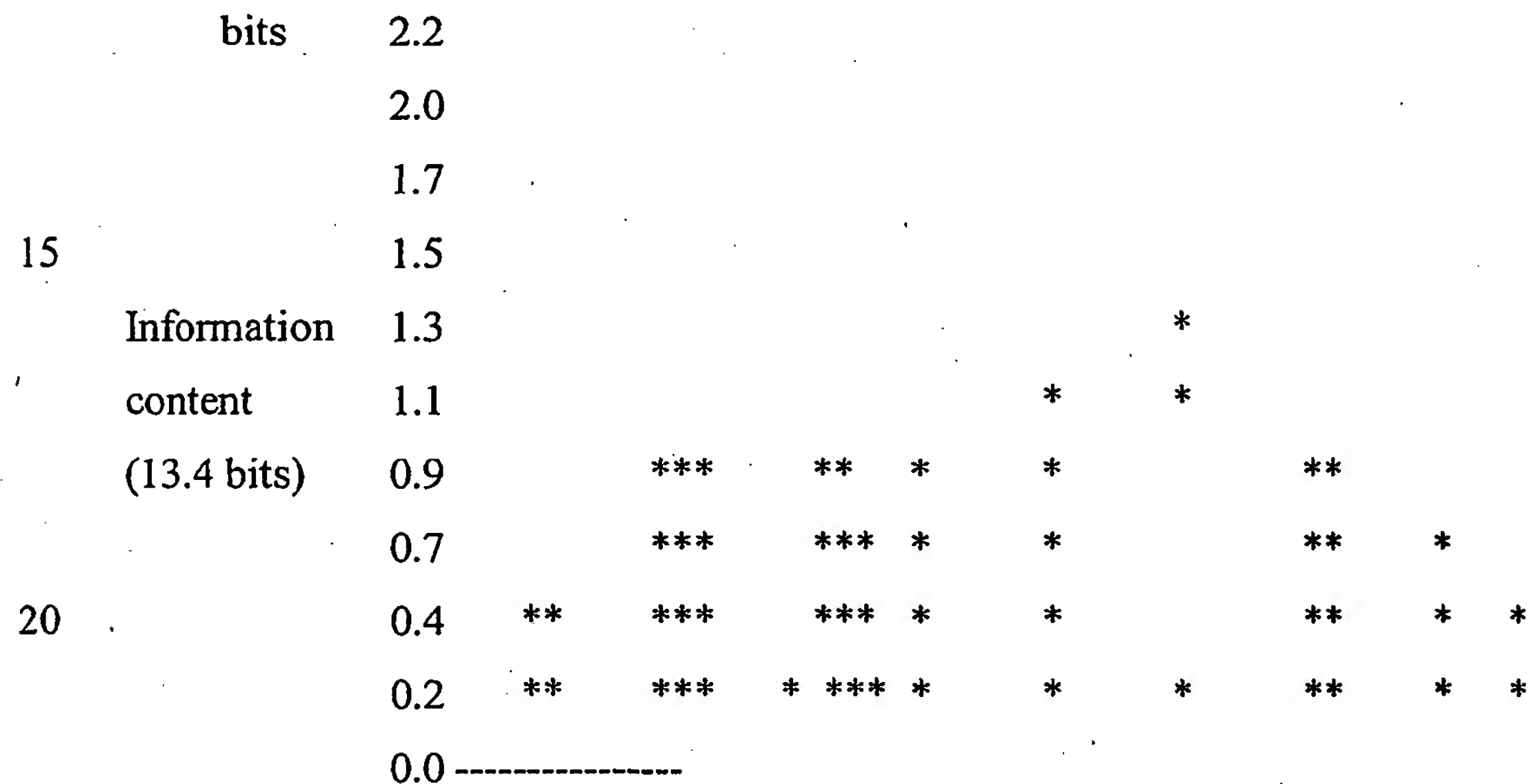
are generally enriched in As or Ts (A/T content in cR7R8 promoters is 70%) and regulatory *cis*-elements usually contain also Cs or Gs.

Motif 1 (CAACA/TA/TTGA/TC/T, SEQ ID NO:710) resembles the type I Myb binding site consensus (MBS;T/CAACT/GG), which is bound by animal and some plant Myb transcription factors (Yang & Klessig, 1996). The 3' portion of the motif 1 consensus allows overlap with binding sites of WRKY (TTTGACC/T; Eulgem et al., 2000) or TGA-bZIP transcription factors (TGACG; Schindler et al. 1992). Interestingly, a gene encoding a putative Myb-like transcription factor (gene identification number 13176) is upregulated along with cR7/R8 genes in an *RPP7/RPP8*-dependent, early and transient manner. The factor encoded by this gene may be a regulator of cR7/R8 genes. Motif 1 is particularly enriched in promoters of the originally defined cR7/R8 cluster (cut off = 75). This motif, which consists of six strictly defined positions and four positions allowing two base pairs each, should occur by random roughly once per 20,000 bp in each of both possible orientations (assuming a T/A content of 70% and a G/C content of 30%). In the 8,441 bp of cR7/R8 promoter sequences, the motif occurs 9 times (roughly 20 times the statistically expected frequency). Consistent with the statistical expectation, motif 1 occurs only two times within 15,873 bp from a set of control promoters of genes showing no defense related expression (data not shown).

In the extended set of cR7/R8 genes (cut off = 50), the enrichment of motif 1 is less striking. It occurs only 9 times within 16,519 bp in total and, more importantly, none of the promoters added to the set by lowering the cut off value contains this motif. Thus, if motif 1 is involved in the specific regulation of cR7/R8 genes it cannot alone be responsible for the particular expression features of these genes, and may rather be responsible for the more pronounced R7/R8-triggered expression of members of the originally defined cluster (cut off = 75).

Motif 2 (A/TTGGGNC/ANAA; SEQ ID NO:711) does not resemble any other known plant *cis*-element. The consensus sequence consists of six strictly defined positions, two positions with two alternatives and two positions with four alternatives; and, hence, should occur by random once per 10,000 bp. Motif 2 can be found 10 times within 8,441 bp of the promoters from the originally defined cR7/R8 (cut off = 75) and 14 times within 16,519 bp of the extended

cR7/R8 promoter set. Thus, its occurrence in cR7/R8 promoters is roughly 10 times the statistical expectation. Motif 2 is absent in the 15,873 bp of promoters of genes showing no defense related expression (data not shown). It is, however, also enriched in the promoters of previously defined clusters of defense related genes, such as the PR1 regulon (SAR genes) and SOMc3 (genes up regulated in Ws-0 after infection with avirulent Noco2; data not shown). The latter two clusters may also include genes sharing expression features with cR7/R8 genes. In addition to AlignAce, a motif 2-like sequence was also recognized by MEME. Within the extended set of cR7/R8 promoters, MEME found the following sequence stretch to be conserved:



25 Multilevel Consensus sequence T/C TTT G/C A/T/G C/T
CCAAG/A/CAA/GAC/A (SEQ ID NO:712)

The reverse complement of this consensus sequence is (positions with three alternatives were given as “N”) given below with motif 2 for comparison:

30 MEME motif: G/T T C/T T N T T G G G N G/C A A A A/C (SEQ ID NO:713)

Motif 2: T G G G N A N/C A A (SEQ ID NO:714)

MEME was run using the default settings of “advanced MEME” choosing the options “one motif per sequence”, “narrow motifs” and “additional strand: reverse complement”.

To confirm these results, Northern blots using probes of representatives of each cluster are performed. In addition, T-DNA lines are screened for knock out in Myb-like gene (AL031394.56_at) and selected members of cR7/R8, such as RNS1 (atu05206_s_at) or the gene encoding a calmodulin-like protein (identification number 13217_s_at). Also, yeast one hybrid screens are performed to clone transcription factors binding to motifs 1 and 2, or other identified motifs. Transgenic *Arabidopsis* plants carrying fusions of GUS with a representative promoter from cR7/R8 can be used to further evaluate the functional significance of motifs 1 and 2, and to perform a genetic screening for mutants impaired in regulation of cR7/R8 genes.

15 Genes Induced by *Peronospora* Infection in a Manner that Requires *RPP7* or *RPP8*

The data sets described above were employed to identify genes that were induced by *Peronospora* infection and were RPP7/8-dependent. All expression values less than 5 were set to 5. Using ratios calculated in Excel, and database sorting using Access, a subset of genes was identified whose expression depends on RPP7 or RPP8 using the following criteria:

Col Hiks1 12 hour/Col untreated > 2.5 AND Col Hiks1 12 hour > 30
AND Col Hiks1 12 hour/Col rpp7 Hiks1 12 hour > 2
OR
25 Col Hiks1 48 hour/Col untreated > 2.5 AND Col Hiks1 48 hour > 30
AND Col Hiks1 48 hour/Col rpp7 Hiks1 48 hour > 2
OR
Col RPP8 Emco5 12 hour/Col RPP8 no treatment > 2.5 AND Col RPP8
Emco5 12 hour > 30 AND Col RPP8 Emco5 12 hour/Col (rpp8) Emco5
30 12 hour > 2
OR
Col RPP8 Emco5 48 hour/Col RPP8 no treatment AND Col RPP8
Emco5 48 hour > 30 AND Col RPP8 Emco5 48 hour/Col (rpp8) Emco5
48 hour > 2

This yielded 217 probe sets ("RPP7 or 8") which correspond to sequences, the expression of which were increased by at least 2.5 fold and were *RPP7*- or *RPP8*-dependent (Table 6).

5

Table 6

ProbeSet	Description
12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]
12091_at (AC004450.116_AT)	gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]
12240_at (AL078579.130_AT)	emb CAB43974.1 (AL078579) putative protein [Arabidopsis thaliana]
12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]
12341_s_at (AL021637.176_S_AT)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
12360_at (AL022347.131_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
12500_s_at (AF081067.3_S_AT)	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
12521_at (AF049236.28_AT)	gb AAC14413.1 (AF049236) unknown [Arabidopsis thaliana]
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
12556_at (AL079344.155_AT)	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]
12630_at (AF024504.13_AT)	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]

12777_i_at (AC006577.16_I_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12778_r_at (AC006577.16_R_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12779_f_at (AC006577.16_F_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
12892_g_at (ATACS6_G_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
12905_s_at (ATERF2_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
12908_s_at (ATERF5_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
12916_s_at (ATHCOR1_S_AT)	gb AAC13947.1 (AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]
12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1 (X96600) pathogenesis-related protein 1 [Arabidopsis thaliana]
12989_s_at (AC004077.149_S_AT)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
13067_s_at (AC003114.16_S_AT)	gb AAC24083.1 (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592, gb T13956, gb T43869 come from from this gene. [Arabidopsis thaliana]

13154_s_at (AC002333.210_S_AT)	gb AAB64047.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]
13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13198_i_at (ATTS0190_I_AT)	emb CAA16892.1 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
13215_s_at (CAFFEROYLCOAMETHYLTRANS_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13217_s_at (CALMODULINLIKE_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
13435_at (AF003102.3_AT)	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ -exchanging protein [Arabidopsis thaliana]
13631_at (AC002387.185_AT)	gb AAB82634.1 (AC002387) putative transketolase precursor [Arabidopsis thaliana]
13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]
13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
13697_at (NI16_AT)	No hits found.

13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana]
13818_s_at (AC006218.175_S_AT)	gb AAD15433.1 (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]
13880_s_at (AL049480.183_S_AT)	emb CAB39611.1 (AL049480) possible apospory-associated like protein [Arabidopsis thaliana]
13966_at (AL022023.172_AT)	emb CAA17775.1 (AL022023) putative protein [Arabidopsis thaliana]
14083_at (AC005662.56_AT)	gb AAC78535.1 (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]
14096_at (AC002291.12_AT)	No hits found. emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]
14110_i_at (AL035528.279_I_AT)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]
14111_s_at (AL035528.279_S_AT)	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
14116_at (AF077407.30_AT)	
14141_at (NOVARTIS31_AT)	No hits found less than or equal to 1e-15. dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
14145_at (NOVARTIS35_AT)	
14146_at (NOVARTIS36_AT)	gb AAD25550.1 AC005850_7 (AC005850) Hypothetical protein [Arabidopsis thaliana]
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
14201_at (NOVARTIS73_AT)	No hits found less than or equal to 1e-15.
14202_at (NOVARTIS73_RC_AT)	No hits found less than or equal to 1e-15.
14223_at (NOVARTIS9_AT)	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
14232_at (NOVARTIS95_AT)	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]

14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb A1100027 come from this gene.
14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
14254_s_at (PAL1-MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14256_f_at (PAL1-INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [Arabidopsis thaliana]
14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]
14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [Arabidopsis thaliana]
14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [Arabidopsis thaliana]
14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
14638_s_at (PRXCB_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
14673_s_at (TSB2_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
14682_i_at (WT1012A_RC_I_AT)	No hits found.
14691_at (WT1096_AT)	No hits found.

14704_s_at (WT768_RC_S_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
14709_at (WT788_AT)	No hits found less than or equal to 1e-15.
14763_at (X86958.1_AT)	emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
14838_s_at (M96073.6_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]
15161_s_at (ATU90522_S_AT)	gb AAB53975.1 (U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
15523_s_at (AL078637.213_S_AT)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]
15532_r_at (AL078637.191_R_AT)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]
15616_s_at (ATHPRO25A_S_AT)	emb CAA08794.1 (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
15629_s_at (AB003280_S_AT)	dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
15641_s_at (AF117063_S_AT)	gb AAD10829.1 (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]
15665_s_at (AF022658_S_AT)	gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]
15778_at (X98676.2_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15779_g_at (X98676.2_G_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15846_at (AC006067.63_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]

15847_g_at (AC006067.63_G_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
15859_at (AC006587.164_AT)	gb AAD21491.1 (AC006587) unknown protein [Arabidopsis thaliana]
15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
15978_at (X68592.6_AT)	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
16053_i_at (Y14251.4_I_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]
16061_s_at (AB004796_S_AT)	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana]
16083_s_at (AF153283_S_AT)	gb AAD34615.1 AF153283_1 (AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
16150_s_at (ATHPEAR_S_AT)	emb CAB41718.1 (AL049730) pEARLI 1 [Arabidopsis thaliana]
16232_s_at (AL080252.77_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana]
16257_at (AC004138.105_AT)	gb AAC32915.1 (AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]
16298_at (AL021890.71_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]
16299_at (AL024486.185_AT)	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]
16357_at (AF149413.38_AT)	gb AAD40144.1 AF149413_25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]
16360_at (AL031187.126_AT)	emb CAA20203.1 (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
16365_at (AC003974.136_AT)	gb AAC04495.1 (AC003974) putative disease resistance protein [Arabidopsis thaliana]
16522_at (X77500.2_AT)	emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]
16536_s_at (AB008107_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]
16609_s_at (AB008104_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
16817_s_at (AL096882.91_S_AT)	emb CAB51412.1 (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]
16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
16995_at (AC002391.188_AT)	gb AAB87114.1 (AC002391) unknown protein [Arabidopsis thaliana]
17008_at (AC006585.212_AT)	gb AAD23027.1 AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
17014_s_at (ATU05206_S_AT)	gb AAC48925.1 (U05206) ribonuclease [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]
17068_s_at (ATHRLPKA_S_AT)	gb AAA32857.1 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
17097_s_at (ATU66345_S_AT)	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
17278_at (AC000107.5_AT)	gb AAD36959.1 AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
17413_s_at (AJ006961.4_S_AT)	emb CAA67551.1 (X99097) peroxidase [Arabidopsis thaliana]
17464_at (AC000132.72_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475, gb ATTS4362 come from this gene. [Arabidopsis thaliana]
17485_s_at (Z97340.345_S_AT)	emb CAB10405.1 (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]

17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
17499_s_at (AF107726_S_AT)	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
17500_s_at (ATHCALLGA_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
17511_s_at (AF067605_S_AT)	gb AAB71482.1 (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
17522_s_at (D78606_S_AT)	dbj BAA28538.1 (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
17544_s_at (ATU40856_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
17653_at (AL035679.144_AT)	emb CAB38823.1 (AL035679) putative protein [Arabidopsis thaliana]
17744_s_at (AC004684.168_S_AT)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
17775_at (AC004392.2_AT)	gb AAC28500.1 (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
17840_s_at (AC002333.223_S_AT)	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
17843_s_at (AC002391.150_S_AT)	gb AAB87109.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
17899_at (Z97339.197_AT)	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]
17930_s_at (AJ006960.4_S_AT)	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]
18012_s_at (AJ002295_S_AT)	emb CAB59428.1 (AJ002295) inositol-1,4,5-trisphosphate 5-Phosphatase [Arabidopsis thaliana]
18022_at (AJ010971_AT)	emb CAB52675.1 (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
18054_at (AJ238846_AT)	emb CAB54517.1 (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18224_s_at (AL021890.57_S_AT)	emb CAA17150.1 (AL021890) putative protein [Arabidopsis thaliana]
18551_at (AC002391.163_AT)	gb AAB87112.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
18567_at (AC004411.25_AT)	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

18590_at (AJ222713.4_AT)	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]
18591_at (X74756.2_AT)	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana] gb AAC72125.1 (AC005278) ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]
18625_at (AC005278.22_AT)	gb AAF26754.1 AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
18716_at (X91916_AT)	gb AAC33239.1 (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
18844_at (AC005315.131_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18909_s_at (AF055848.2_S_AT)	gb AAC16927.1 (AC002338) putative laccase [Arabidopsis thaliana]
18920_at (AC002338.11_AT)	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
18946_at (Y11788.1_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18969_g_at (AF163823.4_G_AT)	emb CAB41722.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
18983_s_at (AL049730.104_S_AT)	emb CAA65053.1 (X95738) proline transporter 2 [Arabidopsis thaliana]
19158_at (X95738.2_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
19171_at (AC002335.160_AT)	emb CAA68191.1 (X99923) male sterility 2-like protein [Arabidopsis thaliana]
19177_at (X99923.1_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]
19182_at (AL031804.245_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
19229_at (AC003027.39_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
19247_at (AF071527.44_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
19415_at (AL080253.32_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana]
19594_i_at (X98321.2_I_AT)	

19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
19664_at (AL050351.172_AT)	emb CAB43638.1 (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
19672_at (AC005687.19_AT)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]
19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]
19914_at (AC005727.175_AT)	gb AAC79593.1 (AC005727) unknown protein [Arabidopsis thaliana]
19951_at (AC005395.47_AT)	gb AAC42241.1 (AC005395) unknown protein [Arabidopsis thaliana]
19982_at (AC002986.28_AT)	gb AAC17040.1 (AC002986) Similarity to A. thaliana gene product F21M12.20, gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
20223_at (AL022347.145_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
20232_s_at (AL022347.12_S_AT)	emb CAA18460.1 (AL022347) protein kinase-like protein [Arabidopsis thaliana]
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
20269_at (AC002387.237_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate

	synthase alpha subunit [Arabidopsis thaliana]
20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
20365_s_at (AC005850.19_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]
20368_at (AC005314.38_AT)	gb AAC36163.1 (AC005314) putative serpin [Arabidopsis thaliana]
20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]
20429_s_at (Z97336.167_S_AT)	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
20620_g_at (AC005896.161_G_AT)	gb AAC98070.1 (AC005896) putative C2H2- type zinc finger protein [Arabidopsis thaliana]
20625_at (AL049658.102_AT)	emb CAB41131.1 (AL049658) hypothetical protein [Arabidopsis thaliana]

The functions of RPP7 and RPP8 are independent of *PAD4*, *NDR1*, *NahG*, *COI1*, and *EDS1*. Consequently, it is unlikely that genes whose expression is reduced in *pad4* or *NahG* backgrounds are important for RPP7- or RPP8- mediated resistance. Although data from *Peronospora* infection of *pad4* or *nahG* plants was not available, data from *Pseudomonas syringae* (ES4326) infection of *pad4* and *NahG* plants was available and employed to determine which genes depended on *PAD4* or were interfered with by *NahG*. Resistance to *P. syringae* mediated by *RPS2* requires *NDR1* function. Genes whose expression requires *RPS2* are less likely to be important for RPP7 or RPP8 mediated resistance than genes whose expression is independent of *RPS2*. Gene expression data was available for wild-type plants infected with *Pseudomonas syringae* pv. tomato DC3000 *avrRpt2*, and *rps2* mutant plants infected with *Pseudomonas syringae* pv. tomato DC3000 *avrRpt2*, 6 hours after infection. *EDM1* is required for resistance mediated by RPP7. Thus, genes whose expression requires *EDM1* are likely to be important for RPP7-mediated resistance. Gene expression data was available for an *edm1* mutant (see above).

The data from the 7 additional data sets (Col Psm ES4326 30 hour; Col Mock 30 hour; Col *NahG* Psm ES4226 30 hour; Col *pad4* Psm ES4326 30 hour; Col water control; Col DC3000 *avrRpt2* and *rps2* DC3000 *avrPrt2* was added to the 217 probe sets in "RPP7 or 8". The following sets were identified:

edm1:

Col edm1 Hiks1 12 hour/Col Hiks1 12 hour < 0.5 OR Col edm1 Hiks1 48 hour/Col Hiks1 48 hour < 0.5.

rps2:

5 Col DC3000 *avrRpt2* 6 hour/Col water control > 2 AND *rps2* DC3000 *avrRpt2* 6 hour/Col DC3000 *avrRpt2* 6 hour < 0.5.

pad4 or NahG:

10 Col Psm ES4326 30 hour/Col Mock 30 hour > 2 AND Col pad4 Psm ES4326 30 hour/Col Psm ES4326 30 hour < 0.5.
OR
Col Psm ES4326 30 hour/Col Mock 30 hour > 2 AND Col NahG Psm ES4326 30 hour/Col Psm ES4326 30 hour < 0.5.

15 There are 8 possible combinations of these three sets. Access was used to divide the 217 probe sets into 8 sets, numbered 2-9 (considering the whole set of 217 probe sets as set 1) as shown in Tables 7 and 8:

Table 7

20	<u>Set</u>	<u>Content</u>	<u>Number of probe</u>
	<u>sets</u>		
	2	RPP7 or 8 not edm1 not rps2 not pad4 o rNahG	62 probe sets
	3	edm1 not rps2 not pad4 or NahG	50 probe sets
	4	rps2 not edm1 not pad4 or NahG	14 probe sets
25	5	pad4 or NahG not edm1 not rps2	21 probe sets
	6	edm1 and rps2 not pad4 or NahG	23 probe sets
	7	edm1 and pad4 or NahG not rps2	25 probe sets
	8	rps2 and pad4 or NahG not edm1	8 probe sets
	9	edm1 and rps2 and pad4 or NahG	<u>14 probe sets</u>
30	Total		217 probe sets

Table 8

2 RPP7 or 8 not edm1 not rps2
not pad4orNahG

ProbeSet	Description
12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]
12240_at (AL078579.130_AT)	emb CAB43974.1 (AL078579) putative protein [Arabidopsis thaliana]
12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
12556_at (AL079344.155_AT)	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]
12777_i_at (AC006577.16_I_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12779_f_at (AC006577.16_F_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
12908_s_at (ATERF5_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1 (X96600) pathogenesis-related protein 1 [Arabidopsis thaliana]
13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]
13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
13880_s_at (AL049480.183_S_AT)	emb CAB39611.1 (AL049480) possible apospory-associated like protein [Arabidopsis thaliana]
13966_at (AL022023.172_AT)	emb CAA17775.1 (AL022023) putative protein [Arabidopsis thaliana]
14111_s_at (AL035528.279_S_AT)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]

14145_at (NOVARTIS35_AT)	dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
14256_f_at (PAL1- INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [Arabidopsis thaliana]
14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]
14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [Arabidopsis thaliana]
14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [Arabidopsis thaliana]
15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
15523_s_at (AL078637.213_S_AT)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]
16083_s_at (AF153283_S_AT)	gb AAD34615.1 AF153283_1 (AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]
16257_at (AC004138.105_AT)	gb AAC32915.1 (AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]
16298_at (AL021890.71_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]
16299_at (AL024486.185_AT)	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]
16522_at (X77500.2_AT)	emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]
16536_s_at (AB008107_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]

17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
17464_at (AC000132.72_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475, gb ATTS4362 come from this gene. [Arabidopsis thaliana]
17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18591_at (X74756.2_AT)	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana]
18625_at (AC005278.22_AT)	gb AAC72125.1 (AC005278) ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]
18844_at (AC005315.131_AT)	gb AAC33239.1 (AC005315) putative ligand- gated ion channel protein [Arabidopsis thaliana]
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18909_s_at (AF055848.2_S_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18920_at (AC002338.11_AT)	gb AAC16927.1 (AC002338) putative laccase [Arabidopsis thaliana]
18983_s_at (AL049730.104_S_AT)	emb CAB41722.1 (AL049730) pEARLI 1- like protein [Arabidopsis thaliana]
19158_at (X95738.2_AT)	emb CAA65053.1 (X95738) proline transporter 2 [Arabidopsis thaliana]
19229_at (AC003027.39_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
19415_at (AL080253.32_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
19594_i_at (X98321.2_I_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana]
19664_at (AL050351.172_AT)	emb CAB43638.1 (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

19982_at (AC002986.28_AT)	gb AAC17040.1 (AC002986) Similarity to A. thaliana gene product F21M12.20, gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana]
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
20368_at (AC005314.38_AT)	gb AAC36163.1 (AC005314) putative serpin [Arabidopsis thaliana]
20620_g_at (AC005896.161_G_AT)	gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]

Duplicates

12777 and 12779 (lipase)

12889 and 20291 (ASA1)

12908 and 16536 (ERF5)

17464 and 19982 (RLK5)

18216 and 18217 (T22C5.18)

18908 and 18909 (subtilisin-like protease)

20238 and 20239 (beta-fructofuranosidase)

3 edm1 without rps2 without pad4orNahG

ProbeSet	Description
12091_at (AC004450.116_AT)	gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]

	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase
12500_s_at (AF081067.3_S_AT)	[Arabidopsis thaliana]
	gb AAC14413.1 (AF049236) unknown
12521_at (AF049236.28_AT)	[Arabidopsis thaliana]
	emb CAA57944.1 (X82624) SRG2At
12574_at (X82624.2_AT)	[Arabidopsis thaliana]
	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12778_r_at (AC006577.16_R_AT)	
	gb AAC63850.1 (U73786) ACC synthase
12891_at (ATACS6_AT)	[Arabidopsis thaliana]
	gb AAC63850.1 (U73786) ACC synthase
12892_g_at (ATACS6_G_AT)	[Arabidopsis thaliana]
	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2
12905_s_at (ATERF2_S_AT)	[Arabidopsis thaliana]
	gb AAC13947.1 (AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]
12916_s_at (ATHCOR1_S_AT)	
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
	emb CAA16892.1 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
13198_i_at (ATTS0190_I_AT)	
	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
13435_at (AF003102.3_AT)	
	gb AAB82634.1 (AC002387) putative transketolase precursor [Arabidopsis thaliana]
13631_at (AC002387.185_AT)	
14096_at (AC002291.12_AT)	No hits found.
	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
14223_at (NOVARTIS9_AT)	
	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]
14232_at (NOVARTIS95_AT)	
14254_s_at (PAL1-MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
14614_at (AC004165.66_AT)	
14691_at (WT1096_AT)	No hits found.
	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase
14838_s_at (M96073.6_S_AT)	[Arabidopsis thaliana]
	gb AAB53975.1 (U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
15161_s_at (ATU90522_S_AT)	

15532_r_at (AL078637.191_R_AT)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana] dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
15629_s_at (AB003280_S_AT)	gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]
15665_s_at (AF022658_S_AT)	
16232_s_at (AL080252.77_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana] dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
16609_s_at (AB008104_S_AT)	
16817_s_at (AL096882.91_S_AT)	emb CAB51412.1 (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana] gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
16981_s_at (U35829.2_S_AT)	gb AAD23027.1 AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
17008_at (AC006585.212_AT)	gb AAC48925.1 (U05206) ribonuclease [Arabidopsis thaliana]
17014_s_at (ATU05206_S_AT)	
17500_s_at (ATHCALLGA_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana] dbj BAA28538.1 (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
17522_s_at (D78606_S_AT)	emb CAB38823.1 (AL035679) putative protein [Arabidopsis thaliana]
17653_at (AL035679.144_AT)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
17744_s_at (AC004684.168_S_AT)	gb AAB87109.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
17843_s_at (AC002391.150_S_AT)	emb CAB52675.1 (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
18022_at (AJ010971_AT)	gb AAB87112.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
18551_at (AC002391.163_AT)	gb AAF26754.1 AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
18716_at (X91916_AT)	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
18946_at (Y11788.1_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
19171_at (AC002335.160_AT)	emb CAA68191.1 (X99923) male sterility 2-like protein [Arabidopsis thaliana]
19177_at (X99923.1_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]
19182_at (AL031804.245_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	

19672_at (AC005687.19_AT)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]
19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
20232_s_at (AL022347.12_S_AT)	emb CAA18460.1 (AL022347) protein kinase-like protein [Arabidopsis thaliana]
20429_s_at (Z97336.167_S_AT)	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
20641_at (X91919.1_AT)	emb CAA63012.1 (X91919) LEA76 homologue type1 [Arabidopsis thaliana] Arabidopsis thaliana. ESTs gb N97082, gb Z27056 and gb Z29902 come from this gene.

Duplicates

12905 and 16609 (ERF2)

13188 and 16981 (thioredoxin h)

12891 and 12892 (ACC
synthase)

14838 (phosphoribosyl
anthranilate transferase) has a
duplicate in set 2 (14620).
Counted in set 2

14254 (PAL1) has a duplicate in
set 2 (14256) Counted in set 2.

12778 (lipase) has duplicates in
set 2 (12777 and 12779) Counted
in set 2.

4 rps2 without edm1 without pad4orNahG

ProbeSet

Description

12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
12360_at (AL022347.131_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
13154_s_at (AC002333.210_S_AT)	gb AAB64047.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]
14141_at (NOVARTIS31_AT)	No hits found less than or equal to 1e-15.

15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
16053_i_at (Y14251.4_I_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]
16995_at (AC002391.188_AT)	gb AAB87114.1 (AC002391) unknown protein [Arabidopsis thaliana]
18054_at (AJ238846_AT)	emb CAB54517.1 (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
18224_s_at (AL021890.57_S_AT)	emb CAA17150.1 (AL021890) putative protein [Arabidopsis thaliana]
19951_at (AC005395.47_AT)	gb AAC42241.1 (AC005395) unknown protein [Arabidopsis thaliana]
20223_at (AL022347.145_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
20365_s_at (AC005850.19_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]

Duplicates

12360 and 20223 (serine threonine kinase)
13685 and 20365 (similar to Mlo)

5 pad4orNahG without rps2 without edm1

ProbeSet

	Description
12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]
13067_s_at (AC003114.16_S_AT)	gb AAC24083.1 (AC003114) Match to calreticulin (AtCTRL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana]

14146_at (NOVARTIS36_AT)	gb AAD25550.1 AC005850_7 (AC005850) Hypothetical protein [Arabidopsis thaliana]
15778_at (X98676.2_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15779_g_at (X98676.2_G_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15859_at (AC006587.164_AT)	gb AAD21491.1 (AC006587) unknown protein [Arabidopsis thaliana]
16360_at (AL031187.126_AT)	emb CAA20203.1 (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3- glucanase 2 (BG2) [Arabidopsis thaliana]
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]
17097_s_at (ATU66345_S_AT)	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]
17278_at (AC000107.5_AT)	gb AAD36959.1 AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
17485_s_at (Z97340.345_S_AT)	emb CAB10405.1 (Z97340) beta-1, 3- glucanase class I precursor [Arabidopsis thaliana]
19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]
20625_at (AL049658.102_AT)	emb CAB41131.1 (AL049658) hypothetical protein [Arabidopsis thaliana]

Duplicates:

15778 and 15779 (zinc finger
protein)

**6 edm1 and rps2 without
pad4orNahG**

ProbeSet

ProbeSet	Description
12630_at (AF024504.13_AT)	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592,gb T13956,gb T43869 come from from this gene. [Arabidopsis thaliana]
13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13189_s_at (ATTHIRED4 S AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]

13215_s_at (CAFFEROYLCOAMETHYLTRANS_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13217_s_at (CALMODULINLIKE_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
14083_at (AC005662.56_AT)	gb AAC78535.1 (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]
14116_at (AF077407.30_AT)	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana] gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
14248_at (PAD3_AT)	No hits found.
14682_i_at (WT1012A_RC_I_AT)	
15641_s_at (AF117063_S_AT)	gb AAD10829.1 (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]
15978_at (X68592.6_AT)	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
16061_s_at (AB004796_S_AT)	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana]
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
17511_s_at (AF067605_S_AT)	gb AAB71482.1 (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
17899_at (Z97339.197_AT)	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]
18012_s_at (AJ002295_S_AT)	emb CAB59428.1 (AJ002295) inositol-1,4,5-trisphosphate 5-Phosphatase [Arabidopsis thaliana]

19640_at (AC004561.78_AT) gb|AAC95192.1| (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Duplicates

13187 and 13189 (thioredoxin h)
There are two duplicates of this in set 3 (13188 and 16981) Count it in set 3.

13215 and 16649 (putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase)

13285 and 16091 (heat shock protein 83)

13217 (calmodulin-like) has a duplicate in set 3 (17500). Count in set 3

16105 (hsf4) has a duplicate in set 4 (13273) Count in set 4

7 pad4orNahG and edm1 without rps2

ProbeSet

Description

14110_i_at (AL035528.279_I_AT)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
14673_s_at (TSB2_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
14704_s_at (WT768_RC_S_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
14709_at (WT788_AT)	No hits found less than or equal to 1e-15.
14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
15616_s_at (ATHPRO25A_S_AT)	emb CAA08794.1 (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

15846_at (AC006067.63_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
15847_g_at (AC006067.63_G_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
16150_s_at (ATHPEAR_S_AT)	emb CAB41718.1 (AL049730) pEARLI 1 [Arabidopsis thaliana]
16357_at (AF149413.38_AT)	gb AAD40144.1 AF149413_25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]
16365_at (AC003974.136_AT)	gb AAC04495.1 (AC003974) putative disease resistance protein [Arabidopsis thaliana]
17068_s_at (ATHRLPKA_S_AT)	gb AAA32857.1 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
17413_s_at (AJ006961.4_S_AT)	emb CAA67551.1 (X99097) peroxidase [Arabidopsis thaliana]
17499_s_at (AF107726_S_AT)	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
17775_at (AC004392.2_AT)	gb AAC28500.1 (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
18590_at (AJ222713.4_AT)	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]
18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18969_g_at (AF163823.4_G_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]

Duplicates

14249 and 14250 (PAD4)

14704 and 15846 and 15847
(unknown protein)

18968 and 18969
(endoxyloglucan transferase)

20287 and 20288 (class IV chitinase)
 14110 (putative disease-resistance gene) is an incomplete probe set with very low signal. It has a duplicate (14111) in set 2.
 Count in set 2.
 14672 (trp synthase alpha) has a duplicate in set 2 (17487)
 Counted in set 2.

8 rps2 and pad4orNahG without edm1

ProbeSet	Description
13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ -exchanging protein [Arabidopsis thaliana]
13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
13818_s_at (AC006218.175_S_AT)	gb AAD15433.1 (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]
14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
17930_s_at (AJ006960.4_S_AT)	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]
19914_at (AC005727.175_AT)	gb AAC79593.1 (AC005727) unknown protein [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]

Duplicates:

14635 and 17128 (PR-1)

9 edm1 and rps2 and pad4orNahG

ProbeSet	Description
12341_s_at (AL021637.176_S_AT)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]

12989_s_at (AC004077.149_S_AT) 13697_at (NI16_AT)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana] No hits found.
14201_at (NOVARTIS73_AT) 14202_at (NOVARTIS73_RC_AT)	No hits found less than or equal to 1e-15. No hits found less than or equal to 1e-15.
14609_at (AC002340.147_AT) 14638_s_at (PRXCB_S_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana] emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
14763_at (X86958.1_AT)	emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana] gb AAC49282.1 (U40856) AIG1
17544_s_at (ATU40856_S_AT) 17840_s_at (AC002333.223_S_AT)	[Arabidopsis thaliana] gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
18567_at (AC004411.25_AT)	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
20269_at (AC002387.237_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]

Duplicates

12879 and 17544 (AIG1)

14201 and 14202 (Novartis 73)

14638 (peroxidase) has a
duplicate in set 7 (15970).

Counted in set 7.

The first set (set 2 above) do not require *EDM1* and are not affected by *rps2*, *pad4* or *NahG*. These genes are less likely to be important for resistance mediated by *RPP7* and *RPP8* than the genes in the second set (set 3 above). The

5 genes in the second set require *EDM1* but are not affected by *rps2*, *pad4* or *NahG*. These genes are more likely to be important for resistance mediated by *RPP7* and *RPP8*. The genes in the third set (set 4 above) are affected by *rps2*, do not require *EDM1*, and are not affected by *pad4* or *NahG*. The genes in the

10 fourth (set 5 above), seventh (set 8 above) and eight (set 9 above) sets include genes that are affected by *pad4* or *NahG*, and so are less likely to be important for resistance mediated by *RPP7* and *RPP8*. The genes in the sixth set (set 7 above) require *RPP7* or *RPP8* for increased expression after infection by

Peronospora and are affected by *rps2*. These genes are also less likely to be important for resistance mediated by *RPP7* and *RPP8*.

Duplicates were identified by sorting "RPP7 or 8" by description, which put duplicated genes adjacent to one another. Most duplicates were in the same set, but there were nine cases of duplicates that had one probe set in one set, and another in another set. Examination of the data revealed that in these cases, the expression values were close to the cut-offs used to define the various sets. If one copy met the criteria, e.g., for *rps2*-dependent, but the other copy did not, the gene was classified as not *rps2*-dependent. Duplicates are noted. One hundred eighty four unique genes remained (SEQ ID NOs:1-211 and 792, Table 9 and Table 10).

Table 9

SEQ ID NO	ProbeSet	Description
1	12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]
2	12091_at (AC004450.116_AT)	gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
3	12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]
4	12240_at (AL078579.130_AT)	emb CAB43974.1 (AL078579) putative protein [Arabidopsis thaliana]
5	12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
6	12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
7	12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]
8	12341_s_at (AL021637.176_S_AT)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
9	12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
10	12360_at (AL022347.131_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
11	20223_at (AL022347.145_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]

- 12 12500_s_at (AF081067.3_S_AT) gb|AAC32192.1| (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
- 13 12521_at (AF049236.28_AT) gb|AAC14413.1| (AF049236) unknown [Arabidopsis thaliana]
- 14 12538_at (AF033205.2_AT) gb|AAC02973.1| (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
- 15 12556_at (AL079344.155_AT) emb|CAB45330.1| (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
- 16 12574_at (X82624.2_AT) emb|CAA57944.1| (X82624) SRG2At [Arabidopsis thaliana]
- 17 12630_at (AF024504.13_AT) gb|AAF18681.1|AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
- 18 12642_at (AC006920.138_AT) gb|AAD22285.1|AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]
- 19 12777_i_at (AC006577.16_I_AT) gb|AAD25772.1|AC006577_8 (AC006577) Belongs to the PF|00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb|T44453, gb|T04815, gb|T45993, gb|R30138, gb|AI099570 and gb|T22281 come from this gene. [Arabidopsis thaliana]
- 20 12778_r_at (AC006577.16_R_AT) gb|AAD25772.1|AC006577_8 (AC006577) Belongs to the PF|00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb|T44453, gb|T04815, gb|T45993, gb|R30138, gb|AI099570 and gb|T22281 come from this gene. [Arabidopsis thaliana]
- 21 12779_f_at (AC006577.16_F_AT) gb|AAD25772.1|AC006577_8 (AC006577) Belongs to the PF|00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb|T44453, gb|T04815, gb|T45993, gb|R30138, gb|AI099570 and gb|T22281 come from this gene. [Arabidopsis thaliana]
- 22 12879_s_at (AIG1_S_AT) gb|AAC49282.1| (U40856) AIG1 [Arabidopsis thaliana]
- 23 17744_s_at (AC004684.168_S_AT) gb|AAC23646.1| (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
- 24 12889_s_at (ASA1_S_AT) gb|AAA32738.1| (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
- 25 20291_s_at (M92353.4_S_AT) gb|AAA32738.1| (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]

26	12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
27	12892_g_at (ATACS6_G_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
28	12905_s_at (ATERF2_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
29	16609_s_at (AB008104_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
30	12908_s_at (ATERF5_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
31	16536_s_at (AB008107_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
32	12916_s_at (ATHCOR1_S_AT)	gb AAC13947.1 (AF021244) coronatine- induced protein 1 [Arabidopsis thaliana]
33	12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1 (X96600) pathogenesis- related protein 1 [Arabidopsis thaliana]
34	12989_s_at (AC004077.149_S_A T)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
35	13067_s_at (AC003114.16_S_AT)	gb AAC24083.1 (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
36	13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
37	13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592, gb T13956, gb T43869 come from from this gene. [Arabidopsis thaliana]
38	13154_s_at (AC002333.210_S_A T)	gb AAB64047.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
39	13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]
40	13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
41	13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
42	13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
43	16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
44	13198_i_at (ATTTS0190_I_AT)	emb CAA16892.1 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

45	13215_s_at (CAFFEROYLCOAMETHYLTRANS_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
46	16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
47	13217_s_at (CALMODULINLIKE_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
48	17500_s_at (ATHCALLGA_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
49	13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
50	16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
51	13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
52	13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
53	16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
54	13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
	13435_at (AF003102.3_AT)	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
55	13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
56	13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ -exchanging protein [Arabidopsis thaliana]
57	13631_at (AC002387.185_AT)	gb AAB82634.1 (AC002387) putative transketolase precursor [Arabidopsis thaliana]
58	13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
59	13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]

		gb AAD25552.1 AC005850_9 (AC005850)
	20365_s_at	Highly Simlilar to Mlo proteins [Arabidopsis
60	(AC005850.19_S_AT)	thaliana]
61	13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
no cds	13697_at (NI16_AT)	No hits found.
	13751_at	gb AAF16751.1 AC010155_4 (AC010155)
62	(NOVARTIS127_AT)	F3M18.8 [Arabidopsis thaliana]
	13764_at	gb AAD39641.1 AC007591_6 (AC007591)
63	(NOVARTIS22_AT)	F9L1.6 [Arabidopsis thaliana]
	13818_s_at	gb AAD15433.1 (AC006218) putative
	(AC006218.175_S_A	aspartate aminotransferase [Arabidopsis
64	T)	thaliana]
	13880_s_at	emb CAB39611.1 (AL049480) possible
	(AL049480.183_S_A	apospory-associated like protein
65	T)	[Arabidopsis thaliana]
	13966_at	emb CAA17775.1 (AL022023) putative
66	(AL022023.172_AT)	protein [Arabidopsis thaliana]
		gb AAC78535.1 (AC005662) putative
	14083_at	embryo-abundant protein [Arabidopsis
67	(AC005662.56_AT)	thaliana]
	14096_at	
68	(AC002291.12_AT)	No hits found.
	14110_i_at	emb CAB36854.1 (AL035528) putative
	(AL035528.279_I_AT	disease resistance protein [Arabidopsis
69)	thaliana]
	14111_s_at	emb CAB36854.1 (AL035528) putative
	(AL035528.279_S_A	disease resistance protein [Arabidopsis
70	T)	thaliana]
		gb AAC26243.1 (AF077407) contains
		similarity to sugar transporters (Pfam:
	14116_at	sugar_tr.hmm, score: 395.39) [Arabidopsis
71	(AF077407.30_AT)	thaliana]
	14141_at	
72	(NOVARTIS31_AT)	No hits found less than or equal to 1e-15.
		dbj BAA22813.1 (D26015) CND41,
	14145_at	chloroplast nucleoid DNA binding protein
73	(NOVARTIS35_AT)	[Nicotiana tabacum]
	14146_at	gb AAD25550.1 AC005850_7 (AC005850)
74	(NOVARTIS36_AT)	Hypothetical protein [Arabidopsis thaliana]
	14148_at	gb AAF34713.1 AF224762_1 (AF224762)
75	(NOVARTIS38_AT)	SigA binding protein [Arabidopsis thaliana]
	14201_at	
76	(NOVARTIS73_AT)	No hits found less than or equal to 1e-15.
	14202_at	
	(NOVARTIS73_RC_	
77	AT)	No hits found less than or equal to 1e-15.
	14223_at	emb CAA19683.1 (AL024486) putative
78	(NOVARTIS9_AT)	protein [Arabidopsis thaliana]

79	14232_at (NOVARTIS95_AT)	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]
80	14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
81	14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
82	14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
83	14254_s_at (PAL1- MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
84	14256_f_at (PAL1- INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
85	14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [Arabidopsis thaliana]
86	14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
87	14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]
88	14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [Arabidopsis thaliana]
89	14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
90	14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
91	14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
92	14838_s_at (M96073.6_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
93	14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [Arabidopsis thaliana]
94	14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
95	17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
96	14638_s_at (PRXCB_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]

97	15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
98	14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
99	17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
100	14673_s_at (TSB2_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
101	14682_i_at (WT1012A_RC_I_AT)	No hits found.
102	14691_at (WT1096_AT)	No hits found.
103	14704_s_at (WT768_RC_S_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
104	15846_at (AC006067.63_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
105	15847_g_at (AC006067.63_G_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
106	14709_at (WT788_AT)	No hits found less than or equal to 1e-15. emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
107	14763_at (X86958.1_AT)	
108	14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
109	15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
110	15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]
111	15161_s_at (ATU90522_S_AT)	gb AAB53975.1 (U90522) lysine- ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
112	15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
113	15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
114	15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
115	15523_s_at (AL078637.213_S_A T)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]
116	15532_r_at (AL078637.191 R A	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]

T)

- 117 15616_s_at
(ATHPRO25A_S_AT) emb|CAA08794.1| (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
) dbj|BAA24440.1| (AB010407)
- 118 15629_s_at
(AB003280_S_AT) phosphoglycerate dehydrogenase
[Arabidopsis thaliana]
gb|AAD10829.1| (AF117063) putative
- 119 15641_s_at
(AF117063_S_AT) inositol polyphosphate 5-phosphatase At5P2
[Arabidopsis thaliana]
gb|AAB80922.1| (AF022658) putative c2h2
- 120; 682 15665_s_at
(AF022658_S_AT) zinc finger transcription factor [Arabidopsis thaliana]
- 121 15778_at
(X98676.2_AT) emb|CAA67234.1| (X98676) zinc finger protein [Arabidopsis thaliana]
- 122 15779_g_at
(X98676.2_G_AT) emb|CAA67234.1| (X98676) zinc finger protein [Arabidopsis thaliana]
- 123 15859_at
(AC006587.164_AT) gb|AAD15461.1| (AC006067) unknown protein [Arabidopsis thaliana]
- 124 15978_at
(X68592.6_AT) gb|AAD15461.1| (AC006067) unknown protein [Arabidopsis thaliana]
- 125 16053_i_at
(Y14251.4_I_AT) emb|CAA74639.1| (Y14251) glutathione S-transferase [Arabidopsis thaliana]
- 126 16061_s_at
(AB004796_S_AT) gb|AAB97145.1| (AF000977) MEK1 [Arabidopsis thaliana] thaliana
gb|AAD34615.1|AF153283_1 (AF153283)
- 127 16083_s_at
(AF153283_S_AT) putative progesterone-binding protein homolog [Arabidopsis thaliana]
- 128 16150_s_at
(ATHPEAR_S_AT) emb|CAB41718.1| (AL049730) pEARLI 1 [Arabidopsis thaliana]
- 129 16232_s_at
(AL080252.77_S_AT) emb|CAB45796.1| (AL080252) putative protein [Arabidopsis thaliana]
gb|AAC32915.1| (AC004138) putative
- 130 16257_at
(AC004138.105_AT) nucleoside triphosphatase [Arabidopsis thaliana]
- 131 16298_at
(AL021890.71_AT) emb|CAA17152.1| (AL021890) putative protein [Arabidopsis thaliana]
- 132 16299_at
(AL024486.185_AT) emb|CAA19705.1| (AL024486) putative protein [Arabidopsis thaliana]
gb|AAD40144.1|AF149413_25 (AF149413)
contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10)
- 133 16357_at
(AF149413.38_AT) [Arabidopsis thaliana]
emb|CAA20203.1| (AL031187) receptor-like
- 134 16360_at
(AL031187.126_AT) serine/threonine protein kinase ARK3 [Arabidopsis thaliana]

- 135 16365_at (AC003974.136_AT) gb|AAC04495.1| (AC003974) putative disease resistance protein [Arabidopsis thaliana]
- 136 16578_s_at (ATHRPRP1B_S_AT) emb|CAB68132.1| (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]
- 137 16817_s_at (AL096882.91_S_AT) emb|CAB51412.1| (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]
- 138 16914_s_at (AL049500.57_S_AT) emb|CAB39936.1| (AL049500) osmotin precursor [Arabidopsis thaliana]
- 139 16995_at (AC002391.188_AT) gb|AAB87114.1| (AC002391) unknown protein [Arabidopsis thaliana]
- 140 17008_at (AC006585.212_AT) gb|AAD23027.1|AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
- 141 17014_s_at (ATU05206_S_AT) gb|AAC48925.1| (U05206) ribonuclease [Arabidopsis thaliana]
- 142 17051_s_at (AF098947_S_AT) gb|AAD09952.1| (AF098947) CTF2B [Arabidopsis thaliana]
- 143 17068_s_at (ATHRLPKA_S_AT) gb|AAA32857.1| (M84658) receptor-like protein kinase [Arabidopsis thaliana]
- 144 17083_s_at (ATU18770_S_AT) gb|AAD25838.1|AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
- 145 17097_s_at (ATU66345_S_AT) gb|AAC49697.1| (U66345) calreticulin [Arabidopsis thaliana]
- 146 17278_at (AC000107.5_AT) gb|AAD36959.1|AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
- 147 17413_s_at (AJ006961.4_S_AT) emb|CAA67551.1| (X99097) peroxidase [Arabidopsis thaliana]
- 148 17464_at (AC000132.72_AT) gb|AAB60752.1| (AC000132) Similar to A. thaliana receptor-like protein kinase (gb|RLK5_ARATH). ESTs gb|ATTS0475,gb|ATTS4362 come from this gene. [Arabidopsis thaliana]
- 149 17485_s_at (Z97340.345_S_AT) emb|CAB10405.1| (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]
- 150 17499_s_at (AF107726_S_AT) gb|AAD19610.1| (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
- 151 17511_s_at (AF067605_S_AT) gb|AAB71482.1| (AC002294) similar to S-linalool synthase gp|U58314|1491939 [Arabidopsis thaliana]
- 152 17522_s_at (D78606_S_AT) dbj|BAA28538.1| (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
- 153 17544_s_at (ATU40856_S_AT) gb|AAC49282.1| (U40856) AIG1 [Arabidopsis thaliana]

- 154 17653_at (AL035679.144_AT) emb|CAB38823.1| (AL035679) putative protein [Arabidopsis thaliana]
gb|AAC28500.1| (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb|AF020814 from Pisum sativum. [Arabidopsis thaliana]
- 155 17775_at (AC004392.2_AT)
- 156 17840_s_at (AC002333.223_S_A T) gb|AAB64049.1| (AC002333) putative endochitinase [Arabidopsis thaliana]
- 157 17843_s_at (AC002391.150_S_A T) gb|AAB87109.1| (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
- 158 17899_at (Z97339.197_AT) emb|CAB10339.1| (Z97339) hypothetical protein [Arabidopsis thaliana]
- 159 17930_s_at (AJ006960.4_S_AT) emb|CAA07352.1| (AJ006960) peroxidase [Arabidopsis thaliana]
- 160 18012_s_at (AJ002295_S_AT) emb|CAB59428.1| (AJ002295) inositol-1,4,5-trisphosphate 5-Phosphatase [Arabidopsis thaliana]
- 161 18022_at (AJ010971_AT) emb|CAB52675.1| (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
- 162 18054_at (AJ238846_AT) emb|CAB54517.1| (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
- 163 18216_at (X95573.2_AT) gb|AAF24959.1|AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
- 164 18217_g_at (X95573.2_G_AT) gb|AAF24959.1|AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
- 165 18551_at (AC002391.163_AT) gb|AAB87112.1| (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
- 166 18567_at (AC004411.25_AT) gb|AAC34217.1| (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
- 167 18590_at (AJ222713.4_AT) emb|CAA10955.1| (AJ222713) unnamed protein product [Arabidopsis thaliana]
- 168; 665 18591_at (X74756.2_AT) emb|CAA52772.1| (X74756) ATAF2 [Arabidopsis thaliana]
- 169 18625_at (AC005278.22_AT) gb|AAC72125.1| (AC005278) ESTs gb|H36966, gb|R65511, gb|T42324 and gb|T20569 come from this gene. [Arabidopsis thaliana]
- 170 18716_at (X91916_AT) gb|AAF26754.1|AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
- 171 18844_at (AC005315.131_AT) gb|AAC33239.1| (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
- 172 18908_i_at (AF055848.2_I_AT) gb|AAC62611.1| (AF055848) subtilisin-like protease [Arabidopsis thaliana]

173	18909_s_at (AF055848.2_S_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
174	18946_at (Y11788.1_AT)	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
175	18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
176	18969_g_at (AF163823.4_G_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
177	18983_s_at (AL049730.104_S_A T)	emb CAB41722.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
178	19158_at (X95738.2_AT)	emb CAA65053.1 (X95738) proline transporter 2 [Arabidopsis thaliana]
179	19171_at (AC002335.160_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
180	19177_at (X99923.1_AT)	emb CAA68191.1 (X99923) male sterility 2-like protein [Arabidopsis thaliana]
181	19182_at (AL031804.245_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]
182	19229_at (AC003027.39_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
183	19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
184	19284_at (AC003028.196_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
185	19415_at (AL080253.32_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
186	19594_i_at (X98321.2_I_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana]
187	19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
188	19664_at (AL050351.172_AT)	emb CAB43638.1 (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
189	19672_at (AC005687.19_AT)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]
190	19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
191	19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
192	19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

193	19914_at (AC005727.175_AT)	gb AAC79593.1 (AC005727) unknown protein [Arabidopsis thaliana]
194	19951_at (AC005395.47_AT)	gb AAC42241.1 (AC005395) unknown protein [Arabidopsis thaliana]
195	19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
196	20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
197	20232_s_at (AL022347.12_S_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
198	20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
199	20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
200	20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
201	20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
202	20269_at (AC002387.237_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
203	20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
204	20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
205	20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
206	20368_at (AC005314.38_AT)	gb AAC36163.1 (AC005314) putative serpin [Arabidopsis thaliana]
207	20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]
208	20429_s_at (Z97336.167_S_AT)	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
209	20620_g_at (AC005896.161_G_A T)	gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
210	20625_at (AL049658.102_AT)	emb CAB41131.1 (AL049658) hypothetical protein [Arabidopsis thaliana]
211	20641_at (X91919.1_AT)	emb CAA63012.1 (X91919) LEA76 homologue type1 [Arabidopsis thaliana]
789	18224_s_at (AL021890.57_S_AT)	Arabidopsis thaliana. ESTs gb N97082, gb Z27056 and gb Z29902 come from this gene.
790	16522_at (X77500.2_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]
		emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]

		gb AAC17040.1 (AC002986) Similarity to
		A. thaliana gene product F21M12.20,
		gb AC000132. EST gb Z25651 comes from
		this gene. [Arabidopsis thaliana]
791	19982_at (AC002986.28_AT)	gb AAC16927.1 (AC002338) putative
367	18920_at (AC002338.11_AT)	laccase [Arabidopsis thaliana]
212	12324_i_at	AC007212
793	12345_at	L36246
213	12500_s_at	AF081067
214; 662	12505_s_at	AC005309
215	12608_i_at	S70188
216	12642_at	AC006920
217	12746_i_at	AL096882
218	12748_f_at	AL096882
219	12761_s_at	AC006577
220	12773_at	AC005727
221	12778_r_at	AC006577
222	12798_at	AC003028
223	12802_at	AL022373
	12842_s_at	No hits found less than or equal to 1e-15
224	12843_s_at	AC007195
	12845_s_at	AJ004810
225	12879_s_at	U40856
226	12891_at	U73786
227	12892_g_at	U73786
228; 658	12904_s_at	AB008103
229	12905_s_at	AB008104
230	12908_s_at	AB008107
231	12909_s_at	Z97343
232	12911_s_at	X84229
233	12916_s_at	AF021244
234	13138_at	AL096882
235	13177_at	AL049640
236	13178_at	U93215
237	13187_i_at	U35829
238	13189_s_at	U35829
239	13198_i_at	AL021749
240	13212_s_at	AL137080
241	13217_s_at	AL049862
242	13258_s_at	AC005309
243	13273_s_at	U68017
244	13284_s_at	AJ002551
245	13604_at	AC000104
246	13615_at	AC002332
247	13617_at	AC006592
248	13718_at	Z72152
249	13771_at	AC006593
250	13785_at	AC007087
251	14052_at	AC004122

252	14096_at	AC002291
253	14097_at	AC005309
254	14116_at	AF077407
255	14141_at	AC011437
256; 683	14148_at	AF224762
257	14196_at	AC012563
258	14201_at	AL163972
259	14219_at	AC068667
260	14223_at	AL024486
261	14248_at	AC007357
262	14250_r_at	AL050300
263	14595_at	AL022580
264	14608_at	AC007357
265	14614_at	AC004165
266	14621_at	AC004747
267	14627_i_at	X76609
268	14628_r_at	X76609
269	14635_s_at	AC005398
270	14636_s_at	AC013258
271	14643_s_at	AC006836
272	14672_s_at	U18993
273	14675_s_at	D85191
274	14691_at	AP002046
275	14704_s_at	AC006067
276	14706_r_at	AL137189
277	14709_at	AP002046
278	14711_s_at	AF085279
279	14731_s_at	AF014960
280	14784_at	AC005310
281	14951_at	AL049481
282	15057_at	AL035440
283	15085_s_at	AL031018
284	15105_s_at	Z14987
285	15116_f_at	AF121356
286	15125_f_at	D85190
287	15141_s_at	D85191
288	15145_s_at	D64155
289	15154_s_at	AL096860
290	15161_s_at	U90522
291	15178_s_at	U43489
292	15216_s_at	U75198
293	15431_at	AL030978
294	15496_at	AC006282
295	15523_s_at	AL078637
296	15593_s_at	U54561
297	15611_s_at	L22567
298	15616_s_at	AJ009696
299	15622_s_at	U43945

300	15629_s_at	AB010407
301	15665_s_at	AF022658
302	15680_s_at	D42061
303	15846_at	AC006067
304	15847_g_at	AC006067
305	15866_s_at	AC005770
306	15950_at	AC006429
307	15954_at	U72155
308	15978_at	X68592
309	16038_s_at	L04173
310	16063_s_at	AB008103
311	16105_s_at	U68017
312	16150_s_at	AL049730
313	16153_s_at	AC013258
314	16393_s_at	AC006436
315	16412_s_at	AL022603
316	16442_s_at	AJ002551
317	16504_s_at	Z97335
318	16510_at	AL034567
319	16536_s_at	AB008107
320	16539_s_at	Z97343
321	16569_s_at	L23968
322	16578_s_at	AL137080
323	16609_s_at	AB008104
324	16620_s_at	AF051338
325	16637_s_at	Z97336
326	16817_s_at	AL096882
327	16864_i_at	AL133248
328	16951_i_at	AC005662
329	16952_s_at	AC005662
330	16981_s_at	U35829
331	17014_s_at	U05206
332	17033_s_at	U83179
333	17054_s_at	AF134128
334	17073_s_at	AC006836
335	17119_s_at	AF132212
336	17123_s_at	AF106087
337	17128_s_at	AC005398
338	17187_at	AF128396
339; 669	17303_s_at	AC005499
340; 663	17379_at	AC018721
341	17386_at	AC006264
342	17413_s_at	X99097
343	17499_s_at	AF107726
344	17500_s_at	AL049862
345	17544_s_at	U40856
346	17567_at	AL162751
347	17886_at	AC004484

348	17899_at	Z97339
349	17917_s_at	AC004261
350	17961_at	AC007323
351	17963_at	AL049730
352	18003_at	AF188334
	18064_r_at	No hits found
	18069_at	No hits found
	18070_r_at	No hits found
353	18216_at	AC012375
354	18217_g_at	AC012375
355	18235_at	AC000348
356	18252_at	AL096882
357	18255_at	AC005770
358	18272_at	AF002109
359	18533_at	AL021684
360	18556_at	AC006264
361	18590_at	AJ222713
362	18591_at	X74756
363	18607_s_at	U78721
364	18635_at	AC004005
365	18716_at	AC007396
366	18876_at	AF002109
367	18920_at	AC002338
368	18928_at	AC002338
369	19034_at	AL021768
370	19171_at	AC002335
371	19178_at	AB035137
372	19182_at	AL031804
373	19251_at	AL035538
374	19640_at	AC004561
375	19977_at	AL049659
376	20017_at	AC004521
377	20034_i_at	A71607
378	20201_at	AL078470
379	20227_s_at	AB027252
380	20269_at	AC002387
381	20297_at	AC007153
382	20314_s_at	AL096882
383	20335_s_at	Y14208
384	20429_s_at	Z97336
385	20585_s_at	AC005309
386	20641_at	X91919
387	12333_at	AJ286345
388	14028_at	
389	14295_s_at	Z54356
390	14965_at	AC002329
391	15969_s_a	AJ133036
392	15982_s_a	X98190

393	16461_I_at	AC004683
394	16462_s_a	AC004683
395	16514_at	AL035538
396	17549_s_a	L37126
397	18706_s_a	X75782
398	19594_i_at	X98321
399	20555_s_a	AL080318
400	16212_at	gb AAD17366.1 (AF128396) similar to human phosphotyrosyl phosphatase activator PTPA (GB:X73478) [Arabidopsis thaliana]
794	14985_s_at	gb AAC32233.2 (AC005168) unknown protein [Arabidopsis thaliana]
401	16411_s_at	emb CAB71046.1 (AL137898) shaggy-like kinase beta [Arabidopsis thaliana]
402	15920_i_at	gb AAD39561.1 AC007067_1 (AC007067) T10024.1 [Arabidopsis thaliana]
403	16299_at	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]
404	18445_at	gb AAC98458.1 (AC005851) putative glucosyltransferase [Arabidopsis thaliana]
405	19215_at	gb AAC23400.1 (AC004005) putative methyl chloride transferase [Arabidopsis thaliana]
406	16439_at	emb CAA50905.1 (X72022) ORF1 [Arabidopsis thaliana]
407	16047_at	gb AAD20710.1 (AC006300) unknown protein [Arabidopsis thaliana]
408	18003_at	gb AAF01328.1 AF188334_1 (AF188334) Toll/interleukin-1 receptor-like protein [Arabidopsis thaliana]
409	20429_s_at	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
410	17917_s_at	gb AAD12002.1 (AC004261) calcium binding protein (CaBP-22) [Arabidopsis thaliana]
411	17963_at	emb CAB41717.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
412	16150_s_at	emb CAB41718.1 (AL049730) pEARLI 1 [Arabidopsis thaliana]
413	20239_g_at	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
414	20238_at	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
415	15616_s_at	emb CAA08794.1 (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
416	18591_at	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana]

417	14116_at	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
418	12759_at	gb AAC72120.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb 84105 and gb A1100071 come from this gene. [Arabidopsis thaliana]
419	19060_at	gb AAC18809.1 (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana]
420	12998_at	emb CAB41863.1 (AL049746) aldose 1-epimerase-like protein [Arabidopsis thaliana]
421	13172_s_at	gb AAD30608.1 AC007369_18 (AC007369) Sugar transporter [Arabidopsis thaliana]
422	14709_at	No hits found less than or equal to 1e-15.
423	15931_at	gb AAD41420.1 AC007727_9 (AC007727) F8K7.9 [Arabidopsis thaliana]
424	20369_s_at	emb CAB41109.1 (AL049656) ammonium transport protein (AMT1) [Arabidopsis thaliana]
425	14201_at	No hits found less than or equal to 1e-15.
426	14691_at	No hits found.
75	14148_at	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
426	16140_s_at	emb CAB42872.1 (AJ012423) wall-associated kinase 2 [Arabidopsis thaliana]
427	13625_s_at	emb CAB42924.1 (AL049862) putative disease resistance protein [Arabidopsis thaliana]
428	13702_s_at	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
429	17886_at	gb AAC14530.1 (AC004484) unknown protein [Arabidopsis thaliana]
430	12354_g_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase [Arabidopsis thaliana]
431	12353_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase [Arabidopsis thaliana]
432	17899_at	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]

433	18894_at	emb CAB43665.1 (AL050352) Ca ²⁺ -transporting ATPase-like protein [Arabidopsis thaliana]
434	14978_at	gb AAB64024.1 (AC002333) putative glucosyltransferase [Arabidopsis thaliana]
435	14223_at	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
436	16109_s_at	gb AAC05342.1 (AC002521) putative protein kinase [Arabidopsis thaliana]
437	18820_at	gb AAD28055.1 AC007166_3 (AC007166) putative protein kinase [Arabidopsis thaliana]
438	20345_at	gb AAC72865.1 (AF104919) similar to class I chitinases (Pfam: PF00182, E=1.2e-142, N=1) [Arabidopsis thaliana]
439	14170_at	gb AAF29406.1 AC022354_5 (AC022354) unknown protein [Arabidopsis thaliana]
440	15143_s_at	gb AAD38519.1 AF138281_1 (AF138281) phospholipase D-gamma-2 [Arabidopsis thaliana]
441	17499_s_at	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
442	20590_at	emb CAB37511.1 (AL035540) Phospholipase like protein [Arabidopsis thaliana]
443	14608_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana]
444	13550_at	emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
445	13355_at	emb CAA71371.1 (Y10342) putative amidase [Arabidopsis thaliana]
446	13564_at	gb AAC78521.1 (AC005312) putative glutathione S-transferase [Arabidopsis thaliana]
447	19845_g_at	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]
448	12764_f_at	gb AAC32912.1 (AC004138) putative glutathione S-transferase [Arabidopsis thaliana]
449	17922_at	gb AAB16855.1 (U71122) pyruvate decarboxylase [Arabidopsis thaliana]

450	15982_s_at	emb CAA66863.1 (X98190) peroxidase ATP2a [Arabidopsis thaliana]
451	12227_at	gb AAD39285.1 AC007576_8 (AC007576) Unknown protein [Arabidopsis thaliana]
452	20555_s_at	emb CAB45975.1 (AL080318) copper amine oxidase like protein (fragment2) [Arabidopsis thaliana]
453	19844_at	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]
454	13985_s_at	gb AAC31242.1 (AC004747) unknown protein [Arabidopsis thaliana]
455	13548_at	gb AAD41421.1 AC007727_10 (AC007727) ESTs gb N96028, gb F14286, gb T20680, gb F14443, gb AA657300 and gb N65244 come from this gene. [Arabidopsis thaliana]
456	15611_s_at	gb AAA32775.1 (L22567) cor78 [Arabidopsis thaliana]
457	19840_s_at	gb AAD25759.1 AC007060_17 (AC007060) Strong similarity to F19I3.2 gi 3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb AC004238. EST gb R90518 comes from this gene.
458	15985_at	emb CAA67340.1 (X98808) peroxidase ATP3a [Arabidopsis thaliana]
459	14584_at	gb AAD32844.1 AC007658_3 (AC007658) unknown protein [Arabidopsis thaliana]
460	15422_at	gb AAD36948.1 AF069441_8 (AF069441) hypothetical protein [Arabidopsis thaliana]
461	20150_at	gb AAB61076.1 (AF007271) A_TM021B04.14 gene product [Arabidopsis thaliana]
462	18844_at	gb AAC33239.1 (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
463	16360_at	emb CAA20203.1 (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
464	20292_at	gb AAB87113.1 (AC002391) putative protein kinase [Arabidopsis thaliana]
465	14554_at	gb AAC18798.1 (AC003671) F1707.4 [Arabidopsis thaliana]
466	18604_at	gb AAC19273.1 (AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]

467	16061_s_at	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana]
468	14145_at	dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
469	16144_s_at	dbj BAA04870.1 (D21843) MAP kinase [Arabidopsis thaliana]
470	17097_s_at	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]
471	19718_at	gb AAB71447.1 (AC000098) Similar to Arabidopsis Fe(II) transport protein (gb U27590). [Arabidopsis thaliana]
472	14298_g_at	gb AAC25507.1 (AC003979) T22J18.6 [Arabidopsis thaliana]
473	12307_at	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
474	20232_s_at	emb CAA18460.1 (AL022347) protein. kinase-like protein [Arabidopsis thaliana]
475	19322_at	gb AAF19738.1 AC012463_12 (AC012463) T2E6.14 [Arabidopsis thaliana]
476	14224_at	gb AAF07386.1 AC010675_9 (AC010675) putative peptide transporter [Arabidopsis thaliana]
477	14270_at	gb AAD39269.1 AC007203_1 (AC007203) Putative UDP-glucose:sterol glucosyltransferase [Arabidopsis thaliana]
478	15479_at	emb CAB39671.1 (AL049483) putative protein [Arabidopsis thaliana]
479	14090_i_at	gb AAD41981.1 AC006438_13 (AC006438) unknown protein [Arabidopsis thaliana]
480	16162_s_at	gb AAB05099.1 (U39944) BELL1 [Arabidopsis thaliana]
481	20149_at	gb AAB70415.1 (AC000106) Similar to Beta integral membrane protein (gb U43629). [Arabidopsis thaliana]
482	12765_at	gb AAD15574.1 (AC006340) unknown protein [Arabidopsis thaliana]
214	12505_s_at	gb AAC63643.1 (AC005309) putative CONSTANS-like B-box zinc finger protein [Arabidopsis thaliana]
483	13140_at	gb AAC79588.1 (AC005727) putative RING zinc finger ankyrin protein [Arabidopsis thaliana]
484	15022_at	gb AAC72124.1 (AC005278) ESTs gb H37641 and gb AA651422 come from this gene. [Arabidopsis thaliana]

485	16306_at	emb CAB41935.1 (AL049751) putative protein [Arabidopsis thaliana] gb AAC26246.1 (AF077407) contains similarity to phosphoenolpyruvate synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
486	18611_at	emb CAB43428.1 (AL050300) putative protein [Arabidopsis thaliana]
487	20199_at	emb CAA18626.1 (AL022580) putative protein [Arabidopsis thaliana]
488	14595_at	gb AAD31337.1 AC007354_10 (AC007354) Strong similarity to gb Y09533 involved in starch metabolism from Solanum tuberosum and contains a PF 01326 Pyruvate phosphate dikinase, PEP/pyruvate binding domain. EST gb N96757 comes from this gene.
489	12532_at	[Arabidopsis thaliana]
490	19977_at	emb CAB41162.1 (AL049659) putative protein [Arabidopsis thaliana] gb AAC79594.1 (AC005727) putative membrane channel protein [Arabidopsis thaliana]
491	12773_at	gb AAD32870.1 AC005489_8 (AC005489) F14N23.8 [Arabidopsis thaliana]
492	19632_at	emb CAA16957.1 (AL021811) putative protein [Arabidopsis thaliana]
493	19359_s_at	emb CAA78712.1 (Z14988) glycine rich protein [Arabidopsis thaliana] thaliana]
494	14716_f_at	gb AAC19269.1 (AF069298) T14P8.18 gene product [Arabidopsis thaliana]
495	13648_at	gb AAD41977.1 AC006438_9 (AC006438) unknown protein [Arabidopsis thaliana]
496	12768_at	gb AAC69134.1 (U78721) putative auxin-regulated protein [Arabidopsis thaliana]
497	16422_at	gb AAC26203.1 (AF053747) dormancy-associated protein [Arabidopsis thaliana]
498	15131_s_at	emb CAB38829.1 (AL035679) drought-inducible cysteine proteinase RD19A precursor
499	14659_s_at	emb CAB38829.1 (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]
500	14658_s_at	emb CAB36513.1 (AL035440) putative protein [Arabidopsis thaliana]
501	15057_at	emb CAB56039.1 (AJ133786) gigantea protein [Arabidopsis thaliana]
502	17581_g_at	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
503	18567_at	

504	17047_s_at	gb AAC68674.1 (AF078825) RING-H2 finger protein RHA3b [Arabidopsis thaliana]
505	15105_s_at	emb CAA78711.1 (Z14987) glycine rich protein [Arabidopsis thaliana]
506	14196_at	gb AAF16557.1 AC012563_10 (AC012563) unknown protein [Arabidopsis thaliana]
507	17599_s_at	gb AAD50976.1 AF170494_1 (AF170494) ionotropic glutamate receptor ortholog GLR6 [Arabidopsis thaliana]
508	18556_at	gb AAD29803.1 AC006264_11 (AC006264) cyclophilin (CYP2) [Arabidopsis thaliana]
509	16486_at	gb AAB04606.1 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana]
510	18272_at	gb AAB95293.1 (AF002109) unknown protein [Arabidopsis thaliana]
795	12219_at	gb AAD31373.1 AC006053_15 (AC006053) unknown protein [Arabidopsis thaliana]
511	20446_s_at	gb AAC80600.1 (AC005106) T25N20.21 [Arabidopsis thaliana]
512	12561_at	emb CAA16701.1 (AL021687) putative protein [Arabidopsis thaliana]
513	12060_at	gb AAD46000.1 AC005916_12 (AC005916) Contains similarity to gb AF113001 silencing mediator of retinoic acid and thyroid hormone receptor alpha and gb AF109179 cyclin T1 from Mus musculus. ESTs gb N95317, gb Z29139 and gb Z30853 come from this gene. [Arabidopsis thaliana]
514	18235_at	gb AAB61480.1 (AC000348) T7N9.4 [Arabidopsis thaliana]
515	14021_r_at	emb CAA04134.1 (AJ000497) Starch branching enzyme II [Arabidopsis thaliana]
516	14020_i_at	emb CAA04134.1 (AJ000497) Starch branching enzyme II [Arabidopsis thaliana] emb CAA44630.1 (X62818) Metallothionein-like protein [Arabidopsis thaliana]
517	16011_s_at	gb AAD09232.1 (U83179) unknown [Arabidopsis thaliana]
518	17033_s_at	gb AAD24630.1 AC006919_10 (AC006919) putative fructose biphosphate aldolase [Arabidopsis thaliana]
519	16050_at	

520	19692_at	gb AAC14039.1 (AC003981) F22O13.13 [Arabidopsis thaliana]
521	19181_s_at	gb AAC39464.1 (AF053065) late embryogenesis abundant protein homolog [Arabidopsis thaliana]
792	13435_at	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
522	17128_s_at	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
523	14635_s_at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
524	15846_at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
525	15847_g_at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
526	14704_s_at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
527	17456_at	gb AAB80678.1 (AC002332) putative steroid dehydrogenase [Arabidopsis thaliana]
528	14895_s_at	emb CAB10562.1 (Z97344) acetylornithine deacetylase [Arabidopsis thaliana]
529	19979_at	gb AAB95235.1 (AC002130) F1N21.7 [Arabidopsis thaliana]
530	20325_s_at	emb CAA78152.1 (Z12162) protein phosphatase 1A [Arabidopsis thaliana]
531	18234_at	gb AAB61479.1 (AC000348) T7N9.3 [Arabidopsis thaliana]
532	16474_s_at	emb CAA35838.1 (X51474) kin1 [Arabidopsis thaliana]
533	18701_s_at	emb CAA38894.1 (X55053) cold regulated [Arabidopsis thaliana]
534	13785_at	gb AAD23000.1 AC007087_19 (AC007087) cold-regulated protein cor15b precursor [Arabidopsis thaliana]
535	20387_at	gb AAC23422.1 (AC004005) putative methionine aminopeptidase [Arabidopsis thaliana]
536	13178_at	gb AAB63086.1 (U93215) unknown protein [Arabidopsis thaliana]
537	12103_at	gb AAD30603.1 AC007369_13 (AC007369) Unknown protein [Arabidopsis thaliana]
538	13225_s_at	emb CAA42483.1 (X59814) Cold and ABA regulated gene [Arabidopsis thaliana]

539	17003_at	gb AAB95275.1 (AF002109) putative LIM-domain protein [Arabidopsis thaliana]
540	15878_at	emb CAA19880.1 (AL031032) putative protein [Arabidopsis thaliana]
541	13004_at	gb AAD03574.1 (AC003952) putative senescence-related protein [Arabidopsis thaliana]
542	14052_at	gb AAC34333.1 (AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]
543	15798_at	gb AAC05351.1 (AC002521) putative receptor-like protein kinase [Arabidopsis thaliana]
793	12345_at	gb AAB67985.1 (L36246) anoxia-induced protein [Arabidopsis thaliana]
544	16818_s_at	emb CAA20206.1 (AL031187) serine/threonine kinase-like protein [Arabidopsis thaliana]
545	13916_at	gb AAC62136.1 (AC005169) unknown protein [Arabidopsis thaliana]
666	20342_at	emb CAB41311.1 (AL049711) putative heat shock transcription factor [Arabidopsis thaliana]
546	20421_at	emb CAB10242.1 (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]
547	14250_r_at	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
548	14249_i_at	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
549	17544_s_at	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
550	12879_s_at	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
551	20017_at	gb AAC16079.1 (AC004521) unknown protein [Arabidopsis thaliana]
552	13177_at	emb CAB40989.1 (AL049640) growth factor like protein [Arabidopsis thaliana]
553	19946_at	gb AAF18611.1 AC005170_1 (AC005170) similar to senescence-associated protein [Arabidopsis thaliana]
554	17894_at	gb AAD08938.1 (AC005724) unknown protein [Arabidopsis thaliana]
555	15855_at	gb AAD15572.1 (AC006340) unknown protein [Arabidopsis thaliana]
556	15558_r_at	emb CAB45807.1 (AL080253) putative protein [Arabidopsis thaliana]
557	15208_s_at	No hits found less than or equal to 1e-15.

558	16153_s_at	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]
559	14636_s_at	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]
560	19178_at	dbj BAA86999.1 (AB035137) blue copper binding protein [Arabidopsis thaliana]
561	17580_at	emb CAB56039.1 (AJ133786) gigantea protein [Arabidopsis thaliana]
562	14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
563	18946_at	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
564	13009_i_at	emb CAA17138.1 (AL021889) putative protein [Arabidopsis thaliana]
565	18508_s_at	gb AAA33709.1 (L16797) glutamate decarboxylase [Petunia x hybrida]
566	12556_at	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
567	13115_at	gb AAB60774.1 (AC000375) ESTs gb U75592, gb T13956, gb T43869 come from from this gene. [Arabidopsis thaliana]
568	15046_s_at	gb AAB87120.1 (AC003000) unknown protein [Arabidopsis thaliana]
339	17303_s_at	gb AAC67339.2 (AC005499) putative WRKY-type DNA binding protein [Arabidopsis thaliana]
569	18597_at	emb CAB45881.1 (AL080282) berberine bridge enzyme-like protein [Arabidopsis thaliana]
570	13908_s_at	emb CAB42588.1 (A71590) unnamed protein product [Arabidopsis thaliana]
571	14553_at	emb CAB41103.1 (AL049655) putative protein [Arabidopsis thaliana]
572	18928_at	gb AAB64044.1 (AC002333) putative endochitinase [Arabidopsis thaliana]

573	12772_at	gb AAC72119.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from <i>Daucus carota</i> . ESTs gb H37281, gb T44167, gb T21813, gb N38437, gb Z26470, gb R65072, gb N76373, gb F15470, gb Z35182, gb H76373, gb Z34678 and gb Z35387>
574	16326_at	emb CAA18124.1 (AL022141) putative receptor protein kinase [<i>Arabidopsis thaliana</i>]
575	20479_i_at	emb CAB38908.1 (AL035708) cytochrome P450-like protein [<i>Arabidopsis thaliana</i>] gb AAD28318.1 AC006436_9 (AC006436) putative receptor-like protein kinase
576	16393_s_at	[<i>Arabidopsis thaliana</i>] emb CAA67551.1 (X99097) peroxidase
577	17413_s_at	[<i>Arabidopsis thaliana</i>] gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase
578	14620_s_at	[<i>Arabidopsis thaliana</i>] emb CAB38908.1 (AL035708) cytochrome P450-like protein [<i>Arabidopsis thaliana</i>] gb AAC79625.1 (AC005770) unknown protein [<i>Arabidopsis thaliana</i>]
579	20480_s_at	emb CAA21214.1 (AL031804) putative protein [<i>Arabidopsis thaliana</i>] gb AAC79625.1 (AC005770) unknown protein [<i>Arabidopsis thaliana</i>]
580	15866_s_at	emb CAA74639.1 (Y14251) glutathione S-transferase [<i>Arabidopsis thaliana</i>]
581	19182_at	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [<i>Arabidopsis thaliana</i>]
582	18255_at	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [<i>Arabidopsis thaliana</i>] emb CAA74639.1 (Y14251) glutathione S-transferase [<i>Arabidopsis thaliana</i>]
583	16054_s_at	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [<i>Arabidopsis thaliana</i>]
584	14672_s_at	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [<i>Arabidopsis thaliana</i>] gb AAD22285.1 AC006920_9 (AC006920) unknown protein [<i>Arabidopsis thaliana</i>]
585	20291_s_at	
586	16053_i_at	
587	17083_s_at	
588	12889_s_at	
589	12642_at	

590	17487_s_at	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
591	14838_s_at	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
592	17104_s_at	dbj BAA13640.1 (D88541) phosphoserine aminotransferase [Arabidopsis thaliana]
593	19892_at	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
594	16105_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
664	13273_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
595	12892_g_at	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
596	15141_s_at	dbj BAA22096.1 (D85191) vegetative storage protein [Arabidopsis thaliana]
597	18231_at	emb CAA55322.1 (X78585) Di21 [Arabidopsis thaliana]
598	15629_s_at	dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
599	15978_at	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
600	20269_at	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
601	14614_at	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
602	17930_s_at	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]
603	16952_s_at	gb AAC78532.1 (AC005662) calmodulin-like protein [Arabidopsis thaliana]
604	12930_s_at 12842_s_at	gb AAC49679.1 (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana] No hits found less than or equal to 1e-15.
605	16063_s_at	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
228	12904_s_at	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
606	12908_s_at	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

607	15937_at	emb CAA17127.1 (AL021889) hypothetical protein [Arabidopsis thaliana]
608	17843_s_at	gb AAB87109.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
609	18966_at	gb AAC95196.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
610	20519_at	gb AAC80599.1 (AC005106) T25N20.20 [Arabidopsis thaliana]
611	19641_at	gb AAC95189.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
612	17408_at	gb AAD32297.1 AC006533_21 (AC006533) putative glucosyltransferase [Arabidopsis thaliana]
613	15646_s_at	gb AAC37474.1 (L42212) serine acetyltransferase [Arabidopsis thaliana]
614	14731_s_at	gb AAC49988.1 (AF014960) multidrug resistance-associated protein 2; AtMRP2 [Arabidopsis thaliana]
615	20685_at	emb CAB41928.1 (AL049751) short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana]
616	16968_at	emb CAA17559.1 (AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]
617	18253_s_at	gb AAC78440.1 (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis thaliana] thaliana]
618	15496_at	gb AAD20156.1 (AC006282) putative glucosyl transferase [Arabidopsis thaliana]
619	19137_at	emb CAA52771.1 (X74755) ATAF1 [Arabidopsis thaliana]
620	19132_s_at	emb CAA18722.1 (AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]
621	13656_at	gb AAD22649.1 AC007138_13 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]
622	17024_s_at	gb AAB67854.1 (U61231) cytochrome P450 [Arabidopsis thaliana]
623	14705_i_at	emb CAB69849.1 (AL137189) anthranilate N-benzoyltransferase-like protein [Arabidopsis thaliana]
624	17500_s_at	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]

625	13217_s_at	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
626	15196_s_at	gb AAC49573.1 (U43412) 3'-phosphoadenosine 5'-phosphosulfate reductase [Arabidopsis thaliana]
627	18590_at	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]
628	14700_at	No hits found less than or equal to 1e-15.
629	14665_r_at	emb CAA69879.1 (Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]
630	12630_at	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
631	18953_at	gb AAC69851.1 (AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
632	13514_s_at	emb CAA16793.1 (AL021713) putative protein [Arabidopsis thaliana]
633	12490_at	gb AAF02787.1 AF195115_7 (AF195115) weak similarity to receptor protein kinase [Arabidopsis thaliana]
634	12246_s_at	emb CAB10404.1 (Z97340) phytochrome D [Arabidopsis thaliana]
635	20536_s_at	emb CAB37488.1 (AL035539) putative protein [Arabidopsis thaliana]
636	18409_at	gb AAC72122.1 (AC005278) F15K9.14 [Arabidopsis thaliana]
637	19387_at	gb AAD21475.1 (AC007017) unknown protein [Arabidopsis thaliana]
638	16117_s_at	gb AAB70244.1 (AF016848) WD-40 repeat protein [Arabidopsis thaliana]
639	18347_s_at	emb CAA21480.1 (AL031986) putative protein [Arabidopsis thaliana]
640	15880_at	emb CAB38906.1 (AL035708) putative protein [Arabidopsis thaliana]
667	20471_at	gb AAC49767.1 (AF003094) AP2 domain containing protein RAP2.1 [Arabidopsis thaliana]
641	16603_s_at	gb AAB58497.1 (U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase [Arabidopsis thaliana]
642	12049_at	gb AAC13598.1 (AF058914) F21E10.13 gene product [Arabidopsis thaliana]
643	12048_at	gb AAC78704.1 (AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

		gb AAB61117.1 (AC002062) ESTs
		gb N38288,gb T43486,gb AA395242 come
644	14064_at	from this gene. [Arabidopsis thaliana]
		gb AAC04492.1 (AC003974) unknown
645	12149_at	protein [Arabidopsis thaliana]
		emb CAA91183.1 (Z54356) HD-ZIP
646	14295_s_at	[Arabidopsis thaliana]
		emb CAA16930.1 (AL021768) TMV
		resistance protein N-like [Arabidopsis
647	19034_at	thaliana]
		gb AAC27848.1 (AC004218) unknown
648	18624_at	protein [Arabidopsis thaliana]
		gb AAC97218.1 (AC005936) unknown
649	13181_at	protein [Arabidopsis thaliana]
		gb AAD10163.1 (AC005917) putative Tal1-
		like non-LTR retroelement protein
650	18866_at	[Arabidopsis thaliana]
		emb CAB44686.1 (AL078620) cytochrome
651	19502_at	P450-like protein [Arabidopsis thaliana]
		emb CAA19807.1 (AL031018) hypothetical
652	16301_s_at	protein [Arabidopsis thaliana]
		gb AAD32774.1 AC007661_11 (AC007661)
653	19411_at	unknown protein [Arabidopsis thaliana]
		emb CAA71588.1 (Y10556) CONSTANS
654	20300_g_at	[Arabidopsis thaliana]
		emb CAA71588.1 (Y10556) CONSTANS
655	20299_at	[Arabidopsis thaliana]
		gb AAB57688.1 (U96045) APS reductase
656	18696_s_at	[Arabidopsis thaliana]
		gb AAC26980.1 (AF016283) 5'-
		adenylylsulfate reductase [Arabidopsis
657	15186_s_at	thaliana] [Arabidopsis thaliana]
659	16609_s_at	AtERF2 (, BAA32419.1; AB008104)
		EREBP4-like, AtERF6 (, CAB10530.1;
660	12909_s_at	Z97343)
661	16536_s_at	AtERF5 (, BAA32422.1; AB008107)
		put. C2H2 zinc finger transcription factor (,
301	15665_s_at	AAB80922.1; AF022658)
		Myb-like (, emb CAA20567.1 (AL031394)
668	13176_at	putative protein
670	15778_at	X98676.2_at
671	20619_at	AC005896.161_at
672	12966_s_at	AL023094.197_s_at
673	20335_s_at	Y14208.2_s_at
674	18949_at	Z54136.1_at
675	13015_s_at	X98673.2 s at emb CAB41311.1

		(AL049711) putative heat shock transcription factor [Arabidopsis thaliana]
676	19646_s_at	AC005819.55_s_at
677	19855_at	AC007260.16_at
		AC007047.101_at gb AAC49767.1
		(AF003094) AP2 domain containing protein
678	18475_at	RAP2.1 [Arabidopsis thaliana]
		unspecified t-factor gb AAC49775.1
		(AF003102) AP2 domain containing protein
679	13001_at	RAP2.9 [Arabidopsis thaliana]
		AC004665.101_at emb CAA67234.1
		(X98676) zinc finger protein [Arabidopsis thaliana]
680	15219_at	ATTHIRED4_s_at gb AAC98070.1
		(AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
681	13189_s_at	hsp70_s_at emb CAA18838.1 (AL023094)
		bZIP transcription factor ATB2 [Arabidopsis thaliana]
684	13284_s_at	

Table 10

<u>Set</u>	<u>Content</u>	<u>Number of unique genes</u>
2	7 or 8 not edm1 not	55 genes
5	rps2 not pad4 or NahG	
3	edm1 not rps2 not pad4 or NahG	44 genes
4	rps2 not edm1 not pad4 or NahG	12 genes
5	pad4 or NahG not edm1 not rps2	20 genes
6	edm1 and rps2 not pad4 or NahG	17 genes
10	7	18 genes
	8	7 genes
	9	<u>11 genes</u>
	Total	184 genes

15 For engineering resistance to pathogens whose growth is restricted by RPP7 or RPP8 dependent responses, such as oomycete pathogens, all 184 genes are potentially useful. The 128 genes in sets 2, 3, 4, and 6 are more likely to be useful, as *pad4* and *NahG* do not interfere with resistance mediated by *RPP7* or *RPP8*, so genes under their control should not be important for this type of

20 resistance. The 99 genes in sets 2 and 3 are even more likely to be useful, because they not affected by *rps2*, and *RPP7* and *RPP8* trigger a different kind of resistance response than the one triggered by *RPS2*. The 44 genes in set 3 are

most likely to be useful, as they require *EDM1*, and *EDM1* is required for resistance.

Example 3

5 Transcriptional Responses Triggered by the RPP7 Defense Signaling Pathway

The *RPP7* defense-signaling pathway (Figure 1) mediates resistance of the *Arabidopsis* ecotype Col-0 against the *Peronospora* isolate Hiks1. In contrast to conventional *R*-gene dependent defense signaling pathways in *Arabidopsis*, such as the *RPP4* pathway, the *RPP7* pathway does not essentially
10 require salicylic acid accumulation or previously described defense regulators, such as *EDS1*, *NDR1*, *NPR1*, *PAD4* and others.

A comparative analysis of transcriptional responses triggered by the *RPP7* and *RPP8* pathways was performed by gene expression profiling using Affymetrix oligonucleotide chips with roughly 8,200 different *Arabidopsis*
15 genes, representing roughly a third of the genome. For the analysis, 2 week old seedlings were harvested 0, 12 or 48 hours post infection with a particular *Peronospora* isolate (Table 11). To examine *RPP8* triggered transcriptional responses, a transgenic line Col-0 line carrying the *RPP8* resistance gene from the *Arabidopsis* ecotype Landsberg erecta was infected with the *Peronospora*
20 isolate Emco5. This interaction is incompatible. The interaction between Emco5 and Col-0 wild type plants served as compatible control. Responses triggered by the *RPP7* pathway were analyzed using the incompatible interaction between the *Peronospora* isolate Hiks1 and Col-0 wild type plants, as well as compatible interactions between Hiks1 and the susceptible mutants *rpp7*, *edm1*,
25 *edm2* and *edm3*. To compare transcriptional responses triggered by the unconventional *RPP7* and *RPP8* pathways with those triggered by the more conventional *RPP4* pathway, Col-0 wild type plants were infected with the *Peronospora* isolate Emoy2, which is avirulent on this ecotype. The interactions between Emoy2 and NahG plants, as well as the mutants *pad4*, *ndr1* and *npr1*,
30 served as compatible controls. Whereas *pad4* and NahG plants are fully Emoy2 susceptible, *ndr1* and *npr1* plants are only partly compromised in Emoy2 resistance.

Table 11

	<u>Plant</u>	<u>Peronospora isolate</u>	<u>Interaction type</u>
	Col-0 (<i>tgRPP8</i>)	Emco5	incompatible
	Col-0 (<i>rpp8</i>)	Emco5	compatible
5	Col-0 (<i>RPP7</i>)	Hiks1	incompatible (2x)
	Col-0 (<i>rpp7</i> ; 3929)	Hiks1	compatible
	Col-0 (<i>edm1</i>)	Hiks1	compatible
	Col-0 (<i>edm2</i>)	Hiks1	compatible
	Col-0 (<i>edm3</i>)	Hiks1	compatible
10	Col-0 (<i>RPP4</i>)	Emoy2	incompatible
	Col-0 (<i>ndr-1-1</i>)	Emoy2	intermediate
	Col-0 (<i>pad4-1</i>)	Emoy2	compatible
	Col-0 (<i>NahG</i>)	Emoy2	compatible
	Col-0 (<i>npr1-1</i>)	Emoy2	intermediate

15

ResultsIdentification of Genes Potentially Required for *RPP7* Mediated *Peronospora* Resistance

Genes that play a role in the establishment of resistance may show differences in their regulation or their expression levels between compatible and incompatible interactions (e.g., genes may show lower expression levels in “loss of Hiks-resistance mutants” as compared to Col-0 wild type plants). Thus, for each gene expression, ratios were calculated between Col-0 and each of the four Hiks response mutants (*rpp7*, *edm1*, *edm2* or *edm3*) at each time point (0, 12 and 48 hours). The resulting data set, consisting of 12 expression ratios for each of the 8,775 probe sets on the chip, was first analyzed with “CLUSTER” and “TREE VIEW”, two commonly used programs for chip and micro-array data analysis (Eisen et al., 1998). Genes that demonstrated only minor or less significant expression differences between Col-0 wild type and the mutants were excluded from analysis. Genes that showed at least one 3-fold expression difference over all 12 calculated expression ratios were first considered for further analysis.

Table 12 shows 194 probe sets corresponding to genes having SEQ ID NOs: 301-494, the expression of which is altered after infection of *Arabidopsis* with *P. parasitica* (wild-type relative to *rpp7*, *edm1*, *edm2*, or *edm3*). Table 13

depicts about 100 genes (genes comprising SEQ ID NOs: 373, 385, 242, 369, 306, 232, 346, 367, 212, 221, 307, 322, 240, 313, 270, 252, 383, 245, 377, 212, 327, 297, 375, 263, 250, 282, 358, 257, 332, 560, 284, 220, 259, 355, 248, 281, 215, 236, 309, 386, 253, 333, 336, 296, 319, 414, 354, 353, 293, 278, 324, 339, 345, 225, 249, 264, 310, 228, 214, 311, 343, 298, 384, 277, 314, 372, 331, 338, 370, 352, 365, 261, 374, 238, 344, 241, 380, 371, 262, 258, 256, 304, 275, 303, 274, 254, 223, 348, 318, 251, 291, 289, 361, 285, 368, 342, 290, 351, 312, 286, 287, 273, 239, 326, 226, 227, 350, 280, 317, 359, 294, 279, 382, 356, 234, 218, 217, 347, 379, 401, 378, 363, 341, 208, 268, 267, 364, 266, 337, 269, 269, 325, 793 and 224) represented by 137 probe sets that show at least one 3-fold-expression difference in comparisons between wild type *Arabidopsis* Col-0 and mutants *rrp7* or *edm1*, *edm2*, or *edm3* infected with *P. parasitica* Hiks1 (i.e., probe sets that show at least one 3-fold difference in expression levels over all 12 expression ratios calculated between Col-0 wild type and each of the 4 Hiks response mutants at each of the time points). Genes were grouped together according to similarities of their expression characteristics. Expression ratios were color encoded. Positive expression ratios were red and negative ratios were green. Black indicated no expression difference. Genes were represented in rows and infection treatments in columns. Red generally indicated that a gene at a given time point is more strongly expressed in Col-0 wild type plants as compared to the respective mutant. One cluster represented genes that are upregulated in response to Hiks1 infection by the *RPP7* pathway (Table 14; genes comprising SEQ ID NOs: 365, 261, 374, 238, 344, 241, 380, 371, 262, 258, 256, 304, 275, 303, 274, 254, 310, 228, 214, 347 and 225, which are induced by Hiks1-infection and which are *RPP7*, *EDM1*, *EDM2*, *EDM3*-dependent genes and so may encode regulators acting downstream of those genes; see probe sets 12505, 13217 and 12904 which correspond to genes that encode potential regulators of Hiks response pathway). Genes in this cluster represent genes that are more strongly expressed in Col-0 wild type than in all four mutants predominantly at the 12 hour time-point in each comparison. The expression difference is less pronounced in the case of *edm2* and *edm3*, but it is consistent over all four comparisons.

Table 12

Affy ID (Probe Set)	Reference No.
12324_i_at	AC007212
12333_at	AJ286345
12345_at	L36246
12500_s_at	AF081067
12505_s_at	AC005309
12608_i_at	S70188
12642_at	AC006920
12746_i_at	AL096882
12748_f_at	AL096882
12761_s_at	AC006577
12773_at	AC005727
12778_r_at	AC006577
12798_at	AC003028
12802_at	AL022373
12842_s_at	
12843_s_at	AC007195
12845_s_at	AJ004810
12879_s_at	U40856
12891_at	U73786
12892_g_at	U73786
12904_s_at	AB008103
12905_s_at	AB008104
12908_s_at	AB008107
12909_s_at	Z97343
12911_s_at	X84229
12916_s_at	AF021244
13138_at	AL096882
13177_at	AL049640
13178_at	U93215
13187_i_at	U35829
13189_s_at	U35829
13198_i_at	AL021749
13212_s_at	AL137080
13217_s_at	AL049862
13258_s_at	AC005309
13273_s_at	U68017
13284_s_at	AJ002551
13604_at	AC000104
13615_at	AC002332
13617_at	AC006592
13718_at	Z72152
13771_at	AC006593
13785_at	AC007087
14028_at	AF075597
14052_at	AC004122
14096_at	AC002291
14097_at	AC005309

14116_at	AF077407
14141_at	AC011437
14148_at	AF224762
14196_at	AC012563
14201_at	AL163972
14219_at	AC068667
14223_at	AL024486
14248_at	AC007357
14250_r_at	AL050300
14295_s_at	Z54356
14595_at	AL022580
14608_at	AC007357
14614_at	AC004165
14621_at	AC004747
14627_i_at	X76609
14628_r_at	X76609
14635_s_at	AC005398
14636_s_at	AC013258
14643_s_at	AC006836
14672_s_at	U18993
14675_s_at	D85191
14691_at	AP002046
14704_s_at	AC006067
14706_r_at	AL137189
14709_at	AP002046
14711_s_at	AF085279
14731_s_at	AF014960
14784_at	AC005310
14951_at	AL049481
14965_at	AC002329
15057_at	AL035440
15085_s_at	AL031018
15105_s_at	Z14987
15116_f_at	AF121356
15125_f_at	D85190
15141_s_at	D85191
15145_s_at	D64155
15154_s_at	AL096860
15161_s_at	U90522
15178_s_at	U43489
15216_s_at	U75198
15431_at	AL030978
15496_at	AC006282
15523_s_at	AL078637
15593_s_at	U54561
15611_s_at	L22567
15616_s_at	AJ009696
15622_s_at	U43945

15629_s_at	AB010407
15665_s_at	AF022658
15680_s_at	D42061
15846_at	AC006067
15847_g_at	AC006067
15866_s_at	AC005770
15950_at	AC006429
15954_at	U72155
15969_s_a	AJ133036
15978_at	X68592
15982_s_a	X98190
16038_s_at	L04173
16063_s_at	AB008103
16105_s_at	U68017
16150_s_at	AL049730
16153_s_at	AC013258
16393_s_at	AC006436
16412_s_at	AL022603
16442_s_at	AJ002551
16461_I_at	AC004683
16462_s_a	AC004683
16504_s_at	Z97335
16510_at	AL034567
16514_at	AL035538
16536_s_at	AB008107
16539_s_at	Z97343
16569_s_at	L23968
16578_s_at	AL137080
16609_s_at	AB008104
16620_s_at	AF051338
16637_s_at	Z97336
16817_s_at	AL096882
16864_i_at	AL133248
16951_i_at	AC005662
16952_s_at	AC005662
16981_s_at	U35829
17014_s_at	U05206
17033_s_at	U83179
17054_s_at	AF134128
17073_s_at	AC006836
17119_s_at	AF132212
17123_s_at	AF106087
17128_s_at	AC005398
17187_at	AF128396
17303_s_at	AC005499
17379_at	AC018721
17386_at	AC006264
17413_s_at	X99097

17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17549_s_a	L37126
17567_at	AL162751
17886_at	AC004484
17899_at	Z97339
17917_s_at	AC004261
17961_at	AC007323
17963_at	AL049730
18003_at	AF188334
18064_r_at	
18069_at	
18070_r_at	
18216_at	AC012375
18217_g_at	AC012375
18235_at	AC000348
18252_at	AL096882
18255_at	AC005770
18272_at	AF002109
18533_at	AL021684
18556_at	AC006264
18590_at	AJ222713
18591_at	X74756
18607_s_at	U78721
18635_at	AC004005
18706_s_a	X75782
18716_at	AC007396
18876_at	AF002109
18920_at	AC002338
18928_at	AC002338
19034_at	AL021768
19171_at	AC002335
19178_at	AB035137
19182_at	AL031804
19251_at	AL035538
19594_i_at	X98321
19640_at	AC004561
19977_at	AL049659
20017_at	AC004521
20034_i_at	A71607
20201_at	AL078470
20227_s_at	AB027252
20269_at	AC002387
20297_at	AC007153
20314_s_at	AL096882
20335_s_at	Y14208
20429_s_at	Z97336

20555_s_a	AL080318
20585_s_at	AC005309
20641_at	X91919

Table 13

Probe Set	Description
12324_i_at	AC007212
12345_at	L36246
12505_s_at	AC005309
12608_i_at	S70188
12746_i_at	AL096882
12748_f_at	AL096882
12761_s_at	AC006577
12773_at	AC005727
12778_r_at	AC006577
12798_at	AC003028
12802_at	AL022373
12842_s_at	
12843_s_at	AC007195
12845_s_at	AJ004810
12879_s_at	U40856
12891_at	U73786
12892_g_at	U73786
12904_s_at	AB008103
12908_s_at	AB008107
12911_s_at	X84229
13138_at	AL096882
13178_at	U93215
13189_s_at	U35829
13198_i_at	AL021749
13212_s_at	AL137080
13217_s_at	AL049862
13258_s_at	AC005309
13604_at	AC000104
13718_at	Z72152
13771_at	AC006593
13785_at	AC007087
14052_at	AC004122
14096_at	AC002291
14097_at	AC005309
14116_at	AF077407
14148_at	AF224762
14196_at	AC012563
14201_at	AL163972
14219_at	AC068667
14248_at	AC007357
14250_r_at	AL050300
14595_at	AL022580

14608_at	AC007357
14621_at	AC004747
14627_i_at	X76609
14628_r_at	X76609
14635_s_at	AC005398
14636_s_at	AC013258
14675_s_at	D85191
14691_at	AP002046
14704_s_at	AC006067
14709_at	AP002046
14711_s_at	AF085279
14731_s_at	AF014960
14784_at	AC005310
14951_at	AL049481
15057_at	AL035440
15105_s_at	Z14987
15116_f_at	AF121356
15125_f_at	D85190
15141_s_at	D85191
15145_s_at	D64155
15154_s_at	AL096860
15161_s_at	U90522
15178_s_at	U43489
15431_at	AL030978
15496_at	AC006282
15593_s_at	U54561
15611_s_at	L22567
15616_s_at	AJ009696
15846_at	AC006067
15847_g_at	AC006067
15950_at	AC006429
15954_at	U72155
16038_s_at	L04173
16063_s_at	AB008103
16105_s_at	U68017
16150_s_at	AL049730
16153_s_at	AC013258
16393_s_at	AC006436
16504_s_at	Z97335
16510_at	AL034567
16536_s_at	AB008107
16578_s_at	AL137080
16620_s_at	AF051338
16637_s_at	Z97336
16817_s_at	AL096882
16864_i_at	AL133248
17014_s_at	U05206
17033_s_at	U83179

17054_s_at	AF134128
17123_s_at	AF106087
17128_s_at	AC005398
17187_at	AF128396
17303_s_at	AC005499
17386_at	AC006264
17413_s_at	X99097
17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17567_at	AL162751
17886_at	AC004484
17899_at	Z97339
17961_at	AC007323
17963_at	AL049730
18003_at	AF188334
18064_r_at	
18069_at	
18216_at	AC012375
18217_g_at	AC012375
18235_at	AC000348
18252_at	AL096882
18272_at	AF002109
18533_at	AL021684
18556_at	AC006264
18590_at	AJ222713
18607_s_at	U78721
18635_at	AC004005
18716_at	AC007396
18920_at	AC002338
18928_at	AC002338
19034_at	AL021768
19171_at	AC002335
19178_at	AB035137
19182_at	AL031804
19251_at	AL035538
19640_at	AC004561
19977_at	AL049659
20034_i_at	A71607
20201_at	AL078470
20227_s_at	AB027252
20269_at	AC002387
20314_s_at	AL096882
20335_s_at	Y14208
20429_s_at	Z97336
20585_s_at	AC005309
20641_at	X91919

Table 14

Probe Set	Description
12505_s_at	AC005309
12879_s_at	U40856
12904_s_at	AB008103
13189_s_at	U35829
13217_s_at	AL049862
14116_at	AF077407
14148_at	AF224762
14201_at	AL163972
14248_at	AC007357
14250_r_at	AL050300
14691_at	AP002046
14704_s_at	AC006067
15846_at	AC006067
15847_g_at	AC006067
16063_s_at	AB008103
17500_s_at	AL049862
17544_s_at	U40856
18716_at	AC007396
19178_at	AB035137
19640_at	AC004561
20269_at	AC002387

Thus, Hiks1 induced upregulation is compromised in all four tested “loss of Hiks1 resistance mutants” and there is a correlation between breakdown of resistance and deregulation of these genes. This may indicate that these genes play important roles in mediating Hiks1 resistance. Furthermore, these genes appear to act downstream of all four genetically defined *RPP7* pathway components, *RPP7*, *EDM1*, *EDM2* and *EDM3*. Some genes of this set may encode important regulators; whereas others may indicate metabolic processes required for Hiks1 resistance.

Seventy-eight genes (Table 15; genes comprising SEQ ID NOs:330, 292, 311, 243, 237, 302, 315, 283, 300, 372, 308, 335, 272, 305, 357, 213, 362, 331, 254, 384, 277, 343, 298, 349, 314, 265, 262, 258, 256, 303, 321, 304, 275, 274, 323, 238, 374, 241, 344, 244, 365, 261, 380, 371, 295, 255, 316, 233, 345, 225, 260, 229, 324, 301, 235, 340, 278, 320, 231, 319, 230, 354, 353, 293, 376, 247, 246, 366, 216, 214, 276, 299, 310, 334, 271, 381 and 228) that show the same, but less pronounced, expression characteristics were selected using relaxed selection criterion (at least one 2-fold expression difference over all 12 calculated expression ratios). With a lower cutoff criterion of at least one 2-fold-expression difference across all twelve expression ratios, this cluster is larger

than that shown in Table 14. Genes that are part of this less stringently defined cluster were included in further analyses so as to not exclude potentially important genes. Potential regulators in this cluster are listed in Table 16 (genes comprising SEQ ID NOs: 220, 323, 231, 319, 214, 301, 340, 243, 227, 321, 235, 5 315, 298, 314, 328, 344 and 349). Four different ERF transcription factors genes are upregulated by the *RPP7*-pathway. Genes encoding ERFs are known to be upregulated in response to several stress-related stimuli, such as wounding, pathogens or ethylene. Moreover, ERF transcription factors bind to GCC boxes, which are ethylene, wounding and pathogen-responsive *cis*-elements. This 10 cluster also contains a gene encoding an ACC synthase, a component of the ethylene biosynthetic pathway. Therefore, ethylene may play a role in the Hiks response pathway.

Table 15

Probe Set	Description
12500_s_at	AF081067
12505_s_at	AC005309
12642_at	AC006920
12879_s_at	U40856
12904_s_at	AB008103
12905_s_at	AB008104
12908_s_at	AB008107
12909_s_at	Z97343
12916_s_at	AF021244
13177_at	AL049640
13187_i_at	U35829
13189_s_at	U35829
13217_s_at	AL049862
13273_s_at	U68017
13284_s_at	AJ002551
13615_at	AC002332
13617_at	AC006592
14116_at	AF077407
14141_at	AC011437
14148_at	AF224762
14201_at	AL163972
14223_at	AL024486
14248_at	AC007357
14250_r_at	AL050300
14614_at	AC004165
14643_s_at	AC006836
14672_s_at	U18993

14691_at	AP002046
14704_s_at	AC006067
14706_r_at	AL137189
14709_at	AP002046
14711_s_at	AF085279
15085_s_at	AL031018
15216_s_at	U75198
15431_at	AL030978
15523_s_at	AL078637
15616_s_at	AL078637
15622_s_at	U43945
15629_s_at	AB010407
15665_s_at	AF022658
15680_s_at	D42061
15846_at	AC006067
15847_g_at	AC006067
15866_s_at	AC005770
15978_at	X68592
16063_s_at	AB008103
16105_s_at	U68017
16393_s_at	AB008103
16412_s_at	U68017
16442_s_at	AJ002551
16536_s_at	AB008107
16539_s_at	Z97343
16569_s_at	L23968
16609_s_at	AB008104
16620_s_at	AF051338
16952_s_at	AC005662
16981_s_at	U35829
17073_s_at	AC006836
17119_s_at	AF132212
17379_at	AC018721
17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17917_s_at	AC004261
18070_r_at	
18216_at	AC012375
18217_g_at	AC012375
18255_at	AC005770
18591_at	X74756
18716_at	AC007396
18876_at	AF002109
19178_at	AB035137
19182_at	AL031804
19640_at	AC004561
20017_at	AC004521

20269_at	AC002387
20297_at	AC007153
20429_s_at	Z97336

Additionally, a gene encoding a lipoxygenase, a component of the jasmonic acid biosynthetic pathway, is upregulated. Other regulators potentially acting downstream of RPP7, EDM1, EDM2 and EDM3 include some putative
 5 zinc finger transcription factors and protein kinases as well as two calmodulin-like proteins and a calcium binding protein, which may point to a role of calcium in the *RPP7*-pathway.

Table 16

10 I. Transcriptional regulators:

- 1.) AtERF1 (12904_s_at, BAA32418.1; AB008103)
- 2.) AtERF2 (16609_s_at, BAA32419.1; AB008104)
- 3.) EREBP4-like (12909_s_at, CAB10530.1; Z97343)
- 4.) AtERF5 (16536_s_at, BAA32422.1; AB008107)
- 15 5.) putative CONSTANS-like zinc finger (12505_s_at, AAC63643.1; AC005309)
- 6.) putative C2H2 zinc finger transcription factor (15665_s_at, AAB80922.1; AF022658)
- 7.) putative C3H zinc finger protein (17379_at, AAF18728.1; AC018721)
- 20 8.) heat shock transcription factor 4 (13273_s_at, AAC31756.1; U68017)
- 9.) SigA binding protein (14148_s_at, AAF34713.1; AF224762)

II. Other signaling proteins

- 10.) AtACS-6 (12892_g_at, CAB51412.1, AL096882, 35400..37154)
- 11.) lipoxygenase (16569_s_at, AAA32749.1; L23968)
- 25 12.) growth factor like protein (13177_at, CAB40989.1; AL049640)
- 13.) serine/threonine protein kinase (16412_s_at, CAA18704.1; AL022603)
- 14.) wall associated kinase 1 (15616_s_at, CAB08794.1; AJ009696)
- 15.) putative receptor-like protein kinase (16393_s_at, AAD28318.1; AC006436)
- 30 16.) calmodulin-like (16951_i_at, AAC78532.1; AC005662)
- 17.) calmodulin-like (17500_s_at; CAB42906.1; AL049862)
- 18.) calcium binding protein (17917_s_at, AAD12002.1; AC004261)

Twenty-six genes (genes comprising SEQ ID NOs: 300, 308, 272, 213, 362, 265, 374, 241, 261, 380, 310, 228, 233, 330, 311, 243, 237, 254, 230, 244, 365, 216, 316, 345, 225, 301, 278, 354, 353, 293, 335, 271 and 321, also shown in Table 15), represented by 33 probe sets, were found to be commonly

5 upregulated in response to both *Peronospora* isolates, Hiks1 and Emco5, in an *RPP7*- or *RPP8*-dependent (and *EDM1*, *EDM2* and *EDM3*-dependent) manner (Table 17). Elevated expression of these genes may be required for resistance against both *Peronospora* isolates or against *Peronospora parasitica* in general. Among these 26 genes are those encoding ERF1, putative zinc finger

10 transcription factors, two proteins potentially involved in calcium signaling, a lipoxygenase, and a cysteine rich antifungal protein.

Table 17

15	26 <i>Peronospora</i> (Hiks1 and Emco5) induced RPP8, RPP7, EDM1,2,3-dependent genes	
	Transcription factors	
	AtERF1	
	Putative salt-tolerance zinc finger transcription factor (18217_g_at)	
20	(ZFPI) hypothetical Cys-3-His zinc finger protein	
	Putative C2H2 zinc finger transcription factor	
	Heat shock transcription factor 4	
	Other potential proteins	
25	Calmodulin-like protein	
	Similarity to centrin, <i>Marsilea vestita</i> contains EF-hand calcium-binding domain (15431_at)	
	Lipoxygenase	
30	Others	
	heat shock protein 70	
	putative steroid sulfotransferase	tryptophan synthase alpha chain
	putative glucosyltransferase	similar to xyloglucan fucosyltransferase (12642_at)
35	phosphoglycerate dehydrogenase	Pad3 (Cytochrome P450)
	ATAF2	putative pectinesterase
	OPDA-reductase homolog	AIG1
	coronatine-induced protein 1	putative glutathione S-transferase
	thioredoxin h	adenosine nucleotide translocator
40	IAA-amino acid hydrolase	contains similarity to sugar transporters
		CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 PRECURSOR (AFP1) (18716_at)

Thirteen of these 26 genes (genes comprising SEQ ID NOs: 308, 300, 272, 362, 265, 242, 261, 380, 228, 243, 254, 216 and 225, *Peronospora* (Hiksl, Emco5 and Emoy2) induced and *RPP4*, *RPP8* and *RPP7* dependent) were also found to be more strongly expressed during the incompatible interaction between the *Peronospora* isolate Emoy2 and Col-0 plants as compared to Emoy2 infections of the compatible or intermediate type (see Table 18). These 13 genes may play an important role in defense against *Peronospora parasitica* in general. Among these genes is PAD3, which was previously demonstrated to be required for pathogen-induced phytoalexin production. Strikingly, Hiksl resistance is partially compromised in the *pad1-1/pad3-1* double mutant, whereas Emoy2 resistance is reduced in the *pad3-1* single mutant (Glazebrook et al. 1997).

Table 18

13 *Peronospora* (Hiksl, Emco5 and Emoy2) induced
RRP4-pathway, RPP7-pathway, and RPP8-dependent genes

- adenosine nucleotide translocator (15978_at)
- phosphoglycerate dehydrogenase (15629_s_at)
- tryptophan synthase alpha chain (14672_s_at)
- ATAF2 (18591_at)
- putative glucosyltransferase (14614_at)
- calmodulin-like protein (13217_s_at)
- pad3 (cytochrome P450)(14248_at)
- putative pectinesterase (20269_at)
- ethylene responsive element binding factor 1 (12904_s_at)
- heat shock transcription factor 4 (13273_s_at)
- sugar transporter-like (14116_at)
- similar to xyloglucan fucosyltransferase (12642_at)
- AIG1 (12879_s_at)

Identification of promoter motifs common to *RPP7* and *RPP8* controlled genes

Sequence motifs conserved in the promoters of genes co-regulated by the *RPP7* or *RPP8* pathways may lead to information about the types of transcription factors controlling expression of these genes and may serve as starting points for isolating and/or cloning of such factors. Sub-categorization of *RPP7*-

5 upregulated genes by K-means clustering, based on the absolute expression levels of the genes, revealed the existence of only a few basic expression profiles. K-means clustering into five gene sets gave the most consistent and tight clusters. For each of the five gene sets (Table 19), the expression changes in two repetitions of the Col-0 wild type/Hiks1 interaction are shown as well as
10 in the *rpp7* mutant and *edm1*, *edm2* and *edm3*.

The first set comprises genes (genes comprising SEQ ID NOs: 292, 302, 315, 300, 308, 213, 265, 374, 241, 344, 261, 299, 365 and 276) that show early and transient upregulation. The genes peak at 12 hours and return to their ground-states at approximately the 48 hours post infection. Genes of the second
15 set (genes comprising SEQ ID NOs: 267, 305, 357, 362, 380, 310, 228, 295, 233, 329, 312, 243, 237, 283, 372, 254, 314, 323, 216, 260, 229 and 235) are also rapidly upregulated, but show a less pronounced or no decline after the peak. In both sets, the response is weaker in the mutants. Only a few genes in the first set respond almost as strongly in *edm2* and *edm3* plants as in wild type plants.
20 Genes of the third (genes comprising SEQ ID NOs: 258, 256, 303, 304, 275, 244, 316, 354 and 225) and fifth (genes comprising SEQ ID NOs: 330, 384, 277, 343, 298, 349, 262, 274, 238 and 301) set show an almost linear increase of transcript level in wild type. In the mutants, this increase is delayed and in some cases less steep. In the fourth set (genes comprising SEQ ID NOs: 432, 347,
25 370, 412, 323, 411, 322, 449, 448, 385, 471, and 339) the expression levels rise in the first repetition of the Col-0 wild type/Hiks interaction, but respond very little in the second one. In *edm3*, the transcript levels drop from a high ground state. The probe sets and genes corresponding to each of these K-means cluster sets are shown in Table 19.

30

Table 19

K-means set 1	Description	K-means set2	Description
12500_s_at	AF081067	12642_at	AC006920
13217_s_at	AL049862	12904_s_at	AB008103
14248_at	AC007357	12905_s_at	AB008104

14614_at	AC004165	12916_s_at	AF021244
14706_r_at	AL137189	13177_at	AL049640
15216_s_at	U75198	13187_i_at	U35829
15622_s_at	U43945	13273_s_at	U68017
15629_s_at	AB010407	14116_at	AF077407
15680_s_at	D42061	14223_at	AL024486
15978_at	X68592	14672_s_at	X76609
16412_s_at	U68017	15085_s_at	AL031018
17500_s_at	AL049862	15523_s_at	AL078637
18070_r_at		15866_s_at	AC005770
18716_at	AC007396	16063_s_at	AB008103
19640_at	AC004561	16105_s_at	AL049730
		16393_s_at	AC006436
		16609_s_at	AB008104
		16952_s_at	AC005662
K-means set 3	Description	18255_at	AC005770
12879_s_at	U40856	18591_at	X74756
13284_s_at	AJ002551	19182_at	AL031804
14148_at	AF224762	20269_at	AC002387
14201_at	AC068667		
14704_s_at	AC006067		
15846_at	AC006067	K-means set 5	Description
15847_g_at	AC006067	13189_s_at	U35829
16442_s_at	AJ002551	14250_r_at	AL050300
17544_s_at	U40856	14691_at	AP002046
		14709_at	AP002046
K-means set4	Description	15616_s_at	AJ009696
12908_s_at	AB008107	15665_s_at	AF022658
12909_s_at	Z97343	16981_s_at	U35829
13617_at	AC006592	17499_s_at	AF107726
14141_at	AC011437	17917_s_at	AC004261
14711_s_at	AF085279	20429_s_at	Z97336
15431_at	AL030978		
16536_s_at	AB008107		
16539_s_at	Z97343		
17379_at	AC018721		
18216_at	AC012375		
18217_g_at	AC012375		
20017_at	AC004521		

Recently, the plant specific family of WRKY transcription factors has been implicated in the regulation of defense-associated genes. Promoters of genes upregulated during systemic acquired resistance were found to be strongly enriched in potential WRKY binding sites. WRKY factors comprise a large family of 72 different members in *Arabidopsis*. Generally these factors appear to bind to sequence motifs containing the core T G A C (W box). It has not yet

been determined whether individual WRKY family members differ in their preferences for distinct W box variations. However, it is probable that a given WRKY protein has a binding preference for a certain variation of the W box motif:

5 Using the program AlignACE, three variations of potential WRKY binding sites were found to be conserved in sub-sets of *RPP7* controlled genes. Two of these motifs are highly enriched in promoters of genes from K-means cluster 3, representing genes that show a linear increase in transcript level after *Peronospora* infection (Table 20; genes comprising SEQ ID NOs: 384, 298, 349, 10 262 and 238 for W box I and genes comprising SEQ ID NOs: 384, 349, 262, 238 and 301 for W box II). These motifs are also present in promoters of K-means cluster 5, which represents a similar expression profile. Focusing on sustained up-regulated genes, that show a particularly pronounced expression difference between Col-0 wild type plants and the Hiks1 response mutants, a third variation 15 of potential WRKY binding sites was found to be significantly enriched (Table 21; genes comprising SEQ ID NOs: 397, 371, 238, 262, 256, 275, 254, 214 and 225). In all three cases, sequence conservation clearly exceeds the core motif of WRKY binding sites that appears to be recognized by all members of this family. These additionally conserved positions may confer specificity for 20 certain WRKY family members. They may provide a highly defined binding site preferentially recognized by a distinct WRKY factor or may serve as binding sites for another transcription factor binding closely adjacent to and specifically interacting with a distinct WRKY factor. In any case, the high conservation of extended potential WRKY binding motifs strongly suggests that specific 25 members of this family participate in the regulation of certain sub-sets of *RPP7*-controlled genes.

Table 20

<u>W box I</u>		MAP Score: 8.98114		
30	GTCATCTTTTAATCTCTGG	0	638	1
	GTCATCTTTTAATCGCCGG	0	932	1
	GCCTTTGCTTATTTATAGG	0	1036	1
	GTCATTTGTTACAAAGAGG	1	318	1
	GTCATTGATCATAAACTGT	1	389	0
35	GCCACTGCTGAATTGTCGG	1	494	1
	GTCCATTGTCAATAAATGG	2	689	1
	GTCCATTGTAAATAAATGT	2	949	1

5 GTCATCTTTTAATCTCTGT 3 475 0
 GTCACGTATGAATGGAAGG 4 73 1
 GTCAACGTTTtagttCATGT 4 226 0
 GTCAAGTTTTTAAATTGTGG 4 352 1
 GTCAACGTTTtagttCATGT 4 401 0
 *** * * * * **

GTCANNNTNTNANTNNNNGG

G A T

10 Expected frequency by chance: 0.02/1kb
 Observed frequency: 1.2/1kb
 Enrichment: ~60 fold

W box II MAP Score: 15.2966

15 ATTAAAAGATGAC 0 638 0
 ATTAAAAGATGAC 0 932 0
 ATTAAATGCTGTC 2 752 0
 ATTAAATGCTGTC 2 1011 0
 AGCAAAAGCTGAC 2 1092 1
 ATTAAAAGATGAC 3 481 1
 ATCAAAAGTTGTC 3 829 1
 20 ACTAAACGTTGAC 4 232 1
 ACTAAACGTTGAC 4 407 1
 ACTAAAAGTGAC 5 755 1
 * * * * *

25 W II ANTAAANGNTGAC
 C A T

W I: CCNNNNANTNANCNNTGAC
 A T A

30 Expected frequency by chance: 0.04/1kb
 Observed frequency: 1.35/1kb
 Enrichment: ~30 fold
 Table 21

35 ATAGGTGGTCAAGT 1 106 0
 AATTGTGGTCATTT 1 823 0
 ACTTGTGGTCAATT 2 804 0
 AAAAGGGGTCATTT 2 970 1
 ATATGTCGTCTCTT 2 994 0
 AGTTGTGGTCTACC 3 502 0
 40 AAAAGTTGTCAATT 3 732 1
 AGACGTCGTAATTT 4 400 0
 ACGTGGCGTCATAT 5 179 0
 ATGTGGCGTCTCCT 6 249 1
 AGTTGGTGTACGCT 6 925 1
 45 ATTCGTGGTCAACT 7 582 1
 ATATGTCGTCACTT 7 875 1
 * * * * *

ANNNGTNGTCANNT

G

50

expected: 0.05/1kb;
 in random set: 0/1kb;
 this set: 1/1kb;
 enrichment: 10-20 fold;

5

Novel, conserved promoter motifs were also found. Genes of K-means set 1, which are early and transient *RPP7*-pathway specific genes, share two similar highly conserved promoter motifs, G G T/C C C A (SEQ ID NO:714; genes comprising SEQ ID NOs: 302, 315, 308, 265, 374, 241, 261, 299 and 365) and G N C C A A A (SEQ ID NO:715; genes comprising SEQ ID NOs: 292, 302, 308, 265, 374, 241, 261, 299, 365 and 276) (Table 22). Both motifs are almost perfectly conserved and are represented in nearly all promoters of this gene set. They are compact six- or seven-mers, which is typical for transcription factor binding sites. For the second motif, the permutations G A C C A A A and G T C C A A A are strongly represented. These permutations may constitute the preferred binding site of a so far unknown transcription factor.

15

Table 22

20

Two related novel motifs are highly enriched in all
 11 promoters of K-means set1

25

30

35

40

GGTCCA 1 232 0
 GGCCCA 1 289 1
 GGTCCA 1 597 1
 GGTCCA 2 517 0
 GGTCCA 3 211 1
 GGCCCA 3 360 1
 GGTCCA 4 597 1
 GGCCCA 4 681 1
 GGTCCA 5 352 0
 GGTCCA 5 1060 1
 GGTCCA 6 358 0
 GGCCCA 7 776 0
 GGCCCA 7 816 0
 GGTCCA 8 285 0
 GGTCCA 9 888 1

 GGTCCA C
 Expected frequency by chance: 0.22/1kb
 Observed frequency: 1.2/1kb
 Enrichment: 5.4 fold
 GCCCAAA 0 601 1
 GTCCAAA 10 1186 1
 GTCCAAA 9 562 1

5 GACCAAA 8 640 0
 GCCCAA 7 774 0
 GTCCAA 7 717 1
 GTCCAA 6 712 1
 GACCAAA 5 970 1
 GTCCAA 5 350 0
 GACCAAA 4 1164 1
 GACCAAA 4 1072 1
 GTCCAA 4 784 0
 10 GACCAAA 4 714 0
 GGCCAA 4 698 0
 GCCCAA 3 361 1
 GACCAAA 1 920 0
 GTCCAA 1 230 0
 15 *****
 GNCCAA
 Expected frequency by chance: 0.32/kb
 Observed frequency: 1.3/kb
 Enrichment: 4 fold
 20

Following a similar approach as for the Hiks1-induced *RPP7* pathway controlled genes, a cluster of early and transiently Emco5-induced *RPP8*-dependent genes were defined (Table 23). In Col-0-*RPP8* plants these genes (genes comprising SEQ ID NOs: 364, 341, 288, 378, 363, 379 and 219) show a very pronounced upregulation 12 hours post Emco5 infection, after which they return to expression ground states. Using AlignACE, two different motifs (see Example 2) were found to be strongly enriched in the promoters of this cluster. The first motif strongly resembles the type I consensus binding site of Myb transcription factors. This motif is also almost identical to a recently identified *cis*-element conferring rapid elicitor responsive gene expression in parley cell culture (Kirsch et al., 2001). Interestingly, a gene encoding a Myb-like transcription factor (highlighted in yellow) is co-regulated with other genes of this cluster. The Myb-like transcription factor gene is the only gene of this cluster that does not contain this conserved motif in its promoter. This MYB-like factor could be a regulator of this cluster. The second motif does not resemble any known stress responsive plant *cis* element or transcription factor binding site. However, the second motif was found to be strongly represented in promoters from other defense related genes, such as SAR genes. As is typical of many transcription factor binding sites, certain permutations of its consensus

sequence may constitute palindromes. This motif was also found to be conserved by the program MEME.

Table 23

5	Glutathione-conjugate transporter AtMRP4 putative GST putative cytochrome P450 (AC002340) PAD3 (similar to cytochrome P450) CTF2B (similarity to proteins involved in	
10	Hydroxylation and oxidation of aromatic rings) Ribonuclease RNS1 Putative Myb-like protein AlignACE Motif 1:	CAACTTTGAC AA TT CAACTG T G
15	type I Myb binding site:	
	Frequency by chance: 0.05/1kb Observed frequency in control cluster: 0.13/1kb	
20	Observed frequency in this cluster: 1.10/1kb AlignACE Motif2:	TTGGGNCNAA A A
	MEME motif:	GTCTNTTGGGNCAAAA TT A G C
25	Frequency by chance: 0.13/1kb Observed frequency in control cluster: 0/1kb Observed frequency in this cluster: 1.2/1kb	

Different types of transcription factors may participate in the control of distinct *RPP7*-pathway dependent expression profiles. Promoters of genes showing a linear sustained increase of transcript are enriched in different variations of WRKY binding sites. However, no *WRKY*-pathway gene was found to be upregulated by the *RPP7* pathway. Therefore, WRKY factors involved in *RPP7* mediated up-regulation of K-means cluster 3 and 5 genes may already be pre-formed when the pathogen signal is perceived. However, only 21 *WRKY* genes out of 72 members of this family in *Arabidopsis* are represented on the oligonucleotide chip. Upregulated WRKY factors participating in *RPP7* mediated gene regulation may not be present on the chip. A novel type of transcription factor may be involved in regulation of early and transient *RPP7*-controlled genes (K-means cluster 1). Promoter stretches containing this motif may be used in yeast one hybrid screenings for novel factors. In addition, transgenic plants carrying appropriate promoter-reporter constructs could be used

as a basis for mutant screenings with the aim of identifying regulators acting on this motif.

A Myb-like transcription factor appears to be involved in the regulation of early and transient *RPP8*-controlled genes. A gene showing a similar pattern of regulation may encode a candidate factor controlling this cluster. The potential role of this factor in regulating *RPP8*-controlled genes may be examined using T-DNA insertion mutants.

Potential constitutive effects of the *RPP7*-pathway

In order to focus on genes showing multiple expression differences between Col-0 wild type plants and Hiks response mutants, all genes that showed at least four 1.8-fold expression differences across all comparisons were selected. The resulting clustergram contains the majority of *RPP7* pathway-dependent Hiks1-induced genes. Two more clusters of genes behaving consistently in all four tested Hiks1-response mutants were found. The first cluster comprises genes that show at all tested time points (including the 0 hpi time point) elevated transcript levels in Col-0 wild type plants as compared to all four mutants (Table 24; genes comprising SEQ ID NOs: 364, 288, 378, 363, 379, 219, 399, 389 and 390). In most cases, expression levels are not affected by Hiks1 infection. These elevated expression levels may be directed by constitutive (non Hiks1-triggered) signal flow via the *RPP7* pathway. This signal flow is disrupted in the *rpp7*, *edm1*, *edm2* and *edm3* mutants. Constitutive expression of these genes may be required for effective disease resistance and may be a prerequisite for induction of subsequent defense responses. A HD-ZIP transcription factor, which is included in this cluster, may act as a pre-formed regulator controlling genes responding to Hiks1-recognition. Its potential role in regulating *RPP7* pathway-dependent genes may be examined using T-DNA insertion mutants.

Table 24

The *RPP7* pathway constitutively activates a cluster of genes including a HD-ZIP transcription factor

PROBE SET	DESCRIPTION
14965 at	AC002329
18635 at	AC004005
14295 s at	Z54356
17386 at	AC006264

15145 s at	D64155
20201 at	AL078470
18607 s at	U78721
20227 s at	AC007153
12761 s at	AC006577
20555 s a	AL080318

Genes of the second cluster show the opposite behavior (Table 25). Their transcript levels are elevated in all four Hiks1 response mutants as compared to Col-0 wild type plants. Hiks1-infection does also not affect their expression levels. Surprisingly, this cluster contains six genes encoding peroxidases. Since peroxidases are believed to play roles in conferring disease resistance, the biological significance of this phenomenon is obscure. Perhaps the mutant plants “realize” disruption of the *RPP7*-defense pathway and compensate for their reduced defense capacity by constitutively up-regulating some defense mechanisms. Alternatively, elevated expression of these peroxidases may be advantageous for invading *Peronospora* hyphae. Therefore, expression of these genes could be constitutively reduced by the *RPP7* pathway.

Table 25

Probe Set	Description
15982_s_at	X98190
15954_at	U72155
12333_at	AJ286345
19594_i_at	X98321
15969_s_at	AJ133036
16462_s_at	AC004683
16461_i_at	AC004683
12324_i_at	AC007212
12778_r_at	AC006577
16514_at	AL035538
17549_s_at	L37126
14028_at	AF075597
17054_s_at	AF134128

Predictions about *RPP7*-pathway hierarchy

Clustering of the Hiks1-infection data in the “treatment” dimension, instead of the “gene” dimension, revealed that at all three infection time points, gene expression profiles of the *rpp7* mutant resemble most those of the *edm1* mutant. Similarly, expression profiles of the *edm2* mutant resemble those of the

edm3 mutant. This may indicate that RPP7 and EDM1 closely act together at a certain level in the *RPP7* signalling cascade, whereas EDM2 and EDM3 may act closely together at a different level of the pathway. Close interaction of RPP7 and EDM1 is also suggested by a T-DNA tagged *rpp7* mutant that

5 phenotypically resembles the *edm1* mutant. In contrast to *rpp7*, *edm2* and *edm3*, which appear only to be compromised in resistance against the *Peronospora* isolate Hiks1, *edm1* is also compromised in resistance to other *Peronospora* isolates that are avirulent on Col-0 plants. Like *edm1*, the putatively T-DNA tagged *rpp7* mutant is also susceptible to a variety of normally Col-0

10 incompatible *Peronospora* isolates. This observation may indicate that the EDM1 protein requires a portion of the RPP7 protein for proper function, which is disrupted in the T- DNA tagged *rpp7* mutant. Assuming that RPP7, which appears to constitute an NBS-LRR receptor, acts at the top of the Hiks1 recognition pathway hierarchy, EDM1 could act at a high level as well and

15 EDM2 and EDM3 may act more downstream in the cascade.

Table 26



Table 27 shows the plant and fungal orthologs of the *Arabidopsis* sequences identified herein.

Table 27

Query= AIG1_s_at 12879_s_at /id_source genbank /description
gb|aac49282.1| (u40856) aig1 [arabidopsis thaliana] /blast_score
1.00e-150

5 (1381 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

10 Searching.....done

	Score	E	
Sequences producing significant alignments:		(bits)	Value
15	gb U64925 NTU64925 Nicotiana tabacum geranylgeranylated protein ...	260	1e-68
	emb AW625701 AW625701 EST319608 tomato radicle, 5 d post-imbibit...	228	6e-59
	emb AW720227 AW720227 LjNEST17c4r Lotus japonicus nodule library...	219	4e-56
	emb AW220184 AW220184 EST302667 tomato root during/after fruit s...	208	7e-53
	emb AI774580 AI774580 EST255680 tomato resistant, Cornell Lycopersicon...	173	2e-42
20	emb AW685484 AW685484 NF030E02NR1F1000 Nodulated root Medicago t...	171	2e-41
	emb AI443867 AI443867 sa44d09.y1 Gm-c1004 Glycine max cDNA clone...	170	3e-41
	emb AW397252 AW397252 sg76f06.y1 Gm-c1007 Glycine max cDNA clone...	168	1e-40
	emb AW033368 AW033368 EST276939 tomato callus, TAMU Lycopersicon...	162	5e-39
	emb AV417858 AV417858 AV417858 Lotus japonicus young plants (two...	153	4e-36
25	emb AI780050 AI780050 EST260929 tomato susceptible, Cornell Lyco...	138	9e-32
	emb AW039095 AW039095 EST281068 tomato mixed elicitor, BTI Lycop...	111	2e-23
	emb AI780139 AI780139 EST261018 tomato susceptible, Cornell Lyco...	86	7e-16
	emb AW164180 AW164180 Ljimpest21-672-c8 Ljimp Lambda HybriZap ...	84	2e-15
	emb AI781596 AI781596 EST262475 tomato susceptible, Cornell Lyco...	75	1e-12
30	emb AW774764 AW774764 EST333915 KV3 Medicago truncatula cDNA clo...	62	7e-09
	emb AW348781 AW348781 GM210003A22H11R Gm-r1021 Glycine max cDNA ...	54	2e-06
	emb AI491210 AI491210 EST241919 tomato shoot, Cornell Lycopersic...	29	0.010
	emb AW651526 AW651526 EST329980 tomato germinating seedlings, TA...	29	0.011
	emb AW220594 AW220594 EST296979 tomato fruit mature green, TAMU ...	29	0.011
35	emb AW926585 AW926585 HVSMeg0007J19 Hordeum vulgare pre-anthesis...	29	0.025
	emb AW032321 AW032321 EST275775 tomato callus, TAMU Lycopersicon...	28	0.026
	emb AW736598 AW736598 EST333090 KV3 Medicago truncatula cDNA clo...	37	0.39
	emb AW736597 AW736597 EST333089 KV3 Medicago truncatula cDNA clo...	37	0.39
	emb AW713727 AW713727 h1f12ne.fl Neurospora crassa evening cDNA ...	35	1.0
40	emb AW711542 AW711542 f3g07ne.fl Neurospora crassa evening cDNA ...	35	1.0
	emb AB009972 AB009972 Aspergillus oryzae gene for beta-1,4-xylos...	35	1.0
	emb AW713709 AW713709 h1e09ne.fl Neurospora crassa evening cDNA ...	35	1.0
	emb AW712721 AW712721 g3a07ne.fl Neurospora crassa evening cDNA ...	35	1.0
	emb AW709185 AW709185 d3e02ne.fl Neurospora crassa evening cDNA ...	35	1.0
45	emb Y09354 SPABC1 S.pombe ABC1 gene.	35	1.4
	emb Z99262 SPAC9E9 S.pombe chromosome I cosmid c9E9.	35	1.4
	emb AJ225108 STA225108 Solanum tuberosum (cultivar Bintje) mitoc...	35	1.4
	emb AW933326 AW933326 EST359169 tomato fruit mature green, TAMU ...	26	1.5
	emb Z25870 CACDC10G C.albicans CDC10 gene for cell division cycl...	31	1.5
50	emb AC008368 AC008368 Trypanosoma brucei chromosome II clone RPC...	35	1.9
	emb AQ942780 AQ942780 Sheared DNA-42B15.TR Sheared DNA Trypanoso...	35	1.9
	emb AQ953508 AQ953508 Sheared DNA-33G8.TR Sheared DNA Trypanosom...	35	1.9
	emb AC009463 AC009463 Trypanosoma brucei chromosome II clone RPC...	35	1.9
	emb AQ950237 AQ950237 Sheared DNA-39C11.TF Sheared DNA Trypanoso...	35	1.9
55	emb AQ643883 AQ643883 RPCI93-DpnII-26C13.TV RPCI93-DpnII Trypano...	35	1.9
	emb AQ948491 AQ948491 Sheared DNA-49H2.TF Sheared DNA Trypanosom...	35	1.9
	emb AW727289 AW727289 GA__Ea0011H24 Gossypium arboreum 7-10 dpa ...	35	1.9
	emb AW729536 AW729536 GA__Ea0025E24 Gossypium arboreum 7-10 dpa ...	35	1.9
	gb L36856 PEAIAP34A Pisum sativum GTP-binding protein (IAP34) mR...	28	2.1
60	emb Z28341 PSCLOEP P.sativum (miranda) mRNA for chloroplast oute...	28	2.1

	emb AW776020 AW776020 EST335085 DSIL Medicago truncatula cDNA cl...	28	2.2
	emb AW685649 AW685649 NF032G04NR1F1000 Nodulated root Medicago t...	28	2.2
	emb AW690755 AW690755 NF037H10ST1F1000 Developing stem Medicago ...	28	2.2
	emb AW256896 AW256896 EST305033 KV2 Medicago truncatula cDNA clo...	28	2.3
5	emb AV422565 AV422565 AV422565 Lotus japonicus young plants (two...	28	2.3
	emb AW832303 AW832303 sm07c04.y1 Gm-cl027 Glycine max cDNA clone...	27	2.3
	emb AL136538 SPAC30 S.pombe chromosome I cosmid c30.	34	2.6
	emb AI724721 AI724721 RHIZ1_26_C05.y2_A001 Rhizome1 Sorghum hale...	34	2.6
	emb AW256609 AW256609 EST304746 KV2 Medicago truncatula cDNA clo...	34	2.6
10	emb AI775696 AI775696 EST256796 tomato resistant, Cornell Lycopersicon...	28	3.1
	emb Z71682 SCYNR067C S.cerevisiae chromosome XIV reading frame O...	34	3.6
	emb AI776315 AI776315 EST257415 tomato resistant, Cornell Lycopersicon...	34	3.6
	emb AF230371 AF230371 Lycopersicon esculentum allene oxide synth...	34	3.6
	emb AA741645 AA741645 LmLv39p3/255A Leishmania major promastigot...	34	3.6
15	gb U08843 PPU08843 Porphyra purpurea putative polysaccharide bin...	34	3.6
	emb AF124792 AF124792 Sporothrix schenckii protein kinase C (PCK...	29	4.7
	emb AQ399149 AQ399149 mgxb0019C01f CUGI Rice Blast BAC Library P...	33	5.0
	emb AW615911 AW615911 EST325409 tomato flower buds 0-3 mm, Corne...	33	5.0
	emb AW035453 AW035453 EST281191 tomato callus, TAMU Lycopersicon...	33	5.0
20	emb AF051695 AF051695 Trypanosoma cruzi sialidase homolog (P85.1...	33	5.0
	emb Z37538 LTGRR4 L.tarentolae mRNA encoding putative NADH subun...	28	5.5
	emb X85021 SCXLTORFS S.cerevisiae DNA from left arm of chromosom...	33	6.8
	gb L25088 YSCMEF2MIT Saccharomyces cerevisiae nuclear-encoded mi...	33	6.8
	emb AQ443826 AQ443826 GSSTc01287 Trypanosoma cruzi random genom...	33	6.8
25	emb AQ502942 AQ502942 V47H4 mTn-3xHA/lacZ Insertion Library Sacc...	33	6.8
	emb Z85962 MSZ85962 Musa sp. DNA for sequence tagged microsatell...	33	6.8
	emb Z49377 SCYJL102W S.cerevisiae chromosome X reading frame ORF...	33	6.8
	emb AW224537 AW224537 EST302980 tomato root, plants pre-anthesis...	31	7.5
	emb AW257183 AW257183 EST305320 KV2 Medicago truncatula cDNA clo...	32	9.4
30	emb AQ642922 AQ642922 RPCI93-DpnII-27E7.TV RPCI93-DpnII Trypanos...	32	9.4
	emb AW738509 AW738509 EST339936 tomato flower buds, anthesis, Co...	32	9.4
	emb AW217351 AW217351 EST296174 tomato flower buds 0-3 mm, Corne...	32	9.4
	emb AW219255 AW219255 EST301737 tomato root during/after fruit s...	32	9.4
	emb AC007865 AC007865 Trypanosoma brucei chromosome II clone RPC...	32	9.4
35	emb AW684118 AW684118 NF012F02NR1F1000 Nodulated root Medicago t...	32	9.4
	emb AW622239 AW622239 EST313037 tomato root during/after fruit s...	32	9.4
	emb AQ651543 AQ651543 Sheared DNA-7C22.TF Sheared DNA Trypanosom...	32	9.4
	emb Y11565 NC11565 N.crassa acu-15 gene.	32	9.4
	emb AW775944 AW775944 EST335009 DSIL Medicago truncatula cDNA cl...	32	9.4
40	emb AB014493 AB014493 Gibberella zeae gene for reductase, partia...	32	9.4

Query= ASA1_s_at 12889_s_at /id_source genbank /description

45 gb|aaa32738.1| (m92353) anthranilate synthase alpha subunit
[arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
/gb_link /ncgi
(1788 letters)

Database: plantfungal

50 661,018 sequences; 426,114,510 total letters

Searching.....done

55 Score E
Sequences producing significant alignments: (bits) Value

60 gb|L34344|RTAANTSYNB Ruta graveolens anthranilate synthase alpha... 772 0.0
gb|L34343|RTAANTSYNB Ruta graveolens anthranilate synthase alpha... 467 0.0
emb|AF079168|AF079168 Nicotiana tabacum feedback-insensitive ant... 365 0.0
emb|AW931942|AW931942 EST357785 tomato fruit mature green, TAMU ... 356 3e-97
emb|AW218352|AW218352 EST303535 tomato radicle, 5 d post-imbibit... 210 1e-73

- emb|AL031966|SPCC1442 *S.pombe* chromosome III cosmid c1442. 209 6e-69
emb|AW651095|AW651095 EST329549 tomato germinating seedlings, TA... 222 2e-64
dbj|D89256|D89256 *Schizosaccharomyces pombe* mRNA, partial cds, c... 205 5e-64
emb|AW982499|AW982499 HVSMeg0003G22f *Hordeum vulgare* pre-anthesi... 215 2e-58
5 emb|AW460005|AW460005 si07d11.y1 *Gm-c1029* Glycine max cDNA clone... 116 1e-57
gb|U18839|SCE9747 *Saccharomyces cerevisiae* chromosome V cosmids ... 123 4e-48
emb|X68327|SCTRP2 *S.cerevisiae* TRP2 gene for anthranilate syntha... 123 4e-48
emb|AW719463|AW719463 LjNEST5b1r *Lotus japonicus* nodule library,... 184 1e-45
emb|AI736775|AI736775 sb33d01.y1 *Gm-c1012* Glycine max cDNA clone... 104 2e-40
10 gb|K01388|YSCTRP2 Yeast (*S.cerevisiae*) TRP2 gene coding for anth... 122 4e-38
emb|AL032684|SPBP8B7 *S.pombe* chromosome II pl p8B7. 95 6e-25
emb|AW509018|AW509018 si39b01.y1 *Gm-r1030* Glycine max cDNA clone... 113 5e-24
gb|T14852|T14852 crs299 *lambda*ZAPST *Ricinus communis* cDNA clone ... 107 2e-22
emb|AW223881|AW223881 EST300692 tomato fruit red ripe, TAMU Lycop... 103 4e-21
15 emb|AF119554|AF119554 *Plasmodium falciparum* para-aminobenzoic ac... 67 6e-10
emb|AL111470|CNS019CM *Botrytis cinerea* strain T4 cDNA library un... 45 2e-05
emb|AI329873|AI329873 b9g02ne.r1 *Neurospora crassa* evening cDNA ... 48 3e-04
emb|AW224247|AW224247 EST300974 tomato fruit red ripe, TAMU Lycop... 46 7e-04
emb|AF149719|AF149719 *Aspergillus fumigatus* para aminobenzoic ac... 42 0.012
20 emb|AQ448372|AQ448372 mgxb0020C12f CUGI Rice Blast BAC Library P... 39 0.15
emb|AQ324360|AQ324360 mgxb0018K01r CUGI Rice Blast BAC Library P... 39 0.15
emb|AQ160089|AQ160089 mgxb0003G09r CUGI Rice Blast BAC Library P... 39 0.15
emb|AW599019|AW599019 gb01b03.y1 Moss EST library PPN Physcomitr... 37 0.38
emb|AW599000|AW599000 ga99h03.y1 Moss EST library PPN Physcomitr... 37 0.38
25 emb|AW678847|AW678847 WS1_1_A04.g1_A002 Water-stressed 1 (WS1) S... 35 0.88
emb|AW680390|AW680390 WS1_52_D12.g1_A002 Water-stressed 1 (WS1) ... 35 0.89
emb|AW678385|AW678385 WS1_15_H06.g1_A002 Water-stressed 1 (WS1) ... 35 0.89
emb|AW747146|AW747146 WS1_66_E07.b1_A002 Water-stressed 1 (WS1) ... 35 0.89
emb|AW678361|AW678361 WS1_15_H06.b1_A002 Water-stressed 1 (WS1) ... 35 0.90
30 emb|AW745749|AW745749 WS1_37_D12.b1_A002 Water-stressed 1 (WS1) ... 35 0.90
emb|AW747427|AW747427 WS1_68_B09.b1_A002 Water-stressed 1 (WS1) ... 35 0.90
emb|AW678071|AW678071 WS1_13_E01.b1_A002 Water-stressed 1 (WS1) ... 35 0.90
emb|AW747468|AW747468 WS1_68_B09.g1_A002 Water-stressed 1 (WS1) ... 35 0.90
emb|AW672427|AW672427 LG1_359_A06.g1_A002 Light Grown 1 (LG1) So... 35 0.90
35 emb|AW744836|AW744836 LG1_384_E07.g1_A002 Light Grown 1 (LG1) So... 35 0.90
emb|AW746170|AW746170 WS1_39_B05.g1_A002 Water-stressed 1 (WS1) ... 35 0.90
emb|AW922317|AW922317 DG1_17_E06.g1_A002 Dark Grown 1 (DG1) Sorg... 35 0.91
emb|AQ648582|AQ648582 RPCI93-EcoRI-1M22.TP RPCI93-EcoRI Trypanos... 36 0.99
emb|AQ643551|AQ643551 RPCI93-EcoRI-3I24.TJ RPCI93-EcoRI Trypanos... 36 0.99
40 emb|AI443370|AI443370 sa31b05.x1 *Gm-c1004* Glycine max cDNA clone... 35 1.4
emb|AW101313|AW101313 sd77d08.y1 *Gm-c1009* Glycine max cDNA clone... 35 1.4
emb|AW678030|AW678030 WS1_12_B10.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
emb|AW349006|AW349006 GM210004A12H10R *Gm-r1021* Glycine max cDNA ... 35 1.4
emb|AW309961|AW309961 sf27b12.x1 *Gm-c1028* Glycine max cDNA clone... 35 1.4
45 emb|AW678582|AW678582 WS1_16_E09.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
emb|AW317198|AW317198 sf38f03.x1 *Gm-c1028* Glycine max cDNA clone... 35 1.4
emb|AW678305|AW678305 WS1_14_G05.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
emb|AW680905|AW680905 WS1_8_A08.b1_A002 Water-stressed 1 (WS1) S... 35 1.4
emb|AW679666|AW679666 WS1_30_B11.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
50 emb|AL031746|PFMAL1P3 *Plasmodium falciparum* MAL1P3, complete seq... 35 1.9
emb|AI959816|AI959816 sc94f02.y1 *Gm-c1019* Glycine max cDNA clone... 35 1.9
emb|AW924277|AW924277 WS1_52_D12.b1_A002 Water-stressed 1 (WS1) ... 35 1.9
gb|J03998|PFAGAR *Plasmodium falciparum* glutamic acid-rich protei... 35 1.9
emb|AW696796|AW696796 NF109A07ST1F1052 Developing stem *Medicago* ... 35 1.9
55 emb|AW396753|AW396753 sf37c11.x1 *Gm-c1028* Glycine max cDNA clone... 35 2.6
gb|M98871|SOYCHS7A Glycine max chalcone synthase (chs7) gene, co... 35 2.6
emb|AI460797|AI460797 sa69d02.y1 *Gm-c1004* Glycine max cDNA clone... 35 2.6
emb|AW348617|AW348617 GM210002B22G1R *Gm-r1021* Glycine max cDNA 3... 35 2.6
emb|AW310362|AW310362 sf35a09.x1 *Gm-c1028* Glycine max cDNA clone... 35 2.6
60 emb|AI437832|AI437832 sa40c07.y1 *Gm-c1004* Glycine max cDNA clone... 35 2.6
gb|BE023927|BE023927 sm94c05.y1 *Gm-c1015* Glycine max cDNA clone ... 35 2.6

	emb AW424189 AW424189 sh62b04.y1 Gm-c1015 Glycine max cDNA clone...	35	2.6
	emb AW101907 AW101907 sd72d01.y1 Gm-c1008 Glycine max cDNA clone...	35	2.6
	emb AW102370 AW102370 sd86h01.y1 Gm-c1009 Glycine max cDNA clone...	35	2.6
	emb AW309356 AW309356 sf16d02.x1 Gm-c1028 Glycine max cDNA clone...	35	2.6
5	emb AL355932 NCB5022 Neurospora crassa DNA linkage group II BAC ...	34	3.5
	emb AQ652663 AQ652663 Sheared DNA-20A9.TR Sheared DNA Trypanosom...	34	3.5
	emb Z98056 SPAC5D6 S.pombe chromosome I cosmid c5D6.	34	3.5
	emb AW348286 AW348286 GM210001B23B6R Gm-r1021 Glycine max cDNA 3...	34	4.9
	emb AB018422 AB018422 Pisum sativum mRNA for DNA binding zinc fi...	34	4.9
10	emb AW734949 AW734949 sk93b10.y1 Gm-c1035 Glycine max cDNA clone...	34	4.9
	emb AW679089 AW679089 WS1_22_A07.g1_A002 Water-stressed 1 (WS1) ...	34	4.9
	emb AW306776 AW306776 sf48c12.y1 Gm-c1009 Glycine max cDNA clone...	34	4.9
	gb M36941 BLYHORDCA Hordeum vulgare C-hordein gene, complete cds.	29	5.3
	gb BE034677 BE034677 ML01H08 ML Mesembryanthemum crystallinum cD...	33	6.7
15	emb Z26877 SCDCHR11 S.cerevisiae (S288C) 36.2kb DNA fragment fro...	33	6.7
	emb AW267708 AW267708 EST305836 DSIR Medicago truncatula cDNA cl...	33	6.7
	emb Z28162 SCYKL162C S.cerevisiae chromosome XI reading frame OR...	33	6.7
	emb AW980990 AW980990 EST392143 GVN Medicago truncatula cDNA clo...	33	6.7
	gb BE037412 BE037412 MP20G03 MP Mesembryanthemum crystallinum cD...	33	6.7
20	emb Z28161 SCYKL161C S.cerevisiae chromosome XI reading frame OR...	33	6.7
	emb AI726247 AI726247 BNLGHi5399 Six-day Cotton fiber Gossypium ...	33	6.7
	emb AE001401 AE001401 Plasmodium falciparum chromosome 2, sectio...	33	6.7
	emb AW573801 AW573801 EST316392 GVN Medicago truncatula cDNA clo...	33	6.7
	emb Z98547 PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque...	33	9.2
25	emb AQ659747 AQ659747 Sheared DNA-16J5.TR Sheared DNA Trypanosom...	33	9.2
	gb BE021269 BE021269 sm56h04.y1 Gm-c1028 Glycine max cDNA clone ...	33	9.2
	emb AW222457 AW222457 EST299268 tomato fruit red ripe, TAMU Lyco...	33	9.2
	emb AB012116 AB012116 Vigna mungo UFGlyT mRNA for UDP-glycose:fl...	33	9.2
	emb AW725836 AW725836 GA__Ea0019N24 Gossypium arboreum 7-10 dpa ...	33	9.2
30	emb AQ324451 AQ324451 mgxb0018L23r CUGI Rice Blast BAC Library P...	33	9.2
	gb M73492 LEIHSP90 Leishmania donovani heat shock protein 90 mRN...	33	9.2
	emb AW132634 AW132634 se06h07.y1 Gm-c1013 Glycine max cDNA clone...	33	9.2
	emb AI166186 AI166186 a032p32u Hybrid aspen plasmid library Popu...	33	9.2
	gb BE053953 BE053953 GA__Ea0031D23f Gossypium arboreum 7-10 dpa ...	33	9.2
35			

Query= AtACS6_at 12891_at /id_source genbank /description
 gb|aac63850.1| (u73786) acc synthase [arabidopsis thaliana]
 40 /blast_score 0 /ec_number /family synthase /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|atacs6|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|atacs6|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|atacs6|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?atacs6>
 (1567 letters)

45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

50

	Score	E
Sequences producing significant alignments:	(bits)	Value

	emb X82273 BOACCS B.oleracea mRNA for ACC synthase.	944	0.0
55	emb X72676 BJMACC B. juncea mRNA for 1-Aminocyclopropane-1-carbo...	833	0.0
	emb AB034992 AB034992 Malus domestica MdACS-5A mRNA for 1-aminoc...	725	0.0
	emb AF057563 AF057563 Nicotiana glutinosa 1-aminocyclopropane-1-...	729	0.0
	emb AJ005002 NTAJ5002 Nicotiana tabacum mRNA for 1-aminocyclopro...	726	0.0
	emb AB034993 AB034993 Malus domestica MdACS-5B mRNA for 1-aminoc...	723	0.0
60	gb U72389 LEU72389 Lycopersicon esculentum 1-aminocyclopropane-1...	724	0.0
	gb U72390 LEU72390 Lycopersicon esculentum 1-aminocyclopropane-1...	720	0.0

	gb U68216 CPU68216	Carica papaya ACC synthase mRNA, complete cds.	435	0.0
	emb AB033503 AB033503	Populus euramericana peacs-2 mRNA for 1-am...	713	0.0
	emb AF061605 AF061605	Nicotiana glutinosa ACC synthase mRNA, com...	712	0.0
	emb AJ012551 CSI012551	Citrus sinensis mRNA for ACC synthase.	420	0.0
5	emb AB033502 AB033502	Populus euphratica peacs-1 mRNA for 1-amin...	591	0.0
	emb AB013100 AB013100	Lycopersicon esculentum LE-ACS6 mRNA for 1...	706	0.0
	emb AB013346 AB013346	Lycopersicon esculentum mRNA for 1-aminocy...	704	0.0
	gb U88971 PHU88971	Pelargonium hortorum 1-aminocyclopropane-1-ca...	423	0.0
	emb Z11613 VRACCSYNM	V.radiata mRNA for ACC synthase.	428	0.0
10	emb X98492 NTACCS	Nicotiana tabacum mRNA for ACC-synthase (clone...	425	0.0
	emb X67100 GMCACCS1	G.max mRNA for ACC synthase.	429	0.0
	emb AJ012696 CSI012696	Citrus sinensis mRNA for ACC synthase (AC...	422	0.0
	emb Z18953 PHAMCRBSY	P.hybrida mRNA for 1-aminocyclopropane 1-ca...	424	0.0
	emb AJ011095 CSI011095	Citrus sinensis mRNA for ACC synthase (ac...	424	0.0
15	emb Z18952 DCAMCRBSY	D.caryophyllus mRNA for 1-aminocyclopropane...	686	0.0
	emb AB006804 AB006804	Cucumis sativus CS-ACS2 mRNA for ACC synth...	423	0.0
	emb AF080258 AF080258	Musa acuminata 1-aminocyclopropane-1-carbo...	680	0.0
	emb AF016459 AF016459	Pisum sativum 1-aminocyclopropane-1-carbox...	415	0.0
	dbj D30805 CUS1A1CS	Melon mRNA for 1-aminocyclopropane-1-carboxy...	678	0.0
20	emb X65982 NTXACCSYN	N.tabacum mRNA for 1-aminocyclopropane-1-ca...	417	0.0
	emb AF109927 AF109927	Musa acuminata 1-aminocyclopropane-1-carbo...	676	0.0
	emb AB006803 AB006803	Cucumis sativus CS-ACS1 mRNA for ACC synth...	676	0.0
	gb U17231 PHU17231	Pelargonium hortorum clone pGAC-2 1-aminocycl...	423	0.0
	emb AB021906 AB021906	Musa acuminata MA-ACS1 mRNA for ACC syntha...	671	0.0
25	emb AF129508 AF129508	Musa acuminata 1-aminocyclopropane-1-carbo...	671	0.0
	emb AB015625 AB015625	Pyrus pyrifolia pPPACS3 mRNA for 1-aminocy...	393	0.0
	emb AB031026 AB031026	Prunus mume PM-ACS1 mRNA for ACC synthase,...	405	0.0
	emb Y11357 CP1A1CS	C.papaya mRNA for 1-aminocyclopropane-1-carbo...	404	0.0
	dbj D01032 CUCACCW	Cucurbita maxima mRNA for 1-aminocyclopropane...	666	0.0
30	dbj E03724 E03724	cDNA encoding detriment induced type 1-aminocy...	666	0.0
	emb X62536 LEACC	L.esculentum mRNA for ACC synthase.	327	0.0
	gb L20634 POTACCSYN	Solanum tuberosum 1-aminocyclopropane-1-carb...	403	0.0
	emb X59145 LEACC2MR	Lycopersicon esculentum LE-ASCC2 mRNA (ptACC...	326	0.0
	gb M58323 CUCACCSYN	Cucurbita pepo 1-aminocyclopropane-1-carboxy...	663	0.0
35	emb AF057562 AF057562	Nicotiana glutinosa 1-aminocyclopropane-1-...	412	0.0
	emb AF239987 AF239987	Prunus persica ACC synthase ACS1 mRNA, par...	662	0.0
	gb M34289 TOMACS	Tomato 1-aminocyclopropane-1-carboxylate syntha...	327	0.0
	gb M63490 TOMACCS	Tomato 1-aminocyclopropane-1-carboxylate synth...	657	0.0
	emb X59146 LEACC4MR	Lycopersicon esculentum LE-ACC4 mRNA (ptACC4...	656	0.0
40	emb Y15739 MAACSYNTH	Musa acuminata mRNA for 1-aminocyclopropane...	655	0.0
	gb U79999 MAU79999	Musa acuminata ACC synthase (acs3) mRNA, comp...	655	0.0
	emb AF178076 AF178076	Carica papaya 1-aminocyclopropane-1-carbox...	395	0.0
	gb U17229 PHU17229	Pelargonium hortorum clone pGAC-1 1-aminocycl...	407	0.0
	emb X82265 CAACCI	C.anuum mRNA for 1-aminocyclopropane-1-carboxyl...	639	0.0
45	gb U70842 STU70842	Solanum tuberosum 1-aminocyclopropane-1-carbo...	637	0.0
	emb AF144746 AF144746	Solanum melongena 1-aminocyclopropane-1-ca...	636	0.0
	emb AJ276295 CSI276295	Citrus sinensis partial mRNA for ACC synt...	418	0.0
	emb AJ012577 CPA012577	Carica papaya mRNA for 1-aminocyclopropan...	387	e-180
	emb AF038945 AF038945	Rumex palustris 1-aminocyclopropane-1-carb...	372	e-179
50	gb U73815 MDU73815	Malus domestica ACC synthase (MdACS-2) mRNA, ...	623	e-178
	dbj D37937 D37937	Cucumis melo mRNA for 1-aminocyclopropane-1-ca...	380	e-177
	emb Z11562 VRACCSYN	V.radiata mRNA for 1-aminocyclopropane-1-car...	375	e-176
	emb AF177769 AF177769	Carica papaya 1-aminocyclopropane-1-carbox...	369	e-175
	emb AF083814 AF083814	Antirrhinum majus ACC synthase 1 (ACS1) mR...	605	e-172
55	emb AF178077 AF178077	Carica papaya 1-aminocyclopropane-1-carbox...	316	e-171
	emb AF239989 AF239989	Prunus persica ACC synthase ACS25 mRNA, pa...	597	e-170
	gb U22523 MIU22523	Mangifera indica 1-aminocyclopropane-carboxyl...	359	e-169
	emb X66605 DCACCS	D.caryophyllus mRNA for 1-aminocyclopropane-1-...	396	e-168
	emb AF049137 AF049137	Dianthus caryophyllus 1-aminocyclopropane-...	338	e-167
60	emb AF170705 AF170705	Mangifera indica 1-aminocyclopropane-1-car...	290	e-167
	emb AJ277160 CPA277160	Carica papaya partial paccs1A gene for 1-...	266	e-165

- emb|AB015624|AB015624 *Pyrus pyrifolia* mRNA for 1-aminocyclopropane-1-carboxylic acid synthase... 359 e-163
 gb|U03294|MSU03294 *Malus sylvestris* 1-aminocyclopropane-1-carboxylic acid synthase... 359 e-163
 gb|L31347|MAUACCSYN *Malus domestica* 1-aminocyclopropane-1-carboxylic acid synthase... 357 e-162
 emb|AB015495|AB015495 *Passiflora edulis* PE-ACS2 mRNA for ACC synthase... 368 e-162
 5 emb|Z77854|PSPACS1 *Phalaenopsis* species mRNA for 1-aminocyclopropane-1-carboxylic acid synthase... 514 e-161
 dbj|D01033|CUCACCA *Cucurbita maxima* mRNA for 1-aminocyclopropane-1-carboxylic acid synthase... 349 e-159
 emb|X87112|PCPCACS1G *P. communis* mRNA for 1-aminocyclopropane-1-carboxylic acid synthase... 346 e-159
 emb|AB007449|AB007449 *Actinidia deliciosa* mRNA for 1-aminocyclopropane-1-carboxylic acid synthase... 336 e-159
 gb|U73816|MDU73816 *Malus domestica* ACC synthase (MdACS-3) mRNA, ... 504 e-158
 10 gb|U17972|LEU17972 *Lycopersicon esculentum* 1-aminocyclopropane-1-carboxylic acid synthase... 343 e-157
 emb|AB007639|AB007639 *Pyrus pyrifolia* mRNA for 1-aminocyclopropane-1-carboxylic acid synthase... 502 e-157
 gb|M66619|DINCARACC *D. caryophyllus* 1-aminocyclopropane-1-carboxylic acid synthase... 495 e-156
 emb|AB006805|AB006805 *Cucumis sativus* CS-ACS3 mRNA for ACC synthase... 342 e-156
 gb|U34987|VRU34987 *Vigna radiata* 1-aminocyclopropane-1-carboxylic acid synthase... 305 e-151
 15 emb|AB000679|AB000679 *Vigna radiata* mRNA for 1-aminocyclopropane-1-carboxylic acid synthase... 340 e-151
 gb|U34986|VRU34986 *Vigna radiata* 1-aminocyclopropane-1-carboxylic acid synthase... 340 e-149
 gb|U64031|DCU64031 *Dendrobium crumenatum* ACC synthase gene, complete cds... 259 e-149
 emb|AF016458|AF016458 *Pisum sativum* 1-aminocyclopropane-1-carboxylic acid synthase... 336 e-148
 emb|Z27233|STACCAS1 *S. tuberosum* (STAC1) gene for amino cyclopropane-1-carboxylic acid synthase... 238 e-147
 20 emb|Z27234|STACCAS2 *S. tuberosum* STACS2 gene for 1-Aminocyclopropane-1-carboxylic acid synthase... 234 e-146
 gb|U37774|CMU37774 *Cucurbita maxima* 1-aminocyclopropane-1-carboxylic acid synthase... 235 e-145
 emb|AF043122|AF043122 *Lycopersicon esculentum* ACC synthase (LE-A-1) mRNA... 237 e-145
 emb|Z12135|VRACCSYN4 *V. radiata* gene for ACC synthase (pMAC-4)... 376 e-145
 gb|L34171|TOMACS3A *Lycopersicon esculentum* 1-aminocyclopropane-1-carboxylic acid synthase... 236 e-143
 25 gb|U18055|LEU18055 *Lycopersicon esculentum* 1-aminocyclopropane-1-carboxylic acid synthase... 236 e-143
 emb|AF074927|AF074927 *Sinapis arvensis* 1-aminocyclopropane-1-carboxylic acid synthase... 330 e-142
 emb|AF083815|AF083815 *Antirrhinum majus* ACC synthase 2 (ACS2) mRNA... 482 e-141
 emb|AF151961|AF151961 *Vigna radiata* 1-aminocyclopropane-1-carboxylic acid synthase... 234 e-141
 emb|AB021907|AB021907 *Musa acuminata* MA-ACS2 mRNA for ACC synthase... 310 e-140
 30 gb|L07883|DORAMICARB *Moth orchid* 1-aminocyclopropane-1-carboxylic acid synthase... 243 e-139
 emb|AB021908|AB021908 *Musa acuminata* MA-ACS3 mRNA for ACC synthase... 298 e-138

35 Query= AtACS6_g_at 12892_g_at /id_source genbank /description
 gb|aac63850.1| (u73786) acc synthase [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
 (1567 letters)

40 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

45	Score	E	(bits)	Value
	Sequences producing significant alignments:			
	emb X82273 BOACCS	<i>B. oleracea</i> mRNA for ACC synthase.	944	0.0
	emb X72676 BJMACC	<i>B. juncea</i> mRNA for 1-Aminocyclopropane-1-carboxylic acid synthase...	833	0.0
50	emb AB034992 AB034992	<i>Malus domestica</i> MdACS-5A mRNA for 1-aminocyclopropane-1-carboxylic acid synthase...	725	0.0
	emb AF057563 AF057563	<i>Nicotiana glutinosa</i> 1-aminocyclopropane-1-carboxylic acid synthase...	729	0.0
	emb AJ005002 NTAJ5002	<i>Nicotiana tabacum</i> mRNA for 1-aminocyclopropane-1-carboxylic acid synthase...	726	0.0
	emb AB034993 AB034993	<i>Malus domestica</i> MdACS-5B mRNA for 1-aminocyclopropane-1-carboxylic acid synthase...	723	0.0
	gb U72389 LEU72389	<i>Lycopersicon esculentum</i> 1-aminocyclopropane-1-carboxylic acid synthase...	724	0.0
55	gb U72390 LEU72390	<i>Lycopersicon esculentum</i> 1-aminocyclopropane-1-carboxylic acid synthase...	720	0.0
	gb U68216 CPU68216	<i>Carica papaya</i> ACC synthase mRNA, complete cds.	435	0.0
	emb AB033503 AB033503	<i>Populus euramericana</i> peacs-2 mRNA for 1-aminocyclopropane-1-carboxylic acid synthase...	713	0.0
	emb AF061605 AF061605	<i>Nicotiana glutinosa</i> ACC synthase mRNA, complete cds.	712	0.0
	emb AJ012551 CSI012551	<i>Citrus sinensis</i> mRNA for ACC synthase.	420	0.0
60	emb AB033502 AB033502	<i>Populus euphratica</i> peacs-1 mRNA for 1-aminocyclopropane-1-carboxylic acid synthase...	591	0.0
	emb AB013100 AB013100	<i>Lycopersicon esculentum</i> LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylic acid synthase...	706	0.0

	emb AB013346 AB013346	Lycopersicon esculentum mRNA for 1-aminocy...	704	0.0
	gb U88971 PHU88971	Pelargonium hortorum 1-aminocyclopropane-1-ca...	423	0.0
	emb Z11613 VRACCSYNM	V.radiata mRNA for ACC synthase.	428	0.0
	emb X98492 NTACCS	Nicotiana tabacum mRNA for ACC-synthase (clone...	425	0.0
5	emb X67100 GMCACCS1	G.max mRNA for ACC synthase.	429	0.0
	emb AJ012696 CSI012696	Citrus sinensis mRNA for ACC synthase (AC...	422	0.0
	emb Z18953 PHAMCRBSY	P.hybrida mRNA for 1-aminocyclopropane 1-ca...	424	0.0
	emb AJ011095 CSI011095	Citrus sinensis mRNA for ACC synthase (ac...	424	0.0
	emb Z18952 DCAMCRBSY	D.caryophyllus mRNA for 1-aminocyclopropane...	686	0.0
10	emb AB006804 AB006804	Cucumis sativus CS-ACS2 mRNA for ACC synth...	423	0.0
	emb AF080258 AF080258	Musa acuminata 1-aminocyclopropane-1-carbo...	680	0.0
	emb AF016459 AF016459	Pisum sativum 1-aminocyclopropane-1-carbox...	415	0.0
	dbj D30805 CUS1A1CS	Melon mRNA for 1-aminocyclopropane-1-carboxy...	678	0.0
	emb X65982 NTXACCSYN	N.tabacum mRNA for 1-aminocyclopropane-1-ca...	417	0.0
15	emb AF109927 AF109927	Musa acuminata 1-aminocyclopropane-1-carbo...	676	0.0
	emb AB006803 AB006803	Cucumis sativus CS-ACS1 mRNA for ACC synth...	676	0.0
	gb U17231 PHU17231	Pelargonium hortorum clone pGAC-2 1-aminocycl...	423	0.0
	emb AB021906 AB021906	Musa acuminata MA-ACS1 mRNA for ACC syntha...	671	0.0
	emb AF129508 AF129508	Musa acuminata 1-aminocyclopropane-1-carbo...	671	0.0
20	emb AB015625 AB015625	Pyrus pyrifolia pPPACS3 mRNA for 1-aminocy...	393	0.0
	emb AB031026 AB031026	Prunus mume PM-ACS1 mRNA for ACC synthase,...	405	0.0
	emb Y11357 CP1A1CS	C.papaya mRNA for 1-aminocyclopropane-1-carbo...	404	0.0
	dbj D01032 CUCACCW	Cucurbita maxima mRNA for 1-aminocyclopropane...	666	0.0
	dbj E03724 E03724	cDNA encoding detriment induced type 1-aminocy...	666	0.0
25	emb X62536 LEACC	L.esculentum mRNA for ACC synthase.	327	0.0
	gb L20634 POTACCSYN	Solanum tuberosum 1-aminocyclopropane-1-carb...	403	0.0
	emb X59145 LEACC2MR	Lycopersicon esculentum LE-ASCC2 mRNA (ptACC...	326	0.0
	gb M58323 CUCACCSYN	Cucurbita pepo 1-aminocyclopropane-1-carboxy...	663	0.0
	emb AF057562 AF057562	Nicotiana glutinosa 1-aminocyclopropane-1-...	412	0.0
30	emb AF239987 AF239987	Prunus persica ACC synthase ACS1 mRNA, par...	662	0.0
	gb M34289 TOMACS	Tomato 1-aminocyclopropane-1-carboxylate syntha...	327	0.0
	gb M63490 TOMACCS	Tomato 1-aminocyclopropane-1-carboxylate synth...	657	0.0
	emb X59146 LEACC4MR	Lycopersicon esculentum LE-ACC4 mRNA (ptACC4...	656	0.0
	emb Y15739 MAACSYNTH	Musa acuminata mRNA for 1-aminocyclopropane...	655	0.0
35	gb U79999 MAU79999	Musa acuminata ACC synthase (acs3) mRNA, comp...	655	0.0
	emb AF178076 AF178076	Carica papaya 1-aminocyclopropane-1-carbox...	395	0.0
	gb U17229 PHU17229	Pelargonium hortorum clone pGAC-1 1-aminocycl...	407	0.0
	emb X82265 CAACC1	C.anuum mRNA for 1-aminocyclopropane-1-carboxyl...	639	0.0
	gb U70842 STU70842	Solanum tuberosum 1-aminocyclopropane-1-carbo...	637	0.0
40	emb AF144746 AF144746	Solanum melongena 1-aminocyclopropane-1-ca...	636	0.0
	emb AJ276295 CSI276295	Citrus sinensis partial mRNA for ACC synt...	418	0.0
	emb AJ012577 CPA012577	Carica papaya mRNA for 1-aminocyclopropan...	387	e-180
	emb AF038945 AF038945	Rumex palustris 1-aminocyclopropane-1-carb...	372	e-179
	gb U73815 MDU73815	Malus domestica ACC synthase (MdACS-2) mRNA, ...	623	e-178
45	dbj D37937 D37937	Cucumis melo mRNA for 1-aminocyclopropane-1-ca...	380	e-177
	emb Z11562 VRACCSYN	V.radiata mRNA for 1-aminocyclopropane-1-car...	375	e-176
	emb AF177769 AF177769	Carica papaya 1-aminocyclopropane-1-carbox...	369	e-175
	emb AF083814 AF083814	Antirrhinum majus ACC synthase 1 (ACS1) mR...	605	e-172
	emb AF178077 AF178077	Carica papaya 1-aminocyclopropane-1-carbox...	316	e-171
50	emb AF239989 AF239989	Prunus persica ACC synthase ACS25 mRNA, pa...	597	e-170
	gb U22523 MIU22523	Mangifera indica 1-aminocyclopropane-carboxyl...	359	e-169
	emb X66605 DCACCS	D.caryophyllus mRNA for 1-aminocyclopropane-1-...	396	e-168
	emb AF049137 AF049137	Dianthus caryophyllus 1-aminocyclopropane-...	338	e-167
	emb AF170705 AF170705	Mangifera indica 1-aminocyclopropane-1-car...	290	e-167
55	emb AJ277160 CPA277160	Carica papaya partial paccs1A gene for 1-...	266	e-165
	emb AB015624 AB015624	Pyrus pyrifolia mRNA for 1-aminocyclopropa...	359	e-163
	gb U03294 MSU03294	Malus sylvestris 1-aminocyclopropane-1-carbox...	359	e-163
	gb L31347 MAUACCSYN	Malus domestica 1-aminocyclopropane-1-carbox...	357	e-162
	emb AB015495 AB015495	Passiflora edulis PE-ACS2 mRNA for ACC syn...	368	e-162
60	emb Z77854 PSPACS1	Phalaenopsis species mRNA for 1-aminocyclopro...	514	e-161
	dbj D01033 CUCACCA	Cucurbita maxima mRNA for 1-aminocyclopropane...	349	e-159

- emb|X87112|PCPCACS1G *P. communis* mRNA for 1-aminocyclopropane-1-c... 346 e-159
 emb|AB007449|AB007449 *Actinidia deliciosa* mRNA for 1-aminocyclop... 336 e-159
 gb|U73816|MDU73816 *Malus domestica* ACC synthase (MdACS-3) mRNA, ... 504 e-158
 gb|U17972|LEU17972 *Lycopersicon esculentum* 1-aminocyclopropane-1... 343 e-157
 5 emb|AB007639|AB007639 *Pyrus pyrifolia* mRNA for 1-aminocyclopropana... 502 e-157
 gb|M66619|DINCARACC *D. caryophyllus* 1-aminocyclopropane-1-carboxy... 495 e-156
 emb|AB006805|AB006805 *Cucumis sativus* CS-ACS3 mRNA for ACC synth... 342 e-156
 gb|U34987|VRU34987 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 305 e-151
 emb|AB000679|AB000679 *Vigna radiata* mRNA for 1-aminocyclopropane... 340 e-151
 10 gb|U34986|VRU34986 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 340 e-149
 gb|U64031|DCU64031 *Dendrobium crumenatum* ACC synthase gene, comp... 259 e-149
 emb|AF016458|AF016458 *Pisum sativum* 1-aminocyclopropane-1-carbox... 336 e-148
 emb|Z27233|STACCAS1 *S. tuberosum* (STAC1) gene for amino cycloprop... 238 e-147
 emb|Z27234|STACCAS2 *S. tuberosum* STACS2 gene for 1-Aminocycloprop... 234 e-146
 15 gb|U37774|CMU37774 *Cucurbita maxima* 1-aminocyclopropane-1-carbox... 235 e-145
 emb|AF043122|AF043122 *Lycopersicon esculentum* ACC synthase (LE-A... 237 e-145
 emb|Z12135|VRACCSYN4 *V. radiata* gene for ACC synthase (pMAC-4). 376 e-145
 gb|L34171|TOMACS3A *Lycopersicon esculentum* 1-aminocyclopropane-1... 236 e-143
 gb|U18055|LEU18055 *Lycopersicon esculentum* 1-aminocyclopropane-1... 236 e-143
 20 emb|AF074927|AF074927 *Sinapis arvensis* 1-aminocyclopropane-1-car... 330 e-142
 emb|AF083815|AF083815 *Antirrhinum majus* ACC synthase 2 (ACS2) mR... 482 e-141
 emb|AF151961|AF151961 *Vigna radiata* 1-aminocyclopropane-1-carbox... 234 e-141
 emb|AB021907|AB021907 *Musa acuminata* MA-ACS2 mRNA for ACC syntha... 310 e-140
 gb|L07883|DORAMICARB *Moth orchid* 1-aminocyclopropane-1-carboxyla... 243 e-139
 25 emb|AB021908|AB021908 *Musa acuminata* MA-ACS3 mRNA for ACC syntha... 298 e-138

30 Query= AtERF2_s_at 12905_s_at /id_source genbank /description
 dbj|baa32419.1| (ab008104) ethylene responsive element binding factor
 2 [arabidopsis thaliana] /blast_score 1.00e-112 /ec_number /family
 /chip nova /gb_link /ncgi
 (921 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

40 Score E
 Sequences producing significant alignments: (bits) Value

dbj|D38126|TOBBY4D Tobacco mRNA for EREBP-2, complete cds. 144 7e-44
 emb|AW220395|AW220395 EST302878 tomato root during/after fruit s... 132 9e-43
 45 dbj|D38123|TOBBY4A *Nicotiana tabacum* mRNA for ERF1, complete cds. 134 6e-41
 emb|AF245119|AF245119 *Mesembryanthemum crystallinum* AP2-related ... 161 5e-39
 emb|AW267820|AW267820 EST305948 *DSIR Medicago truncatula* cDNA cl... 160 1e-38
 emb|AB035270|AB035270 *Matricaria chamomilla* McEREBP1 mRNA for et... 155 5e-37
 gb|U89255|LEU89255 *Lycopersicon esculentum* DNA-binding protein P... 138 3e-32
 50 emb|AI771213|AI771213 EST252409 tomato ovary, TAMU *Lycopersicon* ... 135 1e-31
 emb|AW034216|AW034216 EST277787 tomato callus, TAMU *Lycopersicon*... 134 1e-30
 emb|AW729466|AW729466 GA__Ea0025B11 *Gossypium arboreum* 7-10 dpa ... 132 4e-30
 emb|AF057373|AF057373 *Nicotiana tabacum* ethylene response elemen... 125 4e-28
 emb|AW981151|AW981151 EST392345 *DSIL Medicago truncatula* cDNA cl... 124 8e-28
 55 emb|AW396250|AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone... 116 2e-25
 emb|AW233956|AW233956 sf32e02.y1 Gm-c1028 Glycine max cDNA clone... 115 5e-25
 emb|AW185128|AW185128 se87b10.y1 Gm-c1023 Glycine max cDNA clone... 114 1e-24
 emb|AI897834|AI897834 EST267277 tomato ovary, TAMU *Lycopersicon* ... 113 2e-24
 emb|AW349516|AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA ... 113 2e-24
 60 24
 emb|AV423260|AV423260 AV423260 *Lotus japonicus* young plants (two... 111 6e-24

- emb|AV425560|AV425560 AV425560 Lotus japonicus young plants (two... 111 6e-24
emb|AW981228|AW981228 EST392318 DSIL Medicago truncatula cDNA cl... 89 6e-24
emb|AI899000|AI899000 EST268443 tomato ovary, TAMU Lycopersicon ... 110 2e-23
5 emb|AI965917|AI965917 sc79f12.y1 Gm-c1018 Glycine max cDNA clone... 110 2e-23
emb|AI794657|AI794657 sb67b03.y1 Gm-c1019 Glycine max cDNA clone... 110 2e-23
emb|AW200919|AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone... 109 3e-23
emb|AW507860|AW507860 si45h05.y1 Gm-r1030 Glycine max cDNA clone... 109 3e-23
emb|AW507898|AW507898 si46f03.y1 Gm-r1030 Glycine max cDNA clone... 97 3e-23
dbj|D38125|TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 109 4e-23
10 emb|AW349638|AW349638 GM210005B21A4R Gm-r1021 Glycine max cDNA 3... 109 4e-23
emb|AW278190|AW278190 sf40g11.y1 Gm-c1009 Glycine max cDNA clone... 109 4e-23
emb|AI486689|AI486689 EST245011 tomato ovary, TAMU Lycopersicon ... 108 5e-23
emb|AW618245|AW618245 EST314295 L. pennellii trichome, Cornell U... 108 8e-23
15 emb|AW776671|AW776671 EST335736 DSIL Medicago truncatula cDNA cl... 108 8e-23
emb|AW759181|AW759181 sl38a09.y1 Gm-c1027 Glycine max cDNA clone... 107 1e-22
emb|AW596384|AW596384 sj02f12.y1 Gm-c1032 Glycine max cDNA clone... 107 1e-22
emb|AI897797|AI897797 EST267240 tomato ovary, TAMU Lycopersicon ... 107 1e-22
emb|AI973653|AI973653 sd07h05.y1 Gm-c1020 Glycine max cDNA clone... 107 1e-22
20 emb|AW620490|AW620490 sj05h02.y1 Gm-c1032 Glycine max cDNA clone... 106 2e-22
emb|AI899889|AI899889 sb94g05.y1 Gm-c1017 Glycine max cDNA clone... 105 4e-22
emb|AW574222|AW574222 EST316813 GVN Medicago truncatula cDNA clo... 105 4e-22
emb|AI778693|AI778693 EST259572 tomato susceptible, Cornell Lyco... 105 4e-22
emb|AW776668|AW776668 EST335733 DSIL Medicago truncatula cDNA cl... 105 4e-22
25 emb|AW774176|AW774176 EST333259 KV3 Medicago truncatula cDNA clo... 105 4e-22
emb|AI894873|AI894873 EST264316 tomato callus, TAMU Lycopersicon... 103 2e-21
gb|U89256|LEU89256 Lycopersicon esculentum DNA-binding protein P... 103 2e-21
emb|AW030009|AW030009 EST273264 tomato callus, TAMU Lycopersicon... 103 2e-21
emb|AW030386|AW030386 EST273641 tomato callus, TAMU Lycopersicon... 103 2e-21
30 emb|AI782381|AI782381 EST263260 tomato susceptible, Cornell Lyco... 100 1e-20
emb|AW980654|AW980654 EST391807 GVN Medicago truncatula cDNA clo... 100 2e-20
emb|AV422393|AV422393 AV422393 Lotus japonicus young plants (two... 100 2e-20
emb|AI484961|AI484961 EST243224 tomato ovary, TAMU Lycopersicon ... 100 3e-20
emb|AW781602|AW781602 sl82d06.y1 Gm-c1037 Glycine max cDNA clone... 100 3e-20
35 emb|AW443265|AW443265 EST308195 tomato mixed elicitor, BTI Lycop... 100 3e-20
emb|AI440657|AI440657 sa63d09.y1 Gm-c1004 Glycine max cDNA clone... 99 4e-20
gb|U81157|NTU81157 Nicotiana tabacum S25-XP1 DNA binding protein... 98 8e-20
emb|AJ238740|CRO238740 Catharanthus roseus mRNA for AP2-domain D... 98 8e-20
emb|AW840611|AW840611 00057 leafy spurge Lambda HybriZAP 2.1 two... 97 1e-19
40 emb|AW559315|AW559315 EST306358 DSIR Medicago truncatula cDNA cl... 97 2e-19
emb|AV421566|AV421566 AV421566 Lotus japonicus young plants (two... 97 2e-19
emb|AI966559|AI966559 sc52a04.y1 Gm-c1015 Glycine max cDNA clone... 97 2e-19
emb|AI495036|AI495036 sa90a09.y1 Gm-c1004 Glycine max cDNA clone... 95 5e-19
emb|AI442716|AI442716 sa85d10.y1 Gm-c1004 Glycine max cDNA clone... 95 5e-19
45 emb|AI055252|AI055252 coau0003H16 Cotton Boll Abscission Zone cD... 67 8e-19
emb|AI967551|AI967551 Ljimp05-400-d11 Ljimp Lambda HybriZap... 95 1e-18
emb|AI896308|AI896308 EST265751 tomato callus, TAMU Lycopersicon... 94 1e-18
emb|AI776626|AI776626 EST257726 tomato resistant, Cornell Lycop... 93 3e-18
emb|AW686013|AW686013 NF033D04NR1F1000 Nodulated root Medicago t... 92 5e-18
50 emb|AW981323|AW981323 EST392476 DSIL Medicago truncatula cDNA cl... 92 5e-18
emb|AV417552|AV417552 AV417552 Lotus japonicus young plants (two... 92 5e-18
emb|AW618246|AW618246 EST314296 L. pennellii trichome, Cornell U... 92 5e-18
emb|AW685077|AW685077 NF024H04NR1F1000 Nodulated root Medicago t... 90 2e-17
emb|AW573782|AW573782 EST316373 GVN Medicago truncatula cDNA clo... 90 2e-17
55 emb|AW308784|AW308784 sf71h01.y1 Gm-c1013 Glycine max cDNA clone... 88 1e-16
emb|AW782252|AW782252 sm03d11.y1 Gm-c1027 Glycine max cDNA clone... 59 1e-16
emb|AW980481|AW980481 EST391634 GVN Medicago truncatula cDNA clo... 87 2e-16
gb|BE023264|BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone ... 87 2e-16
emb|AW458901|AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone... 86 4e-16
60 emb|AW348322|AW348322 GM210001B23F6R Gm-r1021 Glycine max cDNA 3... 85 8e-16
emb|AW685799|AW685799 NF030D09NR1F1000 Nodulated root Medicago t... 53 1e-15

emb|AW775819|AW775819 EST334884 DSIL Medicago truncatula cDNA cl... 84 2e-15
emb|AI731242|AI731242 BNLGH9002 Six-day Cotton fiber Gossypium ... 84 2e-15
emb|AI898992|AI898992 EST268435 tomato ovary, TAMU Lycopersicon ... 84 2e-15
emb|AI736796|AI736796 sb33f06.y1 Gm-c1012 Glycine max cDNA clone... 83 3e-15
5 emb|AW560968|AW560968 EST316016 DSIR Medicago truncatula cDNA cl... 57 4e-15
emb|AW560196|AW560196 EST315244 DSIR Medicago truncatula cDNA cl... 57 4e-15
emb|AI489709|AI489709 EST248048 tomato ovary, TAMU Lycopersicon ... 56 6e-15
emb|AW759236|AW759236 sl38f08.y1 Gm-c1027 Glycine max cDNA clone... 80 2e-14
gb|BE057468|BE057468 sm58e08.y1 Gm-c1028 Glycine max cDNA clone ... 55 7e-14
10 gb|T14923|T14923 crs406 lambdaZAPST Ricinus communis cDNA clone ... 56 9e-14
emb|AI489199|AI489199 EST247538 tomato ovary, TAMU Lycopersicon ... 52 1e-13
emb|AI486929|AI486929 EST245251 tomato ovary, TAMU Lycopersicon ... 52 1e-13
emb|AI483636|AI483636 EST249507 tomato ovary, TAMU Lycopersicon ... 52 1e-13
emb|AW033743|AW033743 EST277314 tomato callus, TAMU Lycopersicon... 52 1e-13
15 emb|AI483510|AI483510 EST249359 tomato ovary, TAMU Lycopersicon ... 52 1e-13
emb|AI771755|AI771755 EST252855 tomato ovary, TAMU Lycopersicon ... 52 1e-13
emb|AI485175|AI485175 EST243479 tomato ovary, TAMU Lycopersicon ... 52 1e-13
emb|AI489919|AI489919 EST248258 tomato ovary, TAMU Lycopersicon ... 52 1e-13
emb|AI897787|AI897787 EST267230 tomato ovary, TAMU Lycopersicon ... 52 1e-13
20 emb|AI771834|AI771834 EST252934 tomato ovary, TAMU Lycopersicon ... 52 1e-13
emb|AI485460|AI485460 EST243781 tomato ovary, TAMU Lycopersicon ... 52 1e-13
emb|AI771795|AI771795 EST252895 tomato ovary, TAMU Lycopersicon ... 52 1e-13

25 Query= AtERF5_s_at 12908_s_at /id_source genbank /description
dbj|baa32422.1| (ab008107) ethylene responsive element binding factor
5 [arabidopsis thaliana] /blast_score 1.00e-117 /ec_number /family
/chip nova /gb_link /ncgi
(1059 letters)

30 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

35

	Score	E	
Sequences producing significant alignments:	(bits)	Value	
emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone...	141	4e-37	
40 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone...	149	5e-35	
emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl...	94	5e-33	
emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl...	111	2e-32	
emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon ...	132	2e-30	
emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA ...	130	2e-29	
45 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl...	125	2e-29	
emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon ...	128	3e-29	
emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone...	108	8e-29	
dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds.	127	1e-28	
50 emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon ...	127	2e-28	
gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone ...	103	5e-28	
emb AI897797 AI897797 EST267240 tomato ovary, TAMU Lycopersicon ...	124	1e-27	
emb AI794657 AI794657 sb67b03.y1 Gm-c1019 Glycine max cDNA clone...	124	1e-27	
emb AW507860 AW507860 si45h05.y1 Gm-r1030 Glycine max cDNA clone...	123	2e-27	
55 emb AW775819 AW775819 EST334884 DSIL Medicago truncatula cDNA cl...	95	5e-27	
emb AW685077 AW685077 NF024H04NR1F1000 Nodulated root Medicago t...	93	8e-27	
emb AW573782 AW573782 EST316373 GVN Medicago truncatula cDNA clo...	93	9e-27	
emb AW620490 AW620490 sj05h02.y1 Gm-c1032 Glycine max cDNA clone...	121	1e-26	
emb AW759181 AW759181 sl38a09.y1 Gm-c1027 Glycine max cDNA clone...	121	1e-26	
60 emb AI778693 AI778693 EST259572 tomato susceptible, Cornell Lyco...	120	2e-26	
emb AW774176 AW774176 EST333259 KV3 Medicago truncatula cDNA clo...	118	6e-26	

- emb|AW776668|AW776668 EST335733 DSIL Medicago truncatula cDNA cl... 118 6e-26
 emb|AW574222|AW574222 EST316813 GVN Medicago truncatula cDNA clo... 118 6e-26
 emb|AI899889|AI899889 sb94g05.y1 Gm-c1017 Glycine max cDNA clone... 117 1e-25
 emb|AW185128|AW185128 se87b10.y1 Gm-c1023 Glycine max cDNA clone... 116 2e-25
 5 emb|AW688546|AW688546 NF008H02ST1F1000 Developing stem Medicago ... 89 2e-25
 emb|AV425560|AV425560 AV425560 Lotus japonicus young plants (two... 115 5e-25
 emb|AV423260|AV423260 AV423260 Lotus japonicus young plants (two... 115 5e-25
 emb|AI782381|AI782381 EST263260 tomato susceptible, Cornell Lyco... 115 8e-25
 emb|AF245119|AF245119 Mesembryanthemum crystallinum AP2-related ... 114 1e-24
 10 emb|AW781602|AW781602 sl82d06.y1 Gm-c1037 Glycine max cDNA clone... 114 1e-24
 emb|AW267820|AW267820 EST305948 DSIR Medicago truncatula cDNA cl... 113 2e-24
 emb|AI965917|AI965917 sc79f12.y1 Gm-c1018 Glycine max cDNA clone... 113 3e-24
 emb|AI484961|AI484961 EST243224 tomato ovary, TAMU Lycopersicon ... 112 5e-24
 emb|AB035270|AB035270 Matricaria chamomilla McERE BP1 mRNA for et... 111 1e-23
 15 emb|AW220395|AW220395 EST302878 tomato root during/after fruit s... 110 2e-23
 emb|AV421566|AV421566 AV421566 Lotus japonicus young plants (two... 109 3e-23
 dbj|D38126|TOBBY4D Tobacco mRNA for EREBP-2, complete cds. 109 3e-23
 emb|AW101306|AW101306 sd77c11.y1 Gm-c1009 Glycine max cDNA clone... 89 5e-23
 emb|AW349638|AW349638 GM210005B21A4R Gm-r1021 Glycine max cDNA 3... 107 2e-
 20 22
 emb|AI771213|AI771213 EST252409 tomato ovary, TAMU Lycopersicon ... 107 2e-22
 gb|U89255|LEU89255 Lycopersicon esculentum DNA-binding protein P... 107 2e-22
 emb|AW596384|AW596384 sj02f12.y1 Gm-c1032 Glycine max cDNA clone... 107 2e-22
 dbj|D38123|TOBBY4A Nicotiana tabacum mRNA for ERF1, complete cds. 105 8e-22
 25 emb|AV417552|AV417552 AV417552 Lotus japonicus young plants (two... 103 2e-21
 emb|AW034216|AW034216 EST277787 tomato callus, TAMU Lycopersicon... 103 2e-21
 emb|AW278190|AW278190 sf40g11.y1 Gm-c1009 Glycine max cDNA clone... 103 2e-21
 emb|AJ238740|CRO238740 Catharanthus roseus mRNA for AP2-domain D... 102 4e-21
 emb|AI973653|AI973653 sd07h05.y1 Gm-c1020 Glycine max cDNA clone... 102 4e-21
 30 emb|AW690929|AW690929 NF034G08ST1F1000 Developing stem Medicago ... 73 9e-21
 emb|AW233956|AW233956 sf32e02.y1 Gm-c1028 Glycine max cDNA clone... 101 1e-20
 emb|AW736415|AW736415 EST332429 KV3 Medicago truncatula cDNA clo... 73 2e-20
 emb|AI440657|AI440657 sa63d09.y1 Gm-c1004 Glycine max cDNA clone... 100 2e-20
 35
 emb|AV422393|AV422393 AV422393 Lotus japonicus young plants (two... 100 2e-20
 emb|AI967551|AI967551 Ljirnp05-400-d11 Ljirnp Lambda HybriZap... 100 2e-20
 emb|AI731242|AI731242 BNLGH19002 Six-day Cotton fiber Gossypium ... 100 3e-20
 gb|U89256|LEU89256 Lycopersicon esculentum DNA-binding protein P... 99 5e-20
 40 emb|AW030009|AW030009 EST273264 tomato callus, TAMU Lycopersicon... 99 5e-20
 emb|AI894873|AI894873 EST264316 tomato callus, TAMU Lycopersicon... 99 5e-20
 emb|AW030386|AW030386 EST273641 tomato callus, TAMU Lycopersicon... 99 5e-20
 emb|AW729466|AW729466 GA_Ea0025B11 Gossypium arboreum 7-10 dpa ... 98 1e-19
 emb|AW507898|AW507898 si46f03.y1 Gm-r1030 Glycine max cDNA clone... 98 1e-19
 45 emb|AW618245|AW618245 EST314295 L. pennellii trichome, Cornell U... 98 1e-19
 emb|AW840611|AW840611 00057 leafy spurge Lambda HybriZAP 2.1 two... 97 2e-19
 emb|AI736796|AI736796 sb33f06.y1 Gm-c1012 Glycine max cDNA clone... 97 2e-19
 emb|AI966559|AI966559 sc52a04.y1 Gm-c1015 Glycine max cDNA clone... 97 2e-19
 emb|AF057373|AF057373 Nicotiana tabacum ethylene response elemen... 96 3e-19
 50 emb|AI896308|AI896308 EST265751 tomato callus, TAMU Lycopersicon... 96 5e-19
 emb|AI898992|AI898992 EST268435 tomato ovary, TAMU Lycopersicon ... 95 6e-19
 emb|AW980654|AW980654 EST391807 GVN Medicago truncatula cDNA clo... 95 6e-19
 emb|AI495036|AI495036 sa90a09.y1 Gm-c1004 Glycine max cDNA clone... 94 2e-18
 gb|U81157|NTU81157 Nicotiana tabacum S25-XPI DNA binding protein... 94 2e-18
 55 emb|AW706628|AW706628 sj62g05.y1 Gm-c1033 Glycine max cDNA clone... 70 3e-18
 emb|AI442716|AI442716 sa85d10.y1 Gm-c1004 Glycine max cDNA clone... 93 4e-18
 emb|AW559315|AW559315 EST306358 DSIR Medicago truncatula cDNA cl... 93 4e-18
 emb|AW035119|AW035119 EST280381 tomato callus, TAMU Lycopersicon... 91 1e-17
 emb|AI490591|AI490591 EST249145 tomato ovary, TAMU Lycopersicon ... 91 1e-17
 60 emb|AI489147|AI489147 EST247486 tomato ovary, TAMU Lycopersicon ... 91 1e-17
 emb|AW782252|AW782252 sm03d11.y1 Gm-c1027 Glycine max cDNA clone... 63 1e-17

emb|AW348322|AW348322 GM210001B23F6R Gm-r1021 Glycine max cDNA 3... 90 2e-17
 emb|AW759236|AW759236 sl38f08.y1 Gm-c1027 Glycine max cDNA clone... 90 2e-17
 emb|AW686013|AW686013 NF033D04NR1F1000 Nodulated root Medicago t... 90 2e-17
 emb|AI776626|AI776626 EST257726 tomato resistant, Cornell Lycopersicon... 89 4e-17
 5 emb|AW443265|AW443265 EST308195 tomato mixed elicitor, BTI Lycopersicon... 89 5e-17
 emb|AW308784|AW308784 sf71h01.y1 Gm-c1013 Glycine max cDNA clone... 89 5e-17
 emb|AF211541|AF211541 AF211541 34.1B Nicotiana tabacum cDNA clone... 87 2e-16
 emb|AW621700|AW621700 EST312498 tomato root during/after fruit s... 87 2e-16
 emb|AI489709|AI489709 EST248048 tomato ovary, TAMU Lycopersicon ... 62 2e-16
 10 emb|AW560968|AW560968 EST316016 DSIR Medicago truncatula cDNA cl... 60 4e-16
 emb|AW560196|AW560196 EST315244 DSIR Medicago truncatula cDNA cl... 60 4e-16
 emb|AW185802|AW185802 se59h01.y1 Gm-c1019 Glycine max cDNA clone... 71 5e-16
 emb|AW734757|AW734757 sk88d02.y1 Gm-c1035 Glycine max cDNA clone... 85 1e-15
 emb|AV417624|AV417624 AV417624 Lotus japonicus young plants (two... 58 1e-15
 15 emb|AV407462|AV407462 AV407462 Lotus japonicus young plants (two... 58 1e-15
 emb|AW256448|AW256448 EST304585 KV2 Medicago truncatula cDNA clo... 59 1e-15
 emb|AW560135|AW560135 EST315183 DSIR Medicago truncatula cDNA cl... 59 2e-15
 emb|AW267756|AW267756 EST305884 DSIR Medicago truncatula cDNA cl... 59 2e-15
 emb|AW560134|AW560134 EST315182 DSIR Medicago truncatula cDNA cl... 59 2e-15
 20 emb|AW574073|AW574073 EST316664 GVN Medicago truncatula cDNA clo... 61 2e-15

Query= AthCOR1_s_at 12916_s_at /id_source genbank /description
 gb|aac13947.1| (af021244) coronatine-induced protein 1 [arabidopsis
 25 thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link .
 /ncgi
 (1188 letters)

Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	(bits)	Value
35	Sequences producing significant alignments:			
	emb AF134301 AF134301	Chenopodium album CaCLH (CaCLH) mRNA, comp...	89	4e-57
	emb AB025025 AB025025	Chenopodium album mRNA for chlorophyllase,...	89	4e-57
	emb AF160869 AF160869	Citrus sinensis chlorophyllase mRNA, compl...	84	4e-54
40	emb AW039135 AW039135	EST281108 tomato mixed elicitor, BTI Lycopersicon...	127	2e-38
	gb BE037470 BE037470	MP21E05 MP Mesembryanthemum crystallinum cD...	81	4e-35
	emb AW093776 AW093776	EST286956 tomato mixed elicitor, BTI Lycopersicon...	59	4e-34
	emb AW616099 AW616099	EST296862 L. hirsutum trichome, Cornell Un...	67	1e-29
	emb AW266073 AW266073	L30-2749T3 Ice plant Lambda Uni-Zap XR exp...	79	3e-29
45	emb AA887366 AA887366	L30-338T3 Ice plant Lambda Uni-Zap XR expr...	79	2e-26
	emb AA556157 AA556157	12 Loblolly pine N Pinus taeda cDNA clone ...	120	3e-26
	emb AW042994 AW042994	ST27H11 Pine TriplEx shoot tip library Pin...	106	7e-26
	emb AW265807 AW265807	L30-2522 T3 Ice plant Lambda Uni-Zap XR ex...	84	2e-21
	emb AW678075 AW678075	WS1_13_D09.b1_A002 Water-stressed 1 (WS1) ...	81	1e-19
50	emb AW133452 AW133452	se19b10.y1 Gm-c1015 Glycine max cDNA clone...	62	1e-17
	emb AI777679 AI777679	EST258474 tomato susceptible, Cornell Lyco...	53	7e-17
	emb AW596770 AW596770	sj16e05.y1 Gm-c1032 Glycine max cDNA clone...	89	9e-17
	emb AW596245 AW596245	sj01a09.y1 Gm-c1032 Glycine max cDNA clone...	87	3e-16
	emb AI771244 AI771244	EST252260 tomato ovary, TAMU Lycopersicon ...	67	3e-16
55	emb AW831810 AW831810	sm36f12.y1 Gm-c1028 Glycine max cDNA clone...	85	8e-16
	emb AW678155 AW678155	WS1_13_D09.g1_A002 Water-stressed 1 (WS1) ...	67	2e-10
	emb AI771428 AI771428	EST252528 tomato ovary, TAMU Lycopersicon ...	67	4e-10
	emb AI822354 AI822354	L0-803T3 Ice plant Lambda Uni-Zap XR expre...	59	5e-09
	gb BE058857 BE058857	sn21g11.y1 Gm-c1016 Glycine max cDNA clone ...	41	0.019
60	gb BE058853 BE058853	sn21g06.y1 Gm-c1016 Glycine max cDNA clone ...	41	0.019
	emb AW773701 AW773701	EST332687 KV3 Medicago truncatula cDNA clo...	39	0.094

	emb AV408460 AV408460 AV408460 Lotus japonicus young plants (two...	37	0.33
	emb AV413861 AV413861 AV413861 Lotus japonicus young plants (two...	37	0.33
	emb AV428585 AV428585 AV428585 Lotus japonicus young plants (two...	37	0.33
	emb AV423848 AV423848 AV423848 Lotus japonicus young plants (two...	37	0.33
5	emb AV412195 AV412195 AV412195 Lotus japonicus young plants (two...	37	0.33
	emb AZ216272 AZ216272 Sheared DNA-80A6.TF Sheared DNA Trypanosom...	36	0.46
	emb AQ646813 AQ646813 RPCI93-EcoRI-5A7.TJ RPCI93-EcoRI Trypanoso...	36	0.46
	emb AZ216717 AZ216717 Sheared DNA-85A6.TF Sheared DNA Trypanosom...	36	0.46
	emb AW395857 AW395857 sh01b07.y1 Gm-c1026 Glycine max cDNA clone...	36	0.63
10	emb AV415537 AV415537 AV415537 Lotus japonicus young plants (two...	35	0.86
	gb L33656 L33656 BNAESTF703 Mustard flower buds Brassica rapa cD...	35	0.86
	emb AV417584 AV417584 AV417584 Lotus japonicus young plants (two...	35	0.86
	gb L33647 L33647 BNAESTF649 Mustard flower buds Brassica rapa cD...	35	0.86
	emb AW455247 AW455247 EST311907 tomato root during/after fruit s...	35	0.86
15	emb AQ909224 AQ909224 GSSTc07661 Trypanosome cruzi random genomi...	35	0.86
	emb AQ909223 AQ909223 GSSTc07660 Trypanosome cruzi random genomi...	35	0.86
	emb AV421772 AV421772 AV421772 Lotus japonicus young plants (two...	35	0.86
	emb AL114831 CNS01BXZ Botrytis cinerea strain T4 cDNA library un...	35	0.86
	emb AW625056 AW625056 EST313873 tomato radicle, 5 d post-imbibit...	35	0.86
20	emb AW719366 AW719366 LjNEST3d5r Lotus japonicus nodule library,...	35	0.86
	emb AL023634 SPBC530 S.pombe chromosome II cosmid c530.	35	1.2
	emb AV420271 AV420271 AV420271 Lotus japonicus young plants (two...	35	1.2
	emb AV414699 AV414699 AV414699 Lotus japonicus young plants (two...	35	1.2
	emb AF154666 AF154666 Nicotiana tabacum clone PR58 mRNA sequence.	35	1.2
25	emb AV424919 AV424919 AV424919 Lotus japonicus young plants (two...	35	1.2
	emb AV428060 AV428060 AV428060 Lotus japonicus young plants (two...	35	1.2
	emb AI612620 AI612620 TENG0402 T. Cruzi epimastigote normalised ...	35	1.2
	emb AW615881 AW615881 EST325379 tomato flower buds 0-3 mm, Corne...	35	1.2
	emb AV410945 AV410945 AV410945 Lotus japonicus young plants (two...	35	1.2
30	emb AW616956 AW616956 EST323367 L. hirsutum trichome, Cornell Un...	35	1.6
	emb AW626060 AW626060 EST319967 tomato radicle, 5 d post-imbibit...	35	1.6
	emb AI055068 AI055068 coau0002P04 Cotton Boll Abscission Zone cD...	35	1.6
	emb AJ242531 TAE242531 Triticum aestivum rht-D1a gene for gibber...	35	1.6
	emb AW926582 AW926582 HVSMEg0007J16 Hordeum vulgare pre-anthesis...	27	1.9
35	emb AC067936 AC067936 Neurospora crassa chromosome 7, clone X3-B...	34	2.2
	emb AW649885 AW649885 EST328339 tomato germinating seedlings, TA...	34	2.2
	emb AW092862 AW092862 EST286042 tomato mixed elicitor, BTI Lycop...	34	2.2
	emb AW037417 AW037417 EST278919 tomato mixed elicitor, BTI Lycop...	34	2.2
	emb AI771746 AI771746 EST252846 tomato ovary, TAMU Lycopersicon ...	34	2.2
40	emb AC023489 AC023489 Trypanosoma brucei chromosome IV clone RPC...	34	2.2
	emb X78547 GMREPHYD G.max mRNA for epoxide hydrolase.	34	2.2
	emb AW507737 AW507737 si44e05.y1 Gm-r1030 Glycine max cDNA clone...	34	2.2
	gb U02498 STU02498 Solanum tuberosum Lemhi Russet clone EH9.2 ep...	34	2.2
	emb AV387727 AV387727 AV387727 Chlamydomonas reinhardtii C9 Chla...	34	2.2
45	emb AW217951 AW217951 EST296665 tomato flower buds, anthesis, Co...	34	2.2
	emb AW933299 AW933299 EST359142 tomato fruit mature green, TAMU ...	34	2.2
	emb AW164476 AW164476 se73b10.y1 Gm-c1023 Glycine max cDNA clone...	34	2.2
	dbj D63781 SOYEHA Soybean mRNA for epoxide hydrolase, complete cds.	34	2.2
	gb U02495 STU02495 Solanum tuberosum Lemhi Russet clone EH4.1 ep...	34	2.2
50	emb AI485507 AI485507 EST243828 tomato ovary, TAMU Lycopersicon ...	34	2.2
	emb X78548 GMGEPHYD G.max gene encoding epoxide hydrolase.	34	2.2
	gb U02497 STU02497 Solanum tuberosum Lemhi Russet clone EH10.1 e...	34	2.2
	emb X82454 SHSHST3 S.hamata mRNA for low affinity sulphate trans...	34	2.2
	emb AW930466 AW930466 EST340839 tomato fruit mature green, TAMU ...	34	2.2
55	emb AW308974 AW308974 sf92e06.y1 Gm-c1019 Glycine max cDNA clone...	34	2.2
	emb AI894653 AI894653 EST264096 tomato callus, TAMU Lycopersicon...	34	2.2
	emb AI485258 AI485258 EST243562 tomato ovary, TAMU Lycopersicon ...	34	2.2
	emb AI485798 AI485798 EST244119 tomato ovary, TAMU Lycopersicon ...	34	2.2
	emb AI461013 AI461013 sa77h01.y1 Gm-c1004 Glycine max cDNA clone...	34	2.2
60	emb AW038692 AW038692 EST280553 tomato mixed elicitor, BTI Lycop...	34	2.2
	emb AW706725 AW706725 sk02c03.y1 Gm-c1023 Glycine max cDNA clone...	34	2.2

emb|AW217942|AW217942 EST296656 tomato flower buds, anthesis, Co... 34 2.2
 emb|AW568104|AW568104 si68e03.y1 Gm-r1030 Glycine max cDNA clone... 34 2.2
 gb|BE021125|BE021125 sm55g03.y1 Gm-c1028 Glycine max cDNA clone ... 34 2.2
 emb|AI748138|AI748138 sb48f09.y1 Gm-c1011 Glycine max cDNA clone... 34 2.2
 5 gb|BE037499|BE037499 MP02C04 MP Mesembryanthemum crystallinum cD... 34 2.2
 emb|AW932296|AW932296 EST358139 tomato fruit mature green, TAMU ... 34 2.2
 emb|AI900294|AI900294 sc03f01.y1 Gm-c1012 Glycine max cDNA clone... 34 2.2
 emb|AW694549|AW694549 NF077D06ST1F1057 Developing stem Medicago ... 27 2.5
 emb|AW286854|AW286854 LG1_222_C10.b1_A002 Light Grown 1 (LG1) So... 34 3.1
 10 emb|AQ943121|AQ943121 Sheared DNA-33N2.TF Sheared DNA Trypanosom... 34 3.1
 dbj|D87065|D87065 Triticum aestivum gene for histone H1, complet... 34 3.1
 gb|BE053401|BE053401 GA_Ea0033I09f Gossypium arboreum 7-10 dpa ... 34 3.1
 emb|AW286874|AW286874 LG1_222_E10.b1_A002 Light Grown 1 (LG1) So... 34 3.1
 emb|AA063702|AA063702 T3328 MVAT4 bloodstream form of serodeme W... 34 3.1
 15

Query= ATPR1TAN_r_at 12933_r_at /id_source genbank /description
 emb|caa65420.1| (x96600) pathogenesis-related protein 1 [arabidopsis
 thaliana] /blast_score 1.00e-101 /ec_number /family /chip nova
 20 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|atpr1tan| /ncgi
 http://www.ncgr.org/cgi-bin/ff?atpr1tan
 (2616 letters)

25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E
	Sequences producing significant alignments:	(bits)	Value
	emb X66942 NTPRB1B N.tabacum prb-1b gene.	247	3e-64
	emb AW040954 AW040954 EST283818 tomato mixed elicitor, BTI Lycop...	245	1e-63
35	emb AW219480 AW219480 EST301878 tomato root during/after fruit s...	245	1e-63
	emb AW092623 AW092623 EST285803 tomato mixed elicitor, BTI Lycop...	245	1e-63
	emb AI894650 AI894650 EST264093 tomato callus, TAMU Lycopersicon...	245	1e-63
	emb AW041033 AW041033 EST283897 tomato mixed elicitor, BTI Lycop...	245	1e-63
	emb AW035820 AW035820 EST281974 tomato callus, TAMU Lycopersicon...	245	1e-63
40	emb AW034330 AW034330 EST277901 tomato callus, TAMU Lycopersicon...	245	1e-63
	emb AI894391 AI894391 EST263846 tomato callus, TAMU Lycopersicon...	245	1e-63
	emb AW217013 AW217013 EST295727 tomato callus, TAMU Lycopersicon...	245	1e-63
	emb AW040983 AW040983 EST283847 tomato mixed elicitor, BTI Lycop...	245	1e-63
	emb AW032139 AW032139 EST275593 tomato callus, TAMU Lycopersicon...	245	1e-63
45	emb AW092403 AW092403 EST285583 tomato mixed elicitor, BTI Lycop...	245	1e-63
	emb AI896249 AI896249 EST265692 tomato callus, TAMU Lycopersicon...	245	1e-63
	emb AW219671 AW219671 EST302153 tomato root during/after fruit s...	245	1e-63
	emb AW034206 AW034206 EST277777 tomato callus, TAMU Lycopersicon...	245	1e-63
	emb AW034724 AW034724 EST278526 tomato callus, TAMU Lycopersicon...	245	1e-63
50	emb AW034260 AW034260 EST277831 tomato callus, TAMU Lycopersicon...	245	1e-63
	emb AW625930 AW625930 EST319825 tomato radicle, 5 d post-imbibit...	245	1e-63
	emb AW032514 AW032514 EST276073 tomato callus, TAMU Lycopersicon...	245	1e-63
	emb AW034454 AW034454 EST278025 tomato callus, TAMU Lycopersicon...	245	1e-63
	emb AW032723 AW032723 EST276282 tomato callus, TAMU Lycopersicon...	245	1e-63
55	emb AW033873 AW033873 EST277444 tomato callus, TAMU Lycopersicon...	245	1e-63
	emb AI895090 AI895090 EST264533 tomato callus, TAMU Lycopersicon...	245	1e-63
	emb AW033593 AW033593 EST277164 tomato callus, TAMU Lycopersicon...	243	4e-63
	emb AW032749 AW032749 EST276308 tomato callus, TAMU Lycopersicon...	243	5e-63
	emb AI782621 AI782621 EST263500 tomato susceptible, Cornell Lyco...	242	7e-63
60	emb AW625666 AW625666 EST319573 tomato radicle, 5 d post-imbibit...	240	5e-62
	emb AW622143 AW622143 EST312941 tomato root during/after fruit s...	237	3e-61

- emb|AW033687|AW033687 EST277258 tomato callus, TAMU Lycopersicon... 232 7e-60
emb|AW094536|AW094536 EST287716 tomato mixed elicitor, BTI Lycop... 230 5e-59
emb|AW038553|AW038553 EST280236 tomato mixed elicitor, BTI Lycop... 230 5e-59
emb|AI896011|AI896011 EST265454 tomato callus, TAMU Lycopersicon... 230 5e-59
5 emb|AW218808|AW218808 EST301288 tomato root during/after fruit s... 230 5e-59
emb|AW035735|AW035735 EST281889 tomato callus, TAMU Lycopersicon... 228 2e-58
emb|AW622662|AW622662 EST313462 tomato root during/after fruit s... 227 2e-58
emb|AW031086|AW031086 EST274393 tomato callus, TAMU Lycopersicon... 227 2e-58
emb|AW981257|AW981257 EST392410 DSIL Medicago truncatula cDNA cl... 227 2e-58
10 emb|AW559894|AW559894 EST314942 DSIR Medicago truncatula cDNA cl... 209 3e-58
emb|AW559895|AW559895 EST314943 DSIR Medicago truncatula cDNA cl... 209 3e-58
emb|AW329241|AW329241 N200453e rootphos(-) Medicago truncatula c... 209 3e-58
emb|AW035757|AW035757 EST281911 tomato callus, TAMU Lycopersicon... 227 3e-58
emb|X14065|NTPRP1 Nicotiana tabacum gene for basic form of patho... 149 7e-58
15 emb|AW032727|AW032727 EST276286 tomato callus, TAMU Lycopersicon... 226 9e-58
emb|AW033469|AW033469 EST277040 tomato callus, TAMU Lycopersicon... 224 2e-57
emb|X71592|LEPR1A1A L.esculentum PR-1a1 mRNA. 224 2e-57
emb|AW034455|AW034455 EST278026 tomato callus, TAMU Lycopersicon... 224 2e-57
emb|X52555|NTW381 Tobacco W38/1 gene for PR-1 pathogenesis-relat... 129 6e-57
20 gb|U70666|BNU70666 Brassica napus pathogenesis-related protein P... 154 2e-56
gb|U21849|BNU21849 Brassica napus PR-1a (LSC94) mRNA, complete cds. 154 2e-56
emb|AW035158|AW035158 EST280420 tomato callus, TAMU Lycopersicon... 221 2e-56
emb|AW035469|AW035469 EST281207 tomato callus, TAMU Lycopersicon... 221 3e-56
emb|AW126362|AW126362 N100469e rootphos(-) Medicago truncatula c... 209 3e-56
25 emb|AW040722|AW040722 EST283586 tomato mixed elicitor, BTI Lycop... 220 4e-56
emb|AW559969|AW559969 EST315017 DSIR Medicago truncatula cDNA cl... 194 4e-56
emb|X05959|NTPR1AG Tobacco PR-1a gene for pathogenesis-related p... 134 2e-55
emb|X12737|NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p... 134 2e-55
emb|X06361|NTPR1AG1 Nicotiana tabacum gene for pathogenesis-rela... 134 2e-55
30 emb|X12485|NTPR1A Tobacco mRNA fragment for pathogenesis-related... 134 2e-55
emb|X06930|NTPR1AG2 Tobacco PR-1a gene for pathogenesis-related ... 133 3e-55
emb|X17681|NTPR1CA Tobacco gene for pathogenesis-related protein... 128 3e-55
emb|X05454|NTPR1CR Nicotiana tabacum mRNA for PR-1c protein. 128 3e-55
emb|X12487|NTPR1C Tobacco mRNA fragment for pathogenesis-related... 128 3e-55
35 emb|AJ011520|LES011520 Lycopersicon esculentum pr1a (P4) gene. 147 5e-55
dbj|D90196|TOBPR1A Nicotiana tabacum mRNA for PR1a protein precu... 133 5e-55
gb|M69247|TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat... 147 5e-55
emb|A22634|LEPI4GENE L.esculentum P14 gene. 147 5e-55
gb|BE034214|BE034214 MH01C07 MH Mesembryanthemum crystallinum cD... 116 8e-55
40 emb|AW053720|AW053720 L30-1612T3 Ice plant Lambda Uni-Zap XR exp... 116 8e-55
gb|U64806|BNU64806 Brassica napus pathogenesis-related protein P... 149 1e-54
emb|AW034882|AW034882 EST279111 tomato callus, TAMU Lycopersicon... 144 5e-54
emb|AI782416|AI782416 EST263295 tomato susceptible, Cornell Lyco... 144 7e-54
emb|AW559392|AW559392 EST314440 DSIR Medicago truncatula cDNA cl... 191 9e-54
45 emb|X17680|NTPR1BA Tobacco gene for pathogenesis-related protein... 133 2e-53
emb|X03465|NTPRPR Nicotiana tabacum mRNA for pathogenesis-relate... 133 2e-53
dbj|D90197|TOBPR1B1 Nicotiana tabacum mRNA for PR1b protein. 133 2e-53
emb|AJ250136|STU250136 Solanum tuberosum mRNA for pathogenesis r... 144 2e-53
emb|AI352851|AI352851 MB69-8A PZ204.BNlib Brassica napus cDNA cl... 149 2e-53
50 emb|X12486|NTPR1B Tobacco mRNA fragment for pathogenesis-related... 133 2e-53
emb|Y08804|LEPR1B1 L.esculentum mRNA for PR protein. 139 1e-52
gb|M69248|TOMPRP6 Lycopersicon esculentum PR (pathogenesis relat... 139 1e-52
emb|X68738|LEP1P14A L.esculentum mRNA for ethylene-induced P1(p1... 139 1e-52
emb|AI781499|AI781499 EST262378 tomato susceptible, Cornell Lyco... 139 1e-52
55 emb|AI779424|AI779424 EST260303 tomato susceptible, Cornell Lyco... 139 1e-52
emb|AW031093|AW031093 EST274400 tomato callus, TAMU Lycopersicon... 139 1e-52
emb|AI779425|AI779425 EST260304 tomato susceptible, Cornell Lyco... 139 1e-52
emb|AW040587|AW040587 EST283367 tomato mixed elicitor, BTI Lycop... 141 1e-52
emb|AI782545|AI782545 EST263424 tomato susceptible, Cornell Lyco... 139 1e-52
60 emb|AI782822|AI782822 EST263701 tomato susceptible, Cornell Lyco... 139 1e-52
emb|AI778686|AI778686 EST259565 tomato susceptible, Cornell Lyco... 139 1e-52

emb|AI778680|AI778680 EST259559 tomato susceptible, Cornell Lyco... 139 1e-52
 emb|AW039236|AW039236 EST281471 tomato mixed elicitor, BTI Lycop... 141 1e-52
 emb|AI899514|AI899514 EST268957 tomato susceptible, Cornell Lyco... 139 1e-52
 emb|AI779287|AI779287 EST260166 tomato susceptible, Cornell Lyco... 139 1e-52
 5 emb|AI773130|AI773130 EST254230 tomato resistant, Cornell Lycop... 139 1e-52
 emb|AI778790|AI778790 EST259669 tomato susceptible, Cornell Lyco... 139 1e-52
 emb|AI778791|AI778791 EST259670 tomato susceptible, Cornell Lyco... 139 1e-52
 emb|AI778985|AI778985 EST259864 tomato susceptible, Cornell Lyco... 139 1e-52
 emb|AW032026|AW032026 EST275480 tomato callus, TAMU Lycopersicon... 139 1e-52
 10 emb|AI782288|AI782288 EST263167 tomato susceptible, Cornell Lyco... 139 1e-52

Query= ATTHIRED4_i_at 13187_i_at /id_source genbank /description
 gb|aac49356.1| (u35829) thioredoxin h [arabidopsis thaliana]
 15 /blast_score 2.00e-63 /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|atthired4| /ncgi
 http://www.ncgr.org/cgi-bin/ff?atthired4
 (528 letters)

20 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching:.....done

25

	Score	E
Sequences producing significant alignments:	(bits)	Value
gb U59379 BNU59379 Brassica napus thioredoxin-h-like-1 (THL-1) m...	194	4e-49
30 emb X89759 BOPC17 B.oleracea mRNA for thioredoxin h-like, pollen...	194	4e-49
emb AB010434 AB010434 Brassica rapa PEC-2 mRNA for Thioredoxin, ...	192	2e-48
emb AW255457 AW255457 ML480 peppermint glandular trichome Mentha...	191	4e-48
emb AW569018 AW569018 si74e02.y1 Gm-c1031 Glycine max cDNA clone...	186	1e-46
emb AI988470 AI988470 sd02f07.y1 Gm-c1020 Glycine max cDNA clone...	186	1e-46
35 emb AI161830 AI161830 A007P52U Hybrid aspen plasmid library Popu...	184	3e-46
emb Z70677 RCTHIORXN R.communis mRNA for thioredoxin.	183	9e-46
gb BE053835 BE053835 GA__Ea0009P21f Gossypium arboreum 7-10 dpa ...	182	2e-45
emb AW565750 AW565750 LG1_349_G02.g1_A002 Light Grown 1 (LG1) So...	181	3e-45
emb AW677651 AW677651 WS1_10_F03.b1_A002 Water-stressed 1 (WS1) ...	181	3e-45
40 emb AW671668 AW671668 LG1_349_G02.b1_A002 Light Grown 1 (LG1) So...	181	3e-45
emb AW924685 AW924685 WS1_71_B11.b1_A002 Water-stressed 1 (WS1) ...	181	3e-45
emb AW677726 AW677726 WS1_10_F03.g1_A002 Water-stressed 1 (WS1) ...	181	3e-45
emb AW349345 AW349345 GM210007A20B10R Gm-r1021 Glycine max cDNA ...	180	6e-45
45 emb AI461219 AI461219 sa76f11.y1 Gm-c1004 Glycine max cDNA clone...	180	6e-45
emb AI938238 AI938238 sc41e05.y1 Gm-c1014 Glycine max cDNA clone...	180	6e-45
emb AW164730 AW164730 se77a02.y1 Gm-c1023 Glycine max cDNA clone...	180	8e-45
emb AJ009762 TAE9762 Triticum aestivum mRNA for thioredoxin H.	179	2e-44
emb AW255195 AW255195 ML185 peppermint glandular trichome Mentha...	178	2e-44
50 emb AI165128 AI165128 A076P57U Hybrid aspen plasmid library Popu...	177	5e-44
gb T24347 T24347 crs1466 lambdaZAPST Ricinus communis cDNA clone...	177	5e-44
dbj D87984 D87984 Fagopyrum esculentum mRNA for thioredoxin, com...	177	8e-44
gb BE054543 BE054543 GA__Ea0026K15f Gossypium arboreum 7-10 dpa ...	177	8e-44
emb AW983331 AW983331 HVSMEg0010D20f Hordeum vulgare pre-anthesi...	177	8e-44
55 emb AW329521 AW329521 N200767e rootphos(-) Medicago truncatula c...	176	1e-43
gb BE053246 BE053246 GA__Ea0021K08f Gossypium arboreum 7-10 dpa ...	176	1e-43
emb AW217307 AW217307 EST296026 tomato flower buds 0-3 mm, Corne...	175	2e-43
emb AW781479 AW781479 sl79e04.y1 Gm-c1037 Glycine max cDNA clone...	175	3e-43
emb A48516 A48516 Sequence 4 from Patent WO9603505.	175	3e-43
60 emb AW705063 AW705063 sk57b09.y1 Gm-c1019 Glycine max cDNA clone...	175	3e-43
emb AW164347 AW164347 se71c11.y1 Gm-c1023 Glycine max cDNA clone...	175	3e-43

- emb|AJ001903|TDAJ1903 *Triticum durum* mRNA for thioredoxin H. 175 3e-43
 emb|A48520|A48520 Sequence 8 from Patent WO9603505. 175 3e-43
 emb|X69915|TATHIORDH *T.aestivum* mRNA for thioredoxine H. 175 3e-43
 emb|A48514|A48514 Sequence 2 from Patent WO9603505. 175 3e-43
 5 emb|AW568753|AW568753 si72f07.y1 *Gm-c1031* Glycine max cDNA clone... 175 3e-43
 emb|A48519|A48519 Sequence 7 from Patent WO9603505. 175 3e-43
 emb|AW329764|AW329764 N201033e rootphos(-) *Medicago truncatula* c... 174 4e-43
 emb|AW982237|AW982237 HVSMEg0002G18f *Hordeum vulgare* pre-anthesi... 174 5e-43
 emb|AW983305|AW983305 HVSMEg0010C12f *Hordeum vulgare* pre-anthesi... 174 5e-43
 10 emb|AW626018|AW626018 EST319925 tomato radicle, 5 d post-imbibit... 174 5e-43
 emb|AW349509|AW349509 GM210005A21B12R *Gm-r1021* Glycine max cDNA ... 173 7e-43
 gb|U59380|BNU59380 *Brassica napus* thioredoxin-h-like-2 (THL-2) m... 101 8e-43
 emb|X58527|NTTRNA *N.tabacum* mRNA for thioredoxin. 173 1e-42
 15 gb|C95504|C95504 C95504 *Citrus unshiu* Miyagawa-wase maturation s... 172 1e-42
 emb|AI441505|AI441505 sa87c03.y1 *Gm-c1004* Glycine max cDNA clone... 171 2e-42
 emb|AW277335|AW277335 sf80b02.y1 *Gm-c1019* Glycine max cDNA clone... 171 2e-42
 emb|AW625957|AW625957 EST319852 tomato radicle, 5 d post-imbibit... 171 5e-42
 emb|AW625331|AW625331 EST319154 tomato radicle, 5 d post-imbibit... 171 5e-42
 20 emb|AW650009|AW650009 EST328463 tomato germinating seedlings, TA... 171 5e-42
 emb|AW041395|AW041395 EST284259 tomato mixed elicitor, BTI Lycop... 171 5e-42
 emb|AW096472|AW096472 EST289652 tomato mixed elicitor, BTI Lycop... 171 5e-42
 emb|AW040011|AW040011 EST282502 tomato mixed elicitor, BTI Lycop... 171 5e-42
 emb|AW040001|AW040001 EST282492 tomato mixed elicitor, BTI Lycop... 171 5e-42
 25 emb|AW037831|AW037831 EST279460 tomato mixed elicitor, BTI Lycop... 171 5e-42
 emb|AI773303|AI773303 EST254403 tomato resistant, Cornell Lycop... 171 5e-42
 emb|AW094525|AW094525 EST287705 tomato mixed elicitor, BTI Lycop... 171 5e-42
 emb|AI776110|AI776110 EST257198 tomato resistant, Cornell Lycop... 171 5e-42
 emb|AI775760|AI775760 EST256860 tomato resistant, Cornell Lycop... 171 5e-42
 30 emb|AI780240|AI780240 EST261119 tomato susceptible, Cornell Lyco... 171 5e-42
 emb|AI781827|AI781827 EST262706 tomato susceptible, Cornell Lyco... 171 5e-42
 emb|AI778940|AI778940 EST259819 tomato susceptible, Cornell Lyco... 171 5e-42
 emb|AW621673|AW621673 EST312471 tomato root during/after fruit s... 171 5e-42
 emb|AW038141|AW038141 EST279798 tomato mixed elicitor, BTI Lycop... 171 5e-42
 35 emb|AW038924|AW038924 EST280880 tomato mixed elicitor, BTI Lycop... 171 5e-42
 emb|AW597424|AW597424 si92g01.y1 *Gm-c1031* Glycine max cDNA clone... 169 2e-41
 emb|AW038564|AW038564 EST280247 tomato mixed elicitor, BTI Lycop... 168 2e-41
 emb|AW040201|AW040201 EST282700 tomato mixed elicitor, BTI Lycop... 168 2e-41
 emb|AW040195|AW040195 EST282694 tomato mixed elicitor, BTI Lycop... 168 2e-41
 40 gb|BE057793|BE057793 sn07c11.y1 *Gm-c1016* Glycine max cDNA clone ... 168 2e-41
 emb|AW289622|AW289622 NXNV003H05F Nsf Xylem Normal wood Vertical... 164 4e-40
 emb|AW064893|AW064893 ST37B02 Pine TriplEx shoot tip library Pin... 162 1e-39
 emb|AW043214|AW043214 ST30F08 Pine TriplEx shoot tip library Pin... 162 2e-39
 emb|AW043171|AW043171 ST30B09 Pine TriplEx shoot tip library Pin... 162 2e-39
 45 emb|AW042699|AW042699 ST23E01 Pine TriplEx shoot tip library Pin... 162 2e-39
 emb|AW010199|AW010199 ST03C05 Pine TriplEx shoot tip library Pin... 162 2e-39
 emb|AF051206|AF051206 *Picea mariana* probable thioredoxin H (Sb09... 162 2e-39
 emb|AW043379|AW043379 ST32F12 Pine TriplEx shoot tip library Pin... 162 2e-39
 emb|AW065132|AW065132 ST40A08 Pine TriplEx shoot tip library Pin... 162 2e-39
 50 emb|AW497847|AW497847 PC02B02 Pine TriplEx pollen cone library P... 161 3e-39
 emb|AW736931|AW736931 NXNV_081_G02_F Nsf Xylem Normal wood Verti... 161 3e-39
 emb|AW680784|AW680784 WS1_7_D07.b1_A002 Water-stressed 1 (WS1) S... 161 4e-39
 emb|AW680877|AW680877 WS1_7_D07.g1_A002 Water-stressed 1 (WS1) S... 161 4e-39
 emb|AW011327|AW011327 ST19E02 Pine TriplEx shoot tip library Pin... 160 5e-39
 55 emb|AW011046|AW011046 ST16A08 Pine TriplEx shoot tip library Pin... 160 7e-39
 emb|AI736736|AI736736 sb32g12.y1 *Gm-c1012* Glycine max cDNA clone... 93 1e-38
 emb|AW010836|AW010836 ST14F05 Pine TriplEx shoot tip library Pin... 159 1e-38
 emb|AW290231|AW290231 NXNV015E05F Nsf Xylem Normal wood Vertical... 159 2e-38
 emb|AW011498|AW011498 ST21E10 Pine TriplEx shoot tip library Pin... 158 3e-38
 60 emb|AA740038|AA740038 803 PtiFG2 *Pinus taeda* cDNA clone 9266M 3'... 157 5e-38
 emb|AW009991|AW009991 ST01A09 Pine TriplEx shoot tip library Pin... 157 5e-38

emb|AW684766|AW684766 NF021G12NR1F1000 Nodulated root Medicago t... 124 1e-37
emb|AW706540|AW706540 sj57g11.y1 Gm-c1033 Glycine max cDNA clone... 156 1e-37
emb|AI461254|AI461254 sa60f10.y1 Gm-c1004 Glycine max cDNA clone... 155 2e-37
5 emb|AW924415|AW924415 WS1_69_D02.b1_A002 Water-stressed 1 (WS1) ... 154 4e-37
emb|AW679524|AW679524 WS1_29_F05.g1_A002 Water-stressed 1 (WS1) ... 154 4e-37
emb|AW681036|AW681036 WS1_8_D05.b1_A002 Water-stressed 1 (WS1) S... 154 4e-37
emb|AW754729|AW754729 PC07B04 Pine TriplEx pollen cone library P... 154 4e-37
emb|AW923038|AW923038 DG1_48_B02.g1_A002 Dark Grown 1 (DG1) Sorg... 154 4e-37

10
Query= ATTHIRED4_r_at13188_r_at /id_source genbank /description
gb|aac49356.1| (u35829) thioredoxin h [arabidopsis thaliana]
/blast_score 2.00e-63 /ec_number /family /chip nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-
15 post/entrez/query?db=n&form=6&dopt=g&uid=gb|atthired4| /ncgi
http://www.ncgr.org/cgi-bin/ff?atthired4
(528 letters)

Database: plantfungal
20 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
25 Sequences producing significant alignments: (bits) Value

gb|U59379|BNU59379 Brassica napus thioredoxin-h-like-1 (THL-1) m... 194 4e-49
emb|X89759|BOPC17 B.oleracea mRNA for thioredoxin h-like, pollen... 194 4e-49
emb|AB010434|AB010434 Brassica rapa PEC-2 mRNA for Thioredoxin, ... 192 2e-48
30 emb|AW255457|AW255457 ML480 peppermint glandular trichome Mentha... 191 4e-48
emb|AW569018|AW569018 si74e02.y1 Gm-c1031 Glycine max cDNA clone... 186 1e-46
emb|AI988470|AI988470 sd02f07.y1 Gm-c1020 Glycine max cDNA clone... 186 1e-46
emb|AI161830|AI161830 A007P52U Hybrid aspen plasmid library Popu... 184 3e-46
emb|Z70677|RCTHIORXN R.communis mRNA for thioredoxin. 183 9e-46
35 gb|BE053835|BE053835 GA_Ea0009P21f Gossypium arboreum 7-10 dpa ... 182 2e-45
emb|AW565750|AW565750 LG1_349_G02.g1_A002 Light Grown 1 (LG1) So... 181 3e-45
emb|AW677651|AW677651 WS1_10_F03.b1_A002 Water-stressed 1 (WS1) ... 181 3e-45
emb|AW671668|AW671668 LG1_349_G02.b1_A002 Light Grown 1 (LG1) So... 181 3e-45
emb|AW924685|AW924685 WS1_71_B11.b1_A002 Water-stressed 1 (WS1) ... 181 3e-45
40 emb|AW677726|AW677726 WS1_10_F03.g1_A002 Water-stressed 1 (WS1) ... 181 3e-45
emb|AW349345|AW349345 GM210007A20B10R Gm-r1021 Glycine max cDNA ... 180 6e-45
emb|AI461219|AI461219 sa76f11.y1 Gm-c1004 Glycine max cDNA clone... 180 6e-45
emb|AI938238|AI938238 sc41e05.y1 Gm-c1014 Glycine max cDNA clone... 180 6e-45
45 emb|AW164730|AW164730 se77a02.y1 Gm-c1023 Glycine max cDNA clone... 180 8e-45
emb|AJ009762|TAE9762 Triticum aestivum mRNA for thioredoxin H. 179 2e-44
emb|AW255195|AW255195 ML185 peppermint glandular trichome Mentha... 178 2e-44
emb|AI165128|AI165128 A076P57U Hybrid aspen plasmid library Popu... 177 5e-44
gb|T24347|T24347 crs1466 lambdaZAPST Ricinus communis cDNA clone... 177 5e-44
50 dbj|D87984|D87984 Fagopyrum esculentum mRNA for thioredoxin, com... 177 8e-44
gb|BE054543|BE054543 GA_Ea0026K15f Gossypium arboreum 7-10 dpa ... 177 8e-44
emb|AW983331|AW983331 HVSMEg0010D20f Hordeum vulgare pre-anthesi... 177 8e-44
emb|AW329521|AW329521 N200767e rootphos(-) Medicago truncatula c... 176 1e-43
gb|BE053246|BE053246 GA_Ea0021K08f Gossypium arboreum 7-10 dpa ... 176 1e-43
55 emb|AW217307|AW217307 EST296026 tomato flower buds 0-3 mm, Corne... 175 2e-43
emb|AW781479|AW781479 sl79e04.y1 Gm-c1037 Glycine max cDNA clone... 175 3e-43
emb|A48516|A48516 Sequence 4 from Patent WO9603505. 175 3e-43
emb|AW705063|AW705063 sk57b09.y1 Gm-c1019 Glycine max cDNA clone... 175 3e-43
emb|AW164347|AW164347 se71c11.y1 Gm-c1023 Glycine max cDNA clone... 175 3e-43
60 emb|AJ001903|TDAJ1903 Triticum durum mRNA for thioredoxin H. 175 3e-43
emb|A48520|A48520 Sequence 8 from Patent WO9603505. 175 3e-43

	emb X69915 TATHIORDH T.aestivum mRNA for thioredoxine H.	175 3e-43
	emb A48514 A48514 Sequence 2 from Patent WO9603505.	175 3e-43
	emb AW568753 AW568753 si72f07.yl Gm-c1031 Glycine max cDNA clone...	175 3e-43
	emb A48519 A48519 Sequence 7 from Patent WO9603505.	175 3e-43
5	emb AW329764 AW329764 N201033e rootphos(-) Medicago truncatula c...	174 4e-43
	emb AW982237 AW982237 HVSMEg0002G18f Hordeum vulgare pre-anthesi...	174 5e-43
	emb AW983305 AW983305 HVSMEg0010C12f Hordeum vulgare pre-anthesi...	174 5e-43
	emb AW626018 AW626018 EST319925 tomato radicle, 5 d post-imbibit...	174 5e-43
10	emb AW349509 AW349509 GM210005A21B12R Gm-r1021 Glycine max cDNA ...	173 7e-43
	gb U59380 BNU59380 Brassica napus thioredoxin-h-like-2 (THL-2) m...	101 8e-43
	emb X58527 NTTRNA N.tabacum mRNA for thioredoxin.	173 1e-42
	gb C95504 C95504 C95504 Citrus unshiu Miyagawa-wase maturation s...	172 1e-42
	emb AI441505 AI441505 sa87c03.yl Gm-c1004 Glycine max cDNA clone...	171 2e-42
15	emb AW277335 AW277335 sf80b02.yl Gm-c1019 Glycine max cDNA clone...	171 2e-42
	emb AW625957 AW625957 EST319852 tomato radicle, 5 d post-imbibit...	171 5e-42
	emb AW625331 AW625331 EST319154 tomato radicle, 5 d post-imbibit...	171 5e-42
	emb AW650009 AW650009 EST328463 tomato germinating seedlings, TA...	171 5e-42
	emb AW041395 AW041395 EST284259 tomato mixed elicitor, BTI Lycop...	171 5e-42
20	emb AW096472 AW096472 EST289652 tomato mixed elicitor, BTI Lycop...	171 5e-42
	emb AW040011 AW040011 EST282502 tomato mixed elicitor, BTI Lycop...	171 5e-42
	emb AW040001 AW040001 EST282492 tomato mixed elicitor, BTI Lycop...	171 5e-42
	emb AW037831 AW037831 EST279460 tomato mixed elicitor, BTI Lycop...	171 5e-42
	emb AI773303 AI773303 EST254403 tomato resistant, Cornell Lycope...	171 5e-42
25	emb AW094525 AW094525 EST287705 tomato mixed elicitor, BTI Lycop...	171 5e-42
	emb AI776110 AI776110 EST257198 tomato resistant, Cornell Lycope...	171 5e-42
	emb AI775760 AI775760 EST256860 tomato resistant, Cornell Lycope...	171 5e-42
	emb AI780240 AI780240 EST261119 tomato susceptible, Cornell Lyco...	171 5e-42
	emb AI781827 AI781827 EST262706 tomato susceptible, Cornell Lyco...	171 5e-42
30	emb AI778940 AI778940 EST259819 tomato susceptible, Cornell Lyco...	171 5e-42
	emb AW621673 AW621673 EST312471 tomato root during/after fruit s...	171 5e-42
	emb AW038141 AW038141 EST279798 tomato mixed elicitor, BTI Lycop...	171 5e-42
	emb AW038924 AW038924 EST280880 tomato mixed elicitor, BTI Lycop...	171 5e-42
35	emb AW597424 AW597424 si92g01.yl Gm-c1031 Glycine max cDNA clone...	169 2e-41
	emb AW038564 AW038564 EST280247 tomato mixed elicitor, BTI Lycop...	168 2e-41
	emb AW040201 AW040201 EST282700 tomato mixed elicitor, BTI Lycop...	168 2e-41
	emb AW040195 AW040195 EST282694 tomato mixed elicitor, BTI Lycop...	168 2e-41
	gb BE057793 BE057793 sn07c11.yl Gm-c1016 Glycine max cDNA clone ...	168 2e-41
	emb AW289622 AW289622 NXNV003H05F Nsf Xylem Normal wood Vertical...	164 4e-40
40	emb AW064893 AW064893 ST37B02 Pine TriplEx shoot tip library Pin...	162 1e-39
	emb AW043214 AW043214 ST30F08 Pine TriplEx shoot tip library Pin...	162 2e-39
	emb AW043171 AW043171 ST30B09 Pine TriplEx shoot tip library Pin...	162 2e-39
	emb AW042699 AW042699 ST23E01 Pine TriplEx shoot tip library Pin...	162 2e-39
	emb AW010199 AW010199 ST03C05 Pine TriplEx shoot tip library Pin...	162 2e-39
45	emb AF051206 AF051206 Picea mariana probable thioredoxin H (Sb09...	162 2e-39
	emb AW043379 AW043379 ST32F12 Pine TriplEx shoot tip library Pin...	162 2e-39
	emb AW065132 AW065132 ST40A08 Pine TriplEx shoot tip library Pin...	162 2e-39
	emb AW497847 AW497847 PC02B02 Pine TriplEx pollen cone library P...	161 3e-39
	emb AW736931 AW736931 NXNV_081_G02_F Nsf Xylem Normal wood Verti...	161 3e-39
50	emb AW680784 AW680784 WS1_7_D07.b1_A002 Water-stressed 1 (WS1) S...	161 4e-39
	emb AW680877 AW680877 WS1_7_D07.g1_A002 Water-stressed 1 (WS1) S...	161 4e-39
	emb AW011327 AW011327 ST19E02 Pine TriplEx shoot tip library Pin...	160 5e-39
	emb AW011046 AW011046 ST16A08 Pine TriplEx shoot tip library Pin...	160 7e-39
	emb AI736736 AI736736 sb32g12.yl Gm-c1012 Glycine max cDNA clone...	93 1e-38
55	emb AW010836 AW010836 ST14F05 Pine TriplEx shoot tip library Pin...	159 1e-38
	emb AW290231 AW290231 NXNV015E05F Nsf Xylem Normal wood Vertical...	159 2e-38
	emb AW011498 AW011498 ST21E10 Pine TriplEx shoot tip library Pin...	158 3e-38
	emb AA740038 AA740038 803 PtIFG2 Pinus taeda cDNA clone 9266M 3'...	157 5e-38
	emb AW009991 AW009991 ST01A09 Pine TriplEx shoot tip library Pin...	157 5e-38
60	emb AW684766 AW684766 NF021G12NR1F1000 Nodulated root Medicago t...	124 1e-37
	emb AW706540 AW706540 sj57g11.yl Gm-c1033 Glycine max cDNA clone...	156 1e-37

emb|AI461254|AI461254 sa60f10.y1 Gm-c1004 Glycine max cDNA clone... 155 2e-37
emb|AW924415|AW924415 WS1_69_D02.b1_A002 Water-stressed 1 (WS1) ... 154 4e-37
emb|AW679524|AW679524 WS1_29_F05.g1_A002 Water-stressed 1 (WS1) ... 154 4e-37
emb|AW681036|AW681036 WS1_8_D05.b1_A002 Water-stressed 1 (WS1) S... 154 4e-37
5 emb|AW754729|AW754729 PC07B04 Pine TriplEx pollen cone library P... 154 4e-37
emb|AW923038|AW923038 DG1_48_B02.g1_A002 Dark Grown 1 (DG1) Sorg... 154 4e-37

Query= ATTHIRED4_s_at 13189_s_at /id_source genbank /description
10 gb|aac49356.1| (u35829) thioredoxin h [arabidopsis thaliana]
/blast_score 2.00e-63 /ec_number /family /chip nova /gb_link /ncgi
(528 letters)

Database: plantfungal
15 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
20 Sequences producing significant alignments: (bits) Value

gb|U59379|BNU59379 Brassica napus thioredoxin-h-like-1 (THL-1) m... 194 4e-49
emb|X89759|BOPC17 B.oleracea mRNA for thioredoxin h-like, pollen... 194 4e-49
emb|AB010434|AB010434 Brassica rapa PEC-2 mRNA for Thioredoxin, ... 192 2e-48
25 emb|AW255457|AW255457 ML480 peppermint glandular trichome Mentha... 191 4e-48
emb|AW569018|AW569018 si74e02.y1 Gm-c1031 Glycine max cDNA clone... 186 1e-46
emb|AI988470|AI988470 sd02f07.y1 Gm-c1020 Glycine max cDNA clone... 186 1e-46
emb|AI161830|AI161830 A007P52U Hybrid aspen plasmid library Popu... 184 3e-46
emb|Z70677|RCTHIORXN R.communis mRNA for thioredoxin. 183 9e-46
30 gb|BE053835|BE053835 GA_Ea0009P21f Gossypium arboreum 7-10 dpa ... 182 2e-45
emb|AW565750|AW565750 LG1_349_G02.g1_A002 Light Grown 1 (LG1) So... 181 3e-45
emb|AW677651|AW677651 WS1_10_F03.b1_A002 Water-stressed 1 (WS1) ... 181 3e-45
emb|AW671668|AW671668 LG1_349_G02.b1_A002 Light Grown 1 (LG1) So... 181 3e-45
emb|AW924685|AW924685 WS1_71_B11.b1_A002 Water-stressed 1 (WS1) ... 181 3e-45
35 emb|AW677726|AW677726 WS1_10_F03.g1_A002 Water-stressed 1 (WS1) ... 181 3e-45
emb|AW349345|AW349345 GM210007A20B10R Gm-r1021 Glycine max cDNA ... 180 6e-45
emb|AI461219|AI461219 sa76f11.y1 Gm-c1004 Glycine max cDNA clone... 180 6e-45
emb|AI938238|AI938238 sc41e05.y1 Gm-c1014 Glycine max cDNA clone... 180 6e-45
40 emb|AW164730|AW164730 se77a02.y1 Gm-c1023 Glycine max cDNA clone... 180 8e-45
emb|AJ009762|TAE9762 Triticum aestivum mRNA for thioredoxin H. 179 2e-44
emb|AW255195|AW255195 ML185 peppermint glandular trichome Mentha... 178 2e-44
emb|AI165128|AI165128 A076P57U Hybrid aspen plasmid library Popu... 177 5e-44
gb|T24347|T24347 crs1466 lambdaZAPST Ricinus communis cDNA clone... 177 5e-44
45 dbj|D87984|D87984 Fagopyrum esculentum mRNA for thioredoxin, com... 177 8e-44
gb|BE054543|BE054543 GA_Ea0026K15f Gossypium arboreum 7-10 dpa ... 177 8e-44
emb|AW983331|AW983331 HVSMEg0010D20f Hordeum vulgare pre-anthesi... 177 8e-44
emb|AW329521|AW329521 N200767e rootphos(-) Medicago truncatula c... 176 1e-43
gb|BE053246|BE053246 GA_Ea0021K08f Gossypium arboreum 7-10 dpa ... 176 1e-43
50 emb|AW217307|AW217307 EST296026 tomato flower buds 0-3 mm, Corne... 175 2e-43
emb|AW781479|AW781479 sl79e04.y1 Gm-c1037 Glycine max cDNA clone... 175 3e-43
emb|A48516|A48516 Sequence 4 from Patent WO9603505. 175 3e-43
emb|AW705063|AW705063 sk57b09.y1 Gm-c1019 Glycine max cDNA clone... 175 3e-43
emb|AW164347|AW164347 se71c11.y1 Gm-c1023 Glycine max cDNA clone... 175 3e-43
55 emb|AJ001903|TDAJ1903 Triticum durum mRNA for thioredoxin H. 175 3e-43
emb|A48520|A48520 Sequence 8 from Patent WO9603505. 175 3e-43
emb|X69915|TATHIORDH T.aestivum mRNA for thioredoxine H. 175 3e-43
emb|A48514|A48514 Sequence 2 from Patent WO9603505. 175 3e-43
emb|AW568753|AW568753 si72f07.y1 Gm-c1031 Glycine max cDNA clone... 175 3e-43
60 emb|A48519|A48519 Sequence 7 from Patent WO9603505. 175 3e-43
emb|AW329764|AW329764 N201033e rootphos(-) Medicago truncatula c... 174 4e-43

- emb|AW982237|AW982237 HVSMEg0002G18f Hordeum vulgare pre-anthesi... 174 5e-43
emb|AW983305|AW983305 HVSMEg0010C12f Hordeum vulgare pre-anthesi... 174 5e-43
emb|AW626018|AW626018 EST319925 tomato radicle, 5 d post-imbibit... 174 5e-43
5 emb|AW349509|AW349509 GM210005A21B12R Gm-r1021 Glycine max cDNA ... 173 7e-43
gb|U59380|BNU59380 Brassica napus thioredoxin-h-like-2 (THL-2) m... 101 8e-43
emb|X58527|NTTRNA N.tabacum mRNA for thioredoxin. 173 1e-42
gb|C95504|C95504 C95504 Citrus unshiu Miyagawa-wase maturation s... 172 1e-42
emb|AI441505|AI441505 sa87c03.y1 Gm-c1004 Glycine max cDNA clone... 171 2e-42
10 emb|AW277335|AW277335 sf80b02.y1 Gm-c1019 Glycine max cDNA clone... 171 2e-42
emb|AW625957|AW625957 EST319852 tomato radicle, 5 d post-imbibit... 171 5e-42
emb|AW625331|AW625331 EST319154 tomato radicle, 5 d post-imbibit... 171 5e-42
emb|AW650009|AW650009 EST328463 tomato germinating seedlings, TA... 171 5e-42
emb|AW041395|AW041395 EST284259 tomato mixed elicitor, BTI Lycop... 171 5e-42
15 emb|AW096472|AW096472 EST289652 tomato mixed elicitor, BTI Lycop... 171 5e-42
emb|AW040011|AW040011 EST282502 tomato mixed elicitor, BTI Lycop... 171 5e-42
emb|AW040001|AW040001 EST282492 tomato mixed elicitor, BTI Lycop... 171 5e-42
emb|AW037831|AW037831 EST279460 tomato mixed elicitor, BTI Lycop... 171 5e-42
emb|AI773303|AI773303 EST254403 tomato resistant, Cornell Lycop... 171 5e-42
20 emb|AW094525|AW094525 EST287705 tomato mixed elicitor, BTI Lycop... 171 5e-42
emb|AI776110|AI776110 EST257198 tomato resistant, Cornell Lycop... 171 5e-42
emb|AI775760|AI775760 EST256860 tomato resistant, Cornell Lycop... 171 5e-42
emb|AI780240|AI780240 EST261119 tomato susceptible, Cornell Lyco... 171 5e-42
emb|AI781827|AI781827 EST262706 tomato susceptible, Cornell Lyco... 171 5e-42
25 emb|AI778940|AI778940 EST259819 tomato susceptible, Cornell Lyco... 171 5e-42
emb|AW621673|AW621673 EST312471 tomato root during/after fruit s... 171 5e-42
emb|AW038141|AW038141 EST279798 tomato mixed elicitor, BTI Lycop... 171 5e-42
emb|AW038924|AW038924 EST280880 tomato mixed elicitor, BTI Lycop... 171 5e-42
emb|AW597424|AW597424 si92g01.y1 Gm-c1031 Glycine max cDNA clone... 169 2e-41
30 emb|AW038564|AW038564 EST280247 tomato mixed elicitor, BTI Lycop... 168 2e-41
emb|AW040201|AW040201 EST282700 tomato mixed elicitor, BTI Lycop... 168 2e-41
emb|AW040195|AW040195 EST282694 tomato mixed elicitor, BTI Lycop... 168 2e-41
gb|BE057793|BE057793 sn07c11.y1 Gm-c1016 Glycine max cDNA clone ... 168 2e-41
emb|AW289622|AW289622 NXNV003H05F Nsf Xylem Normal wood Vertical... 164 4e-40
35 emb|AW064893|AW064893 ST37B02 Pine TriplEx shoot tip library Pin... 162 1e-39
emb|AW043214|AW043214 ST30F08 Pine TriplEx shoot tip library Pin... 162 2e-39
emb|AW043171|AW043171 ST30B09 Pine TriplEx shoot tip library Pin... 162 2e-39
emb|AW042699|AW042699 ST23E01 Pine TriplEx shoot tip library Pin... 162 2e-39
emb|AW010199|AW010199 ST03C05 Pine TriplEx shoot tip library Pin... 162 2e-39
40 emb|AF051206|AF051206 Picea mariana probable thioredoxin H (Sb09... 162 2e-39
emb|AW043379|AW043379 ST32F12 Pine TriplEx shoot tip library Pin... 162 2e-39
emb|AW065132|AW065132 ST40A08 Pine TriplEx shoot tip library Pin... 162 2e-39
emb|AW497847|AW497847 PC02B02 Pine TriplEx pollen cone library P... 161 3e-39
emb|AW736931|AW736931 NXNV_081_G02_F Nsf Xylem Normal wood Verti... 161 3e-39
45 emb|AW680784|AW680784 WS1_7_D07.b1_A002 Water-stressed 1 (WS1) S... 161 4e-39
emb|AW680877|AW680877 WS1_7_D07.g1_A002 Water-stressed 1 (WS1) S... 161 4e-39
emb|AW011327|AW011327 ST19E02 Pine TriplEx shoot tip library Pin... 160 5e-39
emb|AW011046|AW011046 ST16A08 Pine TriplEx shoot tip library Pin... 160 7e-39
emb|AI736736|AI736736 sb32g12.y1 Gm-c1012 Glycine max cDNA clone... 93 1e-38
50 emb|AW010836|AW010836 ST14F05 Pine TriplEx shoot tip library Pin... 159 1e-38
emb|AW290231|AW290231 NXNV015E05F Nsf Xylem Normal wood Vertical... 159 2e-38
emb|AW011498|AW011498 ST21E10 Pine TriplEx shoot tip library Pin... 158 3e-38
emb|AA740038|AA740038 803 PtIFG2 Pinus taeda cDNA clone 9266M 3'... 157 5e-38
emb|AW009991|AW009991 ST01A09 Pine TriplEx shoot tip library Pin... 157 5e-38
55 emb|AW684766|AW684766 NF021G12NR1F1000 Nodulated root Medicago t... 124 1e-37
emb|AW706540|AW706540 sj57g11.y1 Gm-c1033 Glycine max cDNA clone... 156 1e-37
emb|AI461254|AI461254 sa60f10.y1 Gm-c1004 Glycine max cDNA clone... 155 2e-37
emb|AW924415|AW924415 WS1_69_D02.b1_A002 Water-stressed 1 (WS1) ... 154 4e-37
emb|AW679524|AW679524 WS1_29_F05.g1_A002 Water-stressed 1 (WS1) ... 154 4e-37
60 emb|AW681036|AW681036 WS1_8_D05.b1_A002 Water-stressed 1 (WS1) S... 154 4e-37
emb|AW754729|AW754729 PC07B04 Pine TriplEx pollen cone library P... 154 4e-37

emb|AW923038|AW923038 DG1_48_B02.g1_A002 Dark Grown 1 (DG1) Sorg... 154 4e-37

5 Query= ATTS0190_i_at 13198_i_at /id_source genbank /description
emb|caa16892.1| (al021749) 12s cruciferin seed storage protein
[arabidopsis thaliana] /blast_score 1.00e-46 /ec_number /family
/chip nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|atts0190| /ncgi
10 http://www.ncgr.org/cgi-bin/ff?atts0190
(433 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

15 Searching.....done

	Score	E	
			(bits) Value
20	Sequences producing significant alignments:		
	emb X62120 BNCRU1 B.napus cru1 gene for cruciferin subunit.	169	4e-48
	gb J05233 BNACRUCA B.napus cruciferin mRNA, 3' end.	169	9e-48
	emb X59808 RSCRUG R.sativus pgCruRsE5 gene for cruciferin.	168	4e-43
	emb X59802 RSCRUI R.sativus pAF7 mRNA for cruciferin.	165	1e-42
25	emb X59804 RSCRUI R.sativus pAC2 mRNA for cruciferin.	123	1e-41
	emb X57850 BNCRU4RN B.napus cru4 mRNA for cruciferin cru4 subunit.	138	2e-32
	emb X57848 BNCRU4RNA B.napus cru4 mRNA for cruciferin cru4 subunit.	137	6e-32
	gb M16860 BNACRUC Rapeseed cruciferin mRNA, complete cds.	132	1e-30
	emb X59294 BNC1G B.napus BnC1 gene for cruciferin storage protein.	132	1e-30
30	emb X14555 BNCRUA Brassica napus cruA gene for cruciferin.	132	1e-30
	emb X57849 BNCRU23 B.napus cru2/3 mRNA for cruciferin cru2/3 sub...	132	1e-30
	emb X59807 RSCRUI R.sativus pAE10 mRNA for cruciferin.	131	3e-30
	emb X59806 RSCRUI R.sativus pBB6 mRNA for cruciferin.	131	3e-30
	emb X59295 BNC2G B.napus BnC2 gene for cruciferin storage protein.	130	5e-30
35	emb X82121 AHGLOBLN A.hypochondriacus mRNA for globulin.	118	3e-26
	gb U38914 CSU38914 Citrus sinensis seed storage protein citrin m...	108	3e-23
	emb X59803 RSCRUI R.sativus pAG4 mRNA for cruciferin.	81	3e-22
	emb AF262998 AF262998 Ricinus communis legumin-like protein mRNA...	104	4e-22
	gb T14851 T14851 crs298 lambdaZAPST Ricinus communis cDNA clone ...	99	2e-20
40	emb X82464 MSLEGA2 M.salicifolia mRNA for legumin precursor (A2).	99	2e-20
	emb X78119 PABTPRU1 P.amygdalus, Batsch (Texas) prul mRNA.	99	2e-20
	gb T23274 T23274 crs1128 lambdaZAPST Ricinus communis cDNA clone...	98	3e-20
	emb AF262999 AF262999 Ricinus communis seed storage protein mRNA...	98	3e-20
	gb T15203 T15203 crs691 lambdaZAPST Ricinus communis cDNA clone ...	98	3e-20
45	gb T14921 T14921 crs404 lambdaZAPST Ricinus communis cDNA clone ...	98	3e-20
	gb T15096 T15096 crs739 lambdaZAPST Ricinus communis cDNA clone ...	98	4e-20
	emb X78120 PABTPRU2 P.amygdalus, Batsch (Texas) pru2 mRNA.	97	6e-20
	emb X82463 MSLEGA11 M.salicifolia mRNA for legumin precursor (A1...	97	8e-20
	gb T15159 T15159 crs641 lambdaZAPST Ricinus communis cDNA clone ...	95	4e-19
50	gb U64443 CAU64443 Coffea arabica 11S storage globulin mRNA, com...	94	5e-19
	gb T24329 T24329 crs1443 lambdaZAPST Ricinus communis cDNA clone...	93	1e-18
	gb U43727 GHU43727 Gossypium hirsutum legumin B (LegB-C134) gene...	92	2e-18
	gb M16936 COTSPB G.hirsutum (cotton) storage protein (beta-globu...	92	2e-18
	emb AF054895 AF054895 Coffea arabica 11S storage globulin mRNA, ...	92	2e-18
55	emb Y16976 CAR16976 Coffea arabica mRNA for 11S storage protein.	92	3e-18
	gb M28832 HNNHAG3D1S Sunflower 11S storage protein (G3-D1) DNA, ...	91	4e-18
	emb AW036288 AW036288 EST278367 tomato seed, TAMU Lycopersicon e...	90	7e-18
	gb T24192 T24192 crs605 lambdaZAPST Ricinus communis cDNA clone ...	90	9e-18
	gb M36407 CUC11SGB Pumpkin 11-S globulin beta-subunit mRNA, comp...	89	2e-17
60	emb Y09116 SSPPLEGUM S.sagittifolia mRNA for pre-pro-legumin.	89	2e-17
	emb X82465 MSLEGB14 M.salicifolia mRNA for legumin precursor (B14).	89	2e-17

- emb|AW395643|AW395643 sg73e07.y1 Gm-c1007 Glycine max cDNA clone... 88 4e-17
 emb|X74740|ASGLAV1G A.sativa GLAV 1 gene for 11S globulin. 88 4e-17
 dbj|D87982|D87982 Fagopyrum esculentum mRNA for legumin-like pro... 88 4e-17
 emb|AF216801|AF216801 Fagopyrum esculentum allergenic protein ge... 87 6e-17
 5 emb|AF152003|AF152003 Fagopyrum esculentum major allergenic stor... 87 6e-17
 emb|AW036551|AW036551 EST283050 tomato seed, TAMU Lycopersicon e... 87 6e-17
 gb|T24206|T24206 crs620 lambdaZAPST Ricinus communis cDNA clone ... 87 6e-17
 gb|T24336|T24336 crs1452 lambdaZAPST Ricinus communis cDNA clone... 87 8e-17
 dbj|D87980|D87980 Fagopyrum esculentum mRNA for legumin-like pro... 86 1e-16
 10 emb|X68648|AS12S A.sativa pseudogene for 12S seed globulin. 86 1e-16
 gb|M69188|COTDGALA Cotton legumin A D-genome alloallele gene, co... 86 1e-16
 gb|M16905|COTSPD G.hirsutum (cotton) storage protein (beta-globu... 86 1e-16
 emb|X74741|ASGLAV3G A.sativa GLAV 3 gene for 11S globulin. 86 1e-16
 emb|AF091842|AF091842 Sesamum indicum strain Tainan 1 11S globul... 86 2e-16
 15 gb|J05485|ASTSSP12S A.sativa 12S globulin seed storage protein g... 85 2e-16
 emb|X17637|AS12SSP Oat gene for 12S seed storage protein. 85 2e-16
 gb|T24158|T24158 crs141 lambdaZAPST Ricinus communis cDNA clone ... 85 3e-16
 emb|X15121|GMGY1 Soybean Gyl gene for glycinin subunit G1. 84 4e-16
 emb|AI941002|AI941002 sb83b02.y1 Gm-c1010 Glycine max cDNA clone... 84 4e-16
 20 gb|M36686|SOYGLYBSU Soybean glycinin A-1a-B-x subunit mRNA, comp... 84 4e-16
 emb|AW318204|AW318204 sg62d03.y1 Gm-c1007 Glycine max cDNA clone... 84 4e-16
 emb|AW397452|AW397452 sg79a12.y1 Gm-c1007 Glycine max cDNA clone... 84 4e-16
 gb|T14825|T14825 crs267 lambdaZAPST Ricinus communis cDNA clone ... 84 4e-16
 emb|AW433058|AW433058 si04a05.y1 Gm-c1029 Glycine max cDNA clone... 84 4e-16
 25 emb|AI748751|AI748751 sb61e06.y1 Gm-c1010 Glycine max cDNA clone... 84 4e-16
 emb|X02985|GMGLY1A Soybean mRNA for glycinin A1aBx precursor. 84 4e-16
 emb|AW317751|AW317751 sg56g11.y1 Gm-c1007 Glycine max cDNA clone... 84 4e-16
 emb|AW317991|AW317991 sg59g07.y1 Gm-c1007 Glycine max cDNA clone... 84 4e-16
 emb|AI735878|AI735878 sb20a12.y1 Gm-c1007 Glycine max cDNA clone... 84 4e-16
 30 emb|AW397311|AW397311 sg77c11.y1 Gm-c1007 Glycine max cDNA clone... 84 4e-16
 emb|AW318315|AW318315 sg63f06.y1 Gm-c1007 Glycine max cDNA clone... 84 4e-16
 emb|X95509|AELEG18GN A.europaeum mRNA for legumin. 84 6e-16
 dbj|E08573|E08573 cDNA encoding 12S globulin A2B of oats. 84 6e-16
 emb|X76738|AS12SGLOB A.sativa (L) mRNA for 12S globulin (1685 bp). 84 6e-16
 35 emb|AW397302|AW397302 sg77c02.y1 Gm-c1007 Glycine max cDNA clone... 84 6e-16
 emb|Y09117|SSPPLTAND S.sagittifolia mRNA for pre-pro-legumin and... 84 8e-16
 emb|AI941031|AI941031 sb83e04.y1 Gm-c1010 Glycine max cDNA clone... 83 1e-15
 emb|AI748075|AI748075 sb47h08.y1 Gm-c1011 Glycine max cDNA clone... 83 1e-15
 emb|AW036363|AW036363 EST278488 tomato seed, TAMU Lycopersicon e... 83 1e-15
 40 emb|AI777374|AI777374 EST263782 tomato seed, TAMU Lycopersicon e... 83 1e-15
 emb|AW036221|AW036221 EST278219 tomato seed, TAMU Lycopersicon e... 83 1e-15
 emb|AW036121|AW036121 EST274497 tomato seed, TAMU Lycopersicon e... 83 1e-15
 emb|AW036283|AW036283 EST278362 tomato seed, TAMU Lycopersicon e... 83 1e-15
 emb|AF261691|AF261691 Elaeis guineensis glutelin mRNA, complete ... 82 2e-15
 45 emb|AW397866|AW397866 sg69c05.y1 Gm-c1007 Glycine max cDNA clone... 82 3e-15
 gb|T24371|T24371 crs1501 lambdaZAPST Ricinus communis cDNA clone... 82 3e-15
 gb|T24377|T24377 crs1511 lambdaZAPST Ricinus communis cDNA clone... 82 3e-15
 gb|T24370|T24370 crs1500 lambdaZAPST Ricinus communis cDNA clone... 82 3e-15
 emb|X15123|GMGY3 Soybean Gy3 gene for glycinin subunit G3. 81 4e-15
 50 emb|AI748727|AI748727 sb61b06.y1 Gm-c1010 Glycine max cDNA clone... 81 4e-15
 emb|AF193433|AF193433 Elaeis guineensis glutelin (PKT9) mRNA, co... 81 4e-15
 emb|X76737|AS12SGL1 A.sativa (L) mRNA for 12S globulin (1556 bp). 81 5e-15
 gb|M21405|ASTSPGLBA Oat seed storage globulin mRNA, complete cds. 81 5e-15
 gb|T23264|T23264 crs1114 lambdaZAPST Ricinus communis cDNA clone... 81 5e-15
 55 gb|M16868|ASTGLOB Oat storage protein 12S globulin mRNA, partial... 81 5e-15
 emb|AW397079|AW397079 sg66g02.y1 Gm-c1007 Glycine max cDNA clone... 81 5e-15
 emb|AF180392|AF180392 Perilla frutescens legumin-like protein mR... 80 7e-15
 emb|AI941048|AI941048 sb83f11.y1 Gm-c1010 Glycine max cDNA clone... 80 7e-15
 gb|T14967|T14967 crs454 lambdaZAPST Ricinus communis cDNA clone ... 80 7e-15
 60

Query= cafferoylCoAmethyltrans_s_at 13215_s_at /id_source genbank
 /description gb|aafl6576.1|ac012563_29 (ac012563) putative
 s-adenosyl-l-methionine:trans-caffeoyl-coenzyme a
 3-o-methyltransferase [arabidopsis thaliana] /blast_score 1.00e-121
 5 /ec_number /family /chip nova /gb_link /ncgi
 (965 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

10 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

15 emb|AB000408|AB000408 Populus kitakamiensis mRNA for caffeoyl-Co... 215 3e-73
 gb|U20736|MSU20736 Medicago sativa S-adenosyl-L-methionine:trans... 142 2e-68
 emb|AW624860|AW624860 EST313689 tomato radicle, 5 d post-imbibit... 139 2e-67
 emb|AF022775|AF022775 Nicotiana tabacum caffeoyl-CoA 3-O-methyltr... 138 2e-67
 20 emb|Z54233|VVCCOAOMT V.vinifera mRNA for caffeoyl-CoA O-methyltr... 136 9e-67
 gb|M69184|PUMCCOAMT Petroselinum crispum caffeoyl-CoA 3-O-methyl... 133 2e-66
 gb|U27116|PTU27116 Populus tremuloides caffeoyl-CoA 3-O-methyltr... 135 3e-66
 emb|AJ224894|PBT AJ4894 Populus balsamifera subsp. trichocarpa mR... 135 3e-66
 gb|U13151|ZEU13151 Zinnia elegans S-adenosyl-L-methionine:trans-... 136 4e-66
 25 emb|AI489305|AI489305 EST247644 tomato ovary, TAMU Lycopersicon ... 139 4e-66
 emb|AJ224895|PBT AJ4895 Populus balsamifera subsp. trichocarpa mR... 136 6e-66
 emb|AJ224896|PBT AJ4896 Populus balsamifera subsp. trichocarpa mR... 136 6e-66
 emb|AF168780|AF168780 Eucalyptus globulus caffeoyl-CoA O-methyltr... 133 8e-66
 emb|AF053553|AF053553 Mesembryanthemum crystallinum caffeoyl-CoA... 132 1e-65
 30 emb|AF240466|AF240466 Populus tomentosa caffeoyl-CoA O-methyltra... 135 1e-65
 emb|A22706|A22706 Caffeoyl-CoA-3-O-Methyltransferase gene. 129 3e-65
 gb|U62734|NTU62734 Nicotiana tabacum caffeoyl-CoA O-methyltransf... 134 5e-65
 emb|Z56282|NTCCOAOMT N.tabacum mRNA for caffeoyl-CoA O-methyltra... 132 5e-65
 gb|U62736|NTU62736 Nicotiana tabacum caffeoyl-CoA O-methyltransf... 136 5e-65
 35 gb|U38612|NTU38612 Nicotiana tabacum caffeoyl-coenzymeA O-methyl... 136 5e-65
 emb|Y12228|EG12228 E.gunnii mRNA for caffeoyl-CoA O-methyltransf... 133 7e-65
 gb|L22203|SLASADEN Stellaria longipes S-adenosyl-L-methionine:tr... 124 8e-65
 emb|AF046122|AF046122 Eucalyptus globulus caffeoyl-CoA 3-O-methy... 133 9e-65
 gb|U62735|NTU62735 Nicotiana tabacum caffeoyl-CoA O-methyltransf... 134 3e-64
 40 emb|AF036095|AF036095 Pinus taeda caffeoyl-CoA O-methyltransfera... 130 6e-64
 emb|AF060180|AF060180 Nicotiana tabacum caffeoyl-coenzyme A trun... 90 9e-60
 emb|AW102353|AW102353 sd86f04.y1 Gm-c1009 Glycine max cDNA clone... 139 5e-58
 emb|AJ130841|PBA130841 Populus balsamifera subsp. trichocarpa mR... 133 2e-57
 emb|AJ001447|FVAJ1447 Fragaria vesca mRNA for putative caffeoyl-... 137 3e-57
 45 gb|BE124003|BE124003 EST394128 DSIL Medicago truncatula cDNA clo... 127 9e-57
 emb|AW775400|AW775400 EST334465 DSIL Medicago truncatula cDNA cl... 142 2e-56
 emb|AW030189|AW030189 EST273444 tomato callus, TAMU Lycopersicon... 133 4e-56
 emb|AW695080|AW695080 NF091D11ST1F1093 Developing stem Medicago ... 142 6e-56
 emb|AW348485|AW348485 GM210002B12A10R Gm-r1021 Glycine max cDNA ... 131 2e-55
 50 emb|AI486500|AI486500 EST244821 tomato ovary, TAMU Lycopersicon ... 139 2e-55
 emb|AI166541|AI166541 xylem.est.363 Poplar xylem Lambda ZAPII li... 135 7e-55
 gb|BE034896|BE034896 ML05H01 ML Mesembryanthemum crystallinum cD... 132 1e-54
 emb|AW306951|AW306951 sf50h03.y1 Gm-c1009 Glycine max cDNA clone... 133 2e-54
 55 emb|AW278810|AW278810 sf98g06.y1 Gm-c1019 Glycine max cDNA clone... 135 3e-54
 emb|AI939180|AI939180 sc67h02.y1 Gm-c1016 Glycine max cDNA clone... 125 3e-54
 emb|AW102461|AW102461 sd88d11.y1 Gm-c1009 Glycine max cDNA clone... 133 3e-54
 emb|AW776700|AW776700 EST335765 DSIL Medicago truncatula cDNA cl... 127 4e-54
 emb|AW757356|AW757356 sl32c10.y1 Gm-c1027 Glycine max cDNA clone... 133 2e-53
 60 emb|AW030736|AW030736 EST273991 tomato callus, TAMU Lycopersicon... 133 8e-53
 emb|AI898029|AI898029 EST267472 tomato ovary, TAMU Lycopersicon ... 133 8e-53

- emb|AW625527|AW625527 EST319434 tomato radicle, 5 d post-imbibit... 133 8e-53
 emb|AW218547|AW218547 EST303730 tomato radicle, 5 d post-imbibit... 133 8e-53
 emb|AW733300|AW733300 sk71f10.y1 Gm-c1016 Glycine max cDNA clone... 134 1e-52
 emb|AW442463|AW442463 EST307393 tomato mixed elicitor, BTI Lycop... 133 1e-52
 5 emb|AW094365|AW094365 EST287545 tomato mixed elicitor, BTI Lycop... 133 1e-52
 gb|BE021597|BE021597 sm60a04.y1 Gm-c1028 Glycine max cDNA clone ... 135 1e-52
 emb|AW034347|AW034347 EST277918 tomato callus, TAMU Lycopersicon... 133 2e-52
 emb|AI443130|AI443130 sa84g01.y1 Gm-c1004 Glycine max cDNA clone... 131 2e-51
 emb|AI898952|AI898952 EST268395 tomato ovary, TAMU Lycopersicon ... 139 2e-51
 10 emb|AW424002|AW424002 sh59c10.y1 Gm-c1015 Glycine max cDNA clone... 115 2e-51
 emb|AW707192|AW707192 sk22a02.y1 Gm-c1028 Glycine max cDNA clone... 132 3e-50
 emb|AI899227|AI899227 EST268670 tomato ovary, TAMU Lycopersicon ... 139 3e-50
 emb|AW980337|AW980337 EST391490 GVN Medicago truncatula cDNA clo... 127 3e-50
 emb|AW648499|AW648499 EST326953 tomato germinating seedlings, TA... 99 7e-50
 15 emb|AW690185|AW690185 NF029D09ST1F1000 Developing stem Medicago ... 142 1e-49
 emb|AI895091|AI895091 EST264534 tomato callus, TAMU Lycopersicon... 99 3e-49
 emb|AW306980|AW306980 sf51c05.y1 Gm-c1009 Glycine max cDNA clone... 135 8e-48
 emb|AW695176|AW695176 NF092D12ST1F1101 Developing stem Medicago ... 142 1e-47
 emb|AW684885|AW684885 NF022F07NR1F1000 Nodulated root Medicago t... 142 2e-47
 20 emb|AA660318|AA660318 00189 MtRHE Medicago truncatula cDNA 5' si... 144 2e-47
 emb|AW703717|AW703717 sk23e07.y1 Gm-c1028 Glycine max cDNA clone... 132 4e-47
 emb|AW776435|AW776435 EST335500 DSIL Medicago truncatula cDNA cl... 142 5e-47
 emb|AI486948|AI486948 EST245270 tomato ovary, TAMU Lycopersicon ... 100 1e-46
 emb|AW620537|AW620537 sj06d09.y1 Gm-c1032 Glycine max cDNA clone... 133 1e-46
 25 emb|AI775483|AI775483 EST256583 tomato resistant, Cornell Lycop... 139 2e-46
 gb|BE124333|BE124333 EST393368 GVN Medicago truncatula cDNA clon... 125 3e-46
 emb|AW704578|AW704578 sk38h08.y1 Gm-c1028 Glycine max cDNA clone... 140 3e-46
 emb|AW350997|AW350997 GM210010A10C11R Gm-r1021 Glycine max cDNA ... 97 6e-46
 emb|AW707224|AW707224 sk22c12.y1 Gm-c1028 Glycine max cDNA clone... 140 9e-46
 30 emb|AW625126|AW625126 EST313943 tomato radicle, 5 d post-imbibit... 133 6e-45
 emb|AI974778|AI974778 T113251e KV2 Medicago truncatula cDNA clon... 142 6e-45
 emb|AI898101|AI898101 EST267544 tomato ovary, TAMU Lycopersicon ... 98 8e-45
 gb|BE124175|BE124175 EST394300 DSIL Medicago truncatula cDNA clo... 127 1e-44
 emb|AW686370|AW686370 NF040G10NR1F1000 Nodulated root Medicago t... 127 4e-44
 35 emb|AI166314|AI166314 xylem.est.159 Poplar xylem Lambda ZAPII li... 136 4e-44
 emb|AW256836|AW256836 EST304973 KV2 Medicago truncatula cDNA clo... 144 5e-44
 emb|AW559274|AW559274 EST306110 DSIR Medicago truncatula cDNA cl... 142 5e-44
 emb|AW278618|AW278618 sf46h04.y1 Gm-c1009 Glycine max cDNA clone... 139 1e-43
 gb|BE059325|BE059325 sn31c09.y1 Gm-c1016 Glycine max cDNA clone ... 140 3e-43
 40 emb|AW831448|AW831448 sm23c03.y1 Gm-c1028 Glycine max cDNA clone... 140 6e-43
 emb|AI938893|AI938893 sc62d08.y1 Gm-c1016 Glycine max cDNA clone... 134 2e-42
 emb|AW257069|AW257069 EST305206 KV2 Medicago truncatula cDNA clo... 142 2e-42
 emb|AW695899|AW695899 NF100E02ST1F1017 Developing stem Medicago ... 125 5e-42
 emb|AW774697|AW774697 EST333848 KV3 Medicago truncatula cDNA clo... 84 8e-42
 45 emb|AW683492|AW683492 NF012H09LF1F1079 Developing leaf Medicago ... 134 2e-41
 emb|AW152892|AW152892 se32d04.y1 Gm-c1015 Glycine max cDNA clone... 82 2e-41
 gb|BE125749|BE125749 DG1_55_H11.b1_A002 Dark Grown 1 (DG1) Sorgh... 127 2e-41
 gb|BE022002|BE022002 sm65c10.y1 Gm-c1028 Glycine max cDNA clone ... 137 3e-41
 emb|AI488060|AI488060 EST246382 tomato ovary, TAMU Lycopersicon ... 100 7e-41
 50 emb|AW622558|AW622558 EST313358 tomato root during/after fruit s... 139 1e-40
 emb|AW625461|AW625461 EST319368 tomato radicle, 5 d post-imbibit... 99 1e-40
 emb|AW625476|AW625476 EST319383 tomato radicle, 5 d post-imbibit... 139 3e-40
 emb|AI960196|AI960196 sc80a08.y1 Gm-c1018 Glycine max cDNA clone... 132 5e-40
 emb|Z82982|NTZ82982 N.tabacum mRNA for caffeoyl-CoA O-methyltran... 136 1e-39
 55 emb|AW218486|AW218486 EST303669 tomato radicle, 5 d post-imbibit... 136 1e-39

Query= calmodulinlike_s_at 13217_s_at /id_source genbank /description
 emb|cab42906.1|(al049862) calmodulin-like protein [arabidopsis
 60 thaliana] /blast_score 6.00e-99 /ec_number /family /chip nova
 /gb_link /ncgi

(827 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5

Searching.....done

	Score	E		(bits)	Value
10	Sequences producing significant alignments:				
	emb AI489346 AI489346	EST247685	tomato ovary, TAMU Lycopersicon ...	79	2e-28
	emb AW350323 AW350323	GM210007B20E12R	Gm-r1021 Glycine max cDNA ...	80	2e-27
	emb AW509006 AW509006	si38h07.y1	Gm-r1030 Glycine max cDNA clone...	79	2e-26
	emb AW685404 AW685404	NF028H10NR1F1000	Nodulated root Medicago t...	74	2e-24
15	emb AW781320 AW781320	sk68d07.y1	Gm-c1016 Glycine max cDNA clone...	86	2e-24
	emb AI897832 AI897832	EST267275	tomato ovary, TAMU Lycopersicon ...	78	1e-23
	emb AW102460 AW102460	sd88d10.y1	Gm-c1009 Glycine max cDNA clone...	70	2e-22
	emb AI490284 AI490284	EST248610	tomato ovary, TAMU Lycopersicon ...	103	2e-22
	emb AI487362 AI487362	EST245684	tomato ovary, TAMU Lycopersicon ...	72	3e-20
20	gb BE125690 BE125690	DG1_54_A02.g1_A002	Dark Grown 1 (DG1) Sorgh...	96	3e-19
	emb X80231 LTCAMA	L.tarentolae CAM A gene	for calmodulin.	73	1e-18
	emb AL115248 CNS01C9K	Botrytis cinerea strain T4	cDNA library un...	65	4e-18
	dbj D10521 TETCALW	T.pyriformis mRNA	for calmodulin.	73	7e-18
	gb M76407 SLECALMODU	Stylonychia lemnae	calmodulin gene, complet...	74	9e-18
25	emb AF007889 AF007889	Symbiodinium microadriaticum	calmodulin (S...	74	1e-17
	emb AF078679 AF078679	Olea europaea	calcium-binding protein (PCA...	57	2e-17
	emb X56511 TBCALUBG	T. brucei	genes for calmodulin, EFH5 and ubi...	77	2e-17
	emb X52096 TCCALB2	Trypanosoma cruzi	CaA2 calmodulin gene.	77	2e-17
	emb AF030033 AF030033	Phaseolus vulgaris	calmodulin (CaM) mRNA, ...	75	2e-17
30	emb X90560 PPCAMPROT	Physcomitrella patens	mRNA for calmodulin.	71	2e-17
	gb U91642 POU91642	Pleurotus ostreatus	calmodulin mRNA, complete...	75	2e-17
	emb AF078680 AF078680	Olea europaea	calcium-binding protein (PCA...	57	2e-17
	emb X85091 MPCAM	M.pyriferi	mRNA for calmodulin.	74	2e-17
	gb M83535 PHTCALPIA	P.infestans	calmodulin (calA) gene, complete...	75	2e-17
35	emb Y08373 TGCM	T.gondii	mRNA for calmodulin.	74	2e-17
	gb C96396 C96396	C96396	Marchantia polymorpha immature sex organ...	73	3e-17
	emb AL113315 CNS01ARV	Botrytis cinerea strain T4	cDNA library un...	72	3e-17
	emb AB044286 AB044286	Chara corallina	ccam mRNA for calmodulin, ...	75	4e-17
	emb AB041712 AB041712	Chara corallina	cccam2 mRNA for calmodulin...	75	4e-17
40	emb AB041711 AB041711	Chara corallina	cccam1 mRNA for calmodulin...	75	4e-17
	gb J05116 ACKCAL	A.klebsiana	calmodulin gene, complete cds.	75	4e-17
	emb X70923 NCCALMOE	N.crassa	mRNA for calmodulin.	74	6e-17
	emb AI328739 AI328739	a6d02ne.fl	Neurospora crassa evening cDNA ...	74	6e-17
	emb AF034964 AF034964	Glomerella cingulata	calmodulin (cam) mRNA...	74	6e-17
45	gb U12505 HCCMD	Histoplasma capsulatum	186AS calmodulin mRNA; co...	74	8e-17
	gb M34540 PARCAM	P.tetraurelia	calmodulin gene, complete cds.	74	8e-17
	gb S68025 S68025	CAM=calmodulin [Paramecium	tetraurelia, Genomic...	74	8e-17
	emb AW164773 AW164773	se77e12.y1	Gm-c1023 Glycine max cDNA clone...	64	8e-17
	emb AW719875 AW719875	LjNEST11d4r	Lotus japonicus nodule library...	57	8e-17
50	emb AW830090 AW830090	sm22a12.y1	Gm-c1028 Glycine max cDNA clone...	64	8e-17
	emb AW126204 AW126204	N100049e	rootphos(-) Medicago truncatula c...	57	8e-17
	emb X52242 TTCALM	T.thermophila	mRNA for calmodulin.	73	1e-16
	gb L02963 NEUCLMDLN	Neurospora crassa	calmodulin mRNA, complete ...	74	1e-16
	emb AW625406 AW625406	EST319229	tomato radicle, 5 d post-imbibit...	62	1e-16
55	gb K02944 TRBCMRSG	Trypanosoma brucei	gambiense calmodulin genes...	73	2e-16
	gb M88307 BNACALM	Brassica juncea	calmodulin mRNA, complete cds.	73	2e-16
	gb U10150 BNU10150	Brassica napus	Naehan calmodulin (bcm1) mRNA,...	73	2e-16
	emb X89890 BPCALMGEN	B.pilosa	mRNA for calmodulin.	73	2e-16
	emb AW099396 AW099396	sd39h01.y1	Gm-c1016 Glycine max cDNA clone...	76	2e-16
60	emb AW101324 AW101324	sd77e09.y1	Gm-c1009 Glycine max cDNA clone...	59	2e-16
	emb AL112713 CNS01AB5	Botrytis cinerea strain T4	cDNA library un...	73	2e-16

emb|AL114582|CNS01BR2 Botrytis cinerea strain T4 cDNA library un... 74 2e-16
 emb|AL112170|CNS019W2 Botrytis cinerea strain T4 cDNA library un... 74 2e-16
 emb|AL114124|CNS01BEC Botrytis cinerea strain T4 cDNA library un... 74 2e-16
 emb|AL115056|CNS01C48 Botrytis cinerea strain T4 cDNA library un... 73 2e-16
 5 emb|AL116760|CNS01DFK Botrytis cinerea strain T4 cDNA library un... 73 2e-16
 emb|AW573768|AW573768 EST316359 GVN Medicago truncatula cDNA clo... 72 2e-16
 emb|Y13784|MSCALMODU Mougeotia scalaris mRNA for calmodulin. 70 3e-16
 emb|AI727960|AI727960 BNLGH19833 Six-day Cotton fiber Gossypium ... 73 3e-16
 emb|AA660367|AA660367 00239 MtRHE Medicago truncatula cDNA 5' si... 71 3e-16
 10 emb|AW164628|AW164628 se74e01.y1 Gm-cl023 Glycine max cDNA clone... 60 3e-16
 emb|AF150059|AF150059 Brassica napus calmodulin (CaM1) mRNA, com... 72 3e-16
 emb|AW738989|AW738989 gb23c06.y1 Moss EST library PPN Physcomitr... 73 3e-16
 gb|U48693|TAU48693 Triticum aestivum calmodulin TaCaM3-1 mRNA, c... 73 4e-16
 gb|M27303|BLYCAMA Barley cam gene encoding calmodulin, complete ... 73 4e-16
 15 gb|BE033450|BE033450 ME02B08 ME Mesembryanthemum crystallinum cD... 73 4e-16
 emb|AF064552|AF064552 Apium graveolens calmodulin mRNA, complete... 73 4e-16
 gb|S81594|S81594 auxin-regulated calmodulin [Vigna radiata=mung ... 73 4e-16
 gb|L20691|VIRCALMOD Vigna radiata calmodulin mRNA, complete cds. 73 4e-16
 emb|AW730911|AW730911 GA__Ea0029I11 Gossypium arboreum 7-10 dpa ... 73 4e-16
 20 gb|BE036340|BE036340 MO23E04 MO Mesembryanthemum crystallinum cD... 73 4e-16
 emb|AF030032|AF030032 Phaseolus vulgaris calmodulin (CaM) mRNA, ... 73 4e-16
 gb|L01431|SOYSCAM2X Soybean calmodulin (SCaM-2) mRNA, complete cds. 73 4e-16
 emb|Y09853|CACAM Cicer arietinum mRNA for CaM protein. 73 4e-16
 gb|L01432|SOYSCAM3X Soybean calmodulin (SCaM-3) mRNA, complete cds. 73 4e-16
 25 gb|U49104|TAU49104 Triticum aestivum calmodulin TaCaM3-3 mRNA, c... 73 4e-16
 gb|U49105|TAU49105 Triticum aestivum calmodulin TaCaM4-1 mRNA, c... 73 4e-16
 emb|AF030034|AF030034 Phaseolus vulgaris calmodulin (CaM) mRNA, ... 73 4e-16
 emb|AW728030|AW728030 GA__Ea0029H21 Gossypium arboreum 7-10 dpa ... 73 4e-16
 gb|L20507|VIRCALMODU Vigna radiata (clone pMBCaM-1) calmodulin m... 73 4e-16
 30 gb|U48242|TAU48242 Triticum aestivum calmodulin TaCaM1-1 mRNA, c... 73 4e-16
 gb|M80836|PETCAM81 Petunia hybrida CAM81 mRNA,. 73 4e-16
 gb|U49103|TAU49103 Triticum aestivum calmodulin TaCaM3-2 mRNA, c... 73 4e-16
 emb|X52398|MSCAL1 Alfalfa call mRNA for calmodulin. 73 4e-16
 gb|U48688|TAU48688 Triticum aestivum calmodulin TaCaM1-2 mRNA, c... 73 4e-16
 35 gb|L01430|SOYSCAM1X Soybean calmodulin (SCaM-1) mRNA, complete cds. 73 4e-16
 emb|AW927068|AW927068 HVSMEg0009G21 Hordeum vulgare pre-anthesis... 73 4e-16
 gb|U48689|TAU48689 Triticum aestivum calmodulin TaCaM1-3 mRNA, c... 73 4e-16
 gb|M80831|PETCALPRO Petunia hybrida CAM53 mRNA, complete cds. 73 4e-16
 emb|AW348582|AW348582 GM210002B22C3R Gm-r1021 Glycine max cDNA 3... 73 4e-16
 40 emb|X59751|DCCAM1G Carrot Ccam-1 gene for calmodulin. 73 4e-16
 emb|AW775754|AW775754 EST334819 DSIL Medicago truncatula cDNA cl... 73 4e-16
 gb|BE052400|BE052400 GA__Ea0001L24f Gossypium arboreum 7-10 dpa ... 73 4e-16
 emb|AW666735|AW666735 GA__Ea0005N08 Gossypium arboreum 7-10 dpa ... 73 4e-16
 gb|U13882|PSU13882 Pisum sativum Alaska calmodulin mRNA, complet... 73 4e-16
 45 gb|BE051931|BE051931 GA__Ea0002G11f Gossypium arboreum 7-10 dpa ... 73 4e-16
 emb|AW666619|AW666619 GA__Ea0005C16 Gossypium arboreum 7-10 dpa ... 73 4e-16
 emb|AW108833|AW108833 gate0001L24f Gossypium arboreum 7-10 dpa f... 73 4e-16
 emb|Z12839|LLCALMOD L.longiflorum mRNA encoding calmodulin. 73 4e-16
 gb|L18912|LILCALMODU Lilium longiflorum calmodulin mRNA, complet... 73 4e-16
 50 Query= HSF4_s_at 13273_s_at /id_source genbank /description
 gb|aac31756.1| (u68017) heat shock transcription factor 4 [arabidopsis
 thaliana] /blast_score 1.00e-113 /ec_number /family /chip nova
 /gb_link /ncgi
 (1408 letters)
 55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
 Searching.....done
 60

Score E

	Sequences producing significant alignments:	(bits) Value
	emb AB014483 AB014483 <i>Nicotiana tabacum</i> NtHSF1 mRNA for heat sho...	213 2e-62
	emb X55347 LPHSF24 Tomato mRNA for heat stress transcription fac...	210 2e-53
5	emb AI900223 AI900223 sc02f05.y1 <i>Gm-c1012</i> Glycine max cDNA clone...	205 3e-53
	emb Z46953 GMHSF34 <i>G.max</i> mRNA for heat shock transcription facto...	203 6e-53
	emb AV408054 AV408054 AV408054 <i>Lotus japonicus</i> young plants (two...	203 3e-51
	emb AV415115 AV415115 AV415115 <i>Lotus japonicus</i> young plants (two...	197 2e-49
	emb AW774951 AW774951 EST334102 KV3 <i>Medicago truncatula</i> cDNA clo...	194 1e-48
10	emb AW689532 AW689532 NF021G10ST1F1000 Developing stem <i>Medicago</i> ...	194 1e-48
	emb AI728175 AI728175 BNLGHi10028 Six-day Cotton fiber <i>Gossypium</i> ...	192 5e-48
	emb AI055366 AI055366 coau0003M17 Cotton Boll Abscission Zone cD...	191 1e-47
	emb AW703969 AW703969 sk14g08.y1 <i>Gm-c1023</i> Glycine max cDNA clone...	191 1e-47
	emb AW428882 AW428882 Ljimpest25-001-b9 Ljirnp Lambda HybriZap ...	190 2e-47
15	emb AW931781 AW931781 EST357624 tomato fruit mature green, TAMU ...	189 3e-47
	emb AW686121 AW686121 NF033H01NR1F1000 Nodulated root <i>Medicago</i> t...	188 1e-46
	emb Z46956 GMHSF5 <i>G.max</i> mRNA for heat shock transcription factor 5.	185 6e-46
	emb AW109013 AW109013 gate0002O16f <i>Gossypium arboreum</i> 7-10 dpa f...	179 4e-44
	gb BE054274 BE054274 GA__Ea0002O16f <i>Gossypium arboreum</i> 7-10 dpa ...	179 4e-44
20	gb BE020791 BE020791 sm52h09.y1 <i>Gm-c1028</i> Glycine max cDNA clone ...	178 1e-43
	emb AW696868 AW696868 NF111F05ST1F1046 Developing stem <i>Medicago</i> ...	166 3e-43
	emb AW686271 AW686271 NF039H06NR1F1000 Nodulated root <i>Medicago</i> t...	171 5e-42
	emb AW931176 AW931176 EST357019 tomato fruit mature green, TAMU ...	168 8e-41
	gb C95479 C95479 C95479 Citrus unshiu Miyagawa-wase maturation s...	166 5e-40
25	emb AW033421 AW033421 EST276992 tomato callus, TAMU <i>Lycopersicon</i> ...	165 1e-39
	emb AW030725 AW030725 EST273980 tomato callus, TAMU <i>Lycopersicon</i> ...	165 1e-39
	emb AW041695 AW041695 EST284559 tomato mixed elicitor, BTI <i>Lycop</i> ...	165 1e-39
	emb AW217982 AW217982 EST296697 tomato flower buds, anthesis, Co...	165 1e-39
	emb X67600 LPHSF8 <i>L.peruvianum</i> Lp-hsf8 mRNA for heat stress tran...	161 1e-38
30	emb AW774397 AW774397 EST333548 KV3 <i>Medicago truncatula</i> cDNA clo...	160 2e-38
	emb AW686582 AW686582 NF042H04NR1F1000 Nodulated root <i>Medicago</i> t...	155 6e-37
	emb AW776460 AW776460 EST335525 DSIL <i>Medicago truncatula</i> cDNA cl...	152 7e-36
	emb AW738023 AW738023 EST339450 tomato flower buds, anthesis, Co...	150 2e-35
	emb AW036683 AW036683 EST278726 tomato fruit mature green, TAMU ...	149 5e-35
35	emb AI729182 AI729182 BNLGHi12855 Six-day Cotton fiber <i>Gossypium</i> ...	149 5e-35
	emb AI489721 AI489721 EST248060 tomato ovary, TAMU <i>Lycopersicon</i> ...	149 5e-35
	emb AW034402 AW034402 EST277973 tomato callus, TAMU <i>Lycopersicon</i> ...	148 7e-35
	emb X67601 LPHSF30 <i>L.peruvianum</i> Lp-hsf30 mRNA for heat stress tr...	148 9e-35
	emb AW906822 AW906822 EST342945 potato stolon, Cornell Universit...	147 2e-34
40	emb AW164509 AW164509 se74f12.y1 <i>Gm-c1023</i> Glycine max cDNA clone...	147 2e-34
	emb AW034874 AW034874 EST279103 tomato callus, TAMU <i>Lycopersicon</i> ...	147 2e-34
	emb AF235958 AF235958 <i>Medicago sativa</i> heat shock transcription f...	145 8e-34
	emb Z46952 GMHSF21 <i>G.max</i> mRNA for heat shock transcription facto...	145 8e-34
	emb AW559623 AW559623 EST314671 DSIR <i>Medicago truncatula</i> cDNA cl...	144 2e-33
45	emb AW222011 AW222011 EST298822 tomato fruit red ripe, TAMU Lyco...	144 2e-33
	emb AW930998 AW930998 EST356841 tomato fruit mature green, TAMU ...	143 4e-33
	emb AW906840 AW906840 EST342963 potato stolon, Cornell Universit...	140 2e-32
	emb AB014484 AB014484 <i>Nicotiana tabacum</i> NtHSF2 mRNA for heat sho...	140 3e-32
	emb AF208544 AF208544 <i>Lycopersicon peruvianum</i> heat stress transc...	139 4e-32
50	emb AW738534 AW738534 EST339961 tomato flower buds, anthesis, Co...	139 5e-32
	emb AI725043 AI725043 942 PtIFG2 <i>Pinus taeda</i> cDNA clone 8824r, m...	139 5e-32
	emb AW874988 AW874988 00109 leafy spurge Lambda HybriZAP 2.1 two...	138 1e-31
	emb AW596493 AW596493 sj13a09.y1 <i>Gm-c1032</i> Glycine max cDNA clone...	138 1e-31
	emb AV415736 AV415736 AV415736 <i>Lotus japonicus</i> young plants (two...	138 1e-31
55	emb AW979619 AW979619 EST341218 tomato root deficiency, Cornell ...	137 2e-31
	emb AW932142 AW932142 EST357985 tomato fruit mature green, TAMU ...	136 3e-31
	emb Z46954 GMHSF33 <i>G.max</i> mRNA for heat shock transcription facto...	135 9e-31
	emb AW569138 AW569138 si63g09.y1 <i>Gm-r1030</i> Glycine max cDNA clone...	134 1e-30
	emb AW569256 AW569256 si64g09.y1 <i>Gm-r1030</i> Glycine max cDNA clone...	134 1e-30
60	emb AW203851 AW203851 sf38h11.y1 <i>Gm-c1028</i> Glycine max cDNA clone...	133 3e-30
	emb AW220758 AW220758 EST297227 tomato fruit mature green, TAMU ...	132 6e-30

- emb|AI728806|AI728806 BNLGHi11701 Six-day Cotton fiber Gossypium... 108 2e-28
 emb|AW736596|AW736596 EST333088 KV3 Medicago truncatula cDNA clo... 103 3e-28
 emb|AI895934|AI895934 EST265377 tomato callus, TAMU Lycopersicon... 123 2e-27
 5 emb|Z46951|GMHSF29 G.max mRNA for heat shock transcription facto... 120 2e-26
 gb|BE019974|BE019974 sm38b12.y1 Gm-c1028 Glycine max cDNA clone ... 119 6e-26
 emb|Z46955|GMHSF31 G.max mRNA for heat shock transcription facto... 115 8e-25
 emb|X67599|LEHSF8 L.esculentum Le-hsf8 gene for heat stress tran... 114 2e-24
 emb|AQ579554|AQ579554 T135016b shotgun sub-library of BAC clone ... 113 4e-24
 emb|AW775388|AW775388 EST334453 DSIL Medicago truncatula cDNA cl... 66 1e-23
 10 emb|AW931892|AW931892 EST357735 tomato fruit mature green, TAMU ... 104 2e-21
 emb|AQ579623|AQ579623 T135087b shotgun sub-library of BAC clone ... 103 4e-21
 emb|AW736595|AW736595 EST333087 KV3 Medicago truncatula cDNA clo... 103 4e-21
 emb|AW697097|AW697097 NF112C08ST1F1065 Developing stem Medicago ... 103 4e-21
 emb|AV420766|AV420766 AV420766 Lotus japonicus young plants (two... 102 8e-21
 15 emb|AV413314|AV413314 AV413314 Lotus japonicus young plants (two... 102 8e-21
 emb|AW693546|AW693546 NF067D12ST1F1101 Developing stem Medicago ... 101 1e-20
 emb|AI895294|AI895294 EST264737 tomato callus, TAMU Lycopersicon... 101 1e-20
 emb|AJ010644|PSA010643 Pisum sativum hsfA gene, exons 1 to 2, pa... 99 7e-20
 emb|AW924303|AW924303 WS1_52_H11.b1_A002 Water-stressed 1 (WS1) ... 99 7e-20
 20 emb|AI895834|AI895834 EST265277 tomato callus, TAMU Lycopersicon... 95 9e-19
 emb|AW756148|AW756148 sl16e07.y1 Gm-c1036 Glycine max cDNA clone... 93 4e-18
 emb|AW132703|AW132703 se09a08.y1 Gm-c1013 Glycine max cDNA clone... 93 6e-18
 gb|M94683|YSPHSF Schizosaccharomyces pombe heat shock transcript... 93 6e-18
 emb|X55149|KLHSFG K. lactis HSF gene for heat shock transcriptio... 76 2e-17
 25 emb|AW933448|AW933448 EST359387 tomato fruit mature green, TAMU ... 89 8e-17
 emb|AI896906|AI896906 EST266349 tomato callus, TAMU Lycopersicon... 89 1e-16
 emb|AZ045432|AZ045432 T234030b shotgun sub-library of BAC clone ... 84 2e-15
 emb|X83031|SCPOS9 S.cerevisiae POS9 gene. 83 5e-15
 gb|U00485|YSCSKN7 Saccharomyces cerevisiae putative transcriptio... 83 5e-15
 30 gb|U00029|YSCH9177 Saccharomyces cerevisiae chromosome VIII cosm... 83 5e-15
 emb|Z69726|SPAC2E12 S.pombe chromosome I cosmid c2E12. 83 6e-15
 gb|M22040|YSCHSF1A S.cerevisiae heat shock transcription factor ... 81 2e-14
 emb|Z72596|SCYGL074C S.cerevisiae chromosome VII reading frame O... 81 2e-14
 gb|J03139|YSCHSF S.cerevisiae heat shock factor gene (HSF), comp... 81 2e-14
 35 emb|AI212342|AI212342 x3c12a1.r1 Aspergillus nidulans 24hr asexu... 73 8e-14
 emb|AW686674|AW686674 NF040F05NR1F1000 Nodulated root Medicago t... 79 8e-14
 emb|AZ048458|AZ048458 PSB119 Barley PstI genomic clones Hordeum ... 78 2e-13
 emb|AW034135|AW034135 EST277706 tomato callus, TAMU Lycopersicon... 57 9e-13
 emb|AW933529|AW933529 EST359288 tomato fruit mature green, TAMU ... 72 1e-11
 40 emb|AW307441|AW307441 sf57a06.y1 Gm-c1009 Glycine max cDNA clone... 70 5e-11
 emb|AW620962|AW620962 sj98b03.y1 Gm-c1023 Glycine max cDNA clone... 70 5e-11

45 Query= hsp176A_i_at13277_i_at /id_source genbank /description
 emb|caa74399.1| (y14070) heat shock protein 17.6a [arabidopsis
 thaliana] /blast_score 2.00e-75 /ec_number /family /chip nova
 /gb_link [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|hsp176a)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|hsp176a](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|hsp176a) /ncgi
<http://www.ncgr.org/cgi-bin/ff?hsp176a>
 50 (613 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

55 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

- 60 gb|M33901|PEAHSP177A Pisum sativum 17.7 kDa heat shock protein (... 126 3e-44
 gb|M99429|PHNSHSPA Ipomoea nil small heat shock protein, complet... 171 4e-42

- emb|X98617|MSSHPI7KD M.sativa mRNA for 17kD heat shock protein. 171 6e-42
emb|AF159562|AF159562 Prunus dulcis cytosolic class II low molec... 105 7e-42
gb|L47740|PIAEMB29R Picea glauca class II cytoplasmic small mole... 169 2e-41
emb|AW569703|AW569703 si79c12.y1 Gm-c1031 Glycine max cDNA clone... 107 6e-41
5 emb|X99346|PASHSP P.abies mRNA for small heat shock protein. 166 1e-40
emb|AW667877|AW667877 GA__Ea0011C02 Gossypium arboreum 7-10 dpa ... 110 2e-40
emb|AW725392|AW725392 GA__Ea0017J18 Gossypium arboreum 7-10 dpa ... 110 2e-40
emb|AW569553|AW569553 si88e08.y1 Gm-c1031 Glycine max cDNA clone... 107 1e-39
emb|AW620261|AW620261 si93g10.y1 Gm-c1031 Glycine max cDNA clone... 107 1e-39
10 gb|BE053976|BE053976 GA__Ea0002N06f Gossypium arboreum 7-10 dpa ... 110 3e-39
emb|AW109163|AW109163 gate0002N06f Gossypium arboreum 7-10 dpa f... 110 3e-39
emb|AW569987|AW569987 si85c01.y1 Gm-c1031 Glycine max cDNA clone... 107 2e-38
emb|X07159|GMHSP179 Soybean gene for heat shock protein Gmhsp17... 103 2e-38
emb|AW620254|AW620254 si93g03.y1 Gm-c1031 Glycine max cDNA clone... 103 2e-38
15 emb|AW569546|AW569546 si88e01.y1 Gm-c1031 Glycine max cDNA clone... 103 2e-38
emb|AW569992|AW569992 si85c07.y1 Gm-c1031 Glycine max cDNA clone... 107 8e-38
emb|AW570000|AW570000 si85d08.y1 Gm-c1031 Glycine max cDNA clone... 104 1e-37
emb|AW730881|AW730881 GA__Ea0029C17 Gossypium arboreum 7-10 dpa ... 103 3e-37
emb|AW870031|AW870031 NXNV_123_C02_F Nsf Xylem Normal wood Verti... 153 1e-36
20 emb|AI812703|AI812703 18B10 Pine Lambda Zap Xylem library Pinus ... 145 3e-34
gb|U72396|LEU72396 Lycopersicon esculentum class II small heat s... 123 8e-31
emb|X95716|PCSHSPGEN P.crispum mRNA for 17.9kDa heat shock prote... 105 3e-28
emb|AI776971|AI776971 EST252063 tomato callus, TAMU Lycopersicon... 123 1e-27
emb|AB027500|AB027500 Daucus carota Dchsp-1 mRNA, complete cds. 98 2e-26
25 emb|AJ225049|LPAJ5049 Lycopersicon peruvianum mRNA for Hsp20.2 p... 105 8e-26
emb|AF090115|AF090115 Lycopersicon esculentum cytosolic class II... 106 3e-25
emb|AI782242|AI782242 EST263121 tomato susceptible, Cornell Lyco... 106 4e-25
emb|AF089846|AF089846 Funaria hygrometrica cytosolic II small he... 73 6e-25
dbj|D21817|LILLIM11 Lily mRNA for small heat shock protein, part... 78 1e-24
30 emb|AW569456|AW569456 si87d04.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
emb|AW569687|AW569687 si79b06.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
emb|AW568954|AW568954 si73e12.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
emb|AW569158|AW569158 si75b01.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
emb|AW568867|AW568867 si73c04.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
35 emb|AW569632|AW569632 si89d12.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
emb|AW569640|AW569640 si89e09.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
emb|AW568707|AW568707 si72b01.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
emb|AW569586|AW569586 si88h09.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
emb|AW620228|AW620228 si93d08.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
40 gb|L47717|PIAEMB27R Picea glauca heat shock protein 17.0 (EMB27)... 110 1e-23
emb|AW570013|AW570013 si85f01.y1 Gm-c1031 Glycine max cDNA clone... 108 3e-23
emb|AW185394|AW185394 se90h07.y1 Gm-c1027 Glycine max cDNA clone... 108 3e-23
emb|AW620212|AW620212 si93c03.y1 Gm-c1031 Glycine max cDNA clone... 108 3e-23
emb|AI900116|AI900116 sc01a11.y1 Gm-c1012 Glycine max cDNA clone... 108 3e-23
45 emb|AW569816|AW569816 si81h07.y1 Gm-c1031 Glycine max cDNA clone... 108 3e-23
emb|AW569179|AW569179 si75e02.y1 Gm-c1031 Glycine max cDNA clone... 108 3e-23
emb|AW289617|AW289617 NXNV003E01F Nsf Xylem Normal wood Vertical... 108 5e-23
emb|Z29554|HA179HSP H.annuus (Sunweed) mRNA for 17.9 kDa heat-sh... 105 3e-22
emb|X92983|PMLMWHSPA P.menziesii mRNA for low molecular weight h... 104 6e-22
50 emb|AW569996|AW569996 si85c11.y1 Gm-c1031 Glycine max cDNA clone... 104 6e-22
emb|X92984|PMLMWHSPB P.menziesii mRNA for low molecular weight h... 104 6e-22
dbj|D21816|LILLIM10 Lily mRNA for small heat shock protein, part... 68 1e-21
emb|X58279|TAHSP173 T.aestivum mRNA for heat shock protein 17.3. 102 1e-21
gb|M99430|PHNSHSPB Ipomoea nil small heat shock protein, complet... 102 3e-21
55 gb|M33899|PEAHSP181A Pisum sativum 18.1 kDa heat shock protein (... 65 5e-21
emb|AF089843|AF089843 Funaria hygrometrica cytosolic I small hea... 64 9e-21
gb|U63631|FXU63631 Fragaria x ananassa LMW heat shock protein mR... 63 2e-20
gb|U46545|HAU46545 Helianthus annuus 17.7 kDa heat-shock protein... 63 2e-20
emb|X13431|TAHSPLW Wheat mRNA for putative low molecular weight ... 65 2e-20
60 emb|AF123255|AF123255 Lycopersicon esculentum 17.7 kD class I sm... 61 3e-20
emb|X58711|MSHSP182 M.sativa mRNA for heat shock protein (clone ... 61 3e-20

emb|AW929084|AW929084 EST337788 tomato flower buds 8 mm to pre-a... 61 3e-20
 emb|AW443699|AW443699 EST308629 tomato mixed elicitor, BTI Lycop... 61 3e-20
 gb|BE034047|BE034047 MG04B07 MG Mesembryanthemum crystallinum cD... 61 4e-20
 gb|U08601|PSU08601 Papaver somniferum low molecular weight heat-... 98 5e-20
 5 emb|AW289567|AW289567 NXNV002G05F Nsf Xylem Normal wood Vertical... 98 5e-20
 emb|X70688|NTHSP18P N.tabacum hsp18p mRNA for heat shock protein... 61 8e-20
 emb|AF022217|AF022217 Brassica rapa low molecular weight heat-sh... 63 8e-20
 emb|X07160|GMHSP185 Soybean gene for heat shock protein Gmhsp18... 61 1e-19
 emb|AF161179|AF161179 Malus domestica low molecular weight heat ... 60 1e-19
 10 emb|AW597262|AW597262 si91d02.y1 Gm-c1031 Glycine max cDNA clone... 61 1e-19
 emb|AW568968|AW568968 si73g03.y1 Gm-c1031 Glycine max cDNA clone... 61 1e-19
 emb|AW569326|AW569326 si76f03.y1 Gm-c1031 Glycine max cDNA clone... 61 1e-19
 emb|X56138|LEHSP18 Lycopersicon esculentum mRNA for small heat-s... 61 2e-19
 emb|A15448|A15448 tomato fruit ripening related gene pTOM66 Seq ... 61 2e-19
 15 emb|AF123256|AF123256 Lycopersicon esculentum 17.8 kD class I sm... 61 2e-19
 emb|AF087640|AF087640 Funaria hygrometrica cytosolic I small hea... 66 3e-19
 emb|AF123257|AF123257 Lycopersicon esculentum 17.6 kD class I sm... 59 4e-19
 emb|AJ225047|LPAJ5047 Lycopersicon peruvianum mRNA for Hsp19.9 p... 59 4e-19
 emb|AW029721|AW029721 EST272976 tomato callus, TAMU Lycopersicon... 62 4e-19
 20 emb|AW221905|AW221905 EST298716 tomato fruit red ripe, TAMU Lyco... 62 4e-19
 emb|X58710|MSHSP181 M.sativa mRNA for heat shock protein (clone ... 58 4e-19
 emb|AW980952|AW980952 EST392105 GVN Medicago truncatula cDNA clo... 58 4e-19
 emb|AW569926|AW569926 si83d04.y1 Gm-c1031 Glycine max cDNA clone... 63 4e-19
 emb|AW569343|AW569343 si76g12.y1 Gm-c1031 Glycine max cDNA clone... 63 4e-19
 25 emb|AJ225046|LPAJ5046 Lycopersicon peruvianum mRNA for Hsp20.1 p... 59 5e-19
 emb|AW678863|AW678863 WS1_1_C05.g1_A002 Water-stressed 1 (WS1) S... 95 6e-19
 emb|AW678637|AW678637 WS1_1_C05.b1_A002 Water-stressed 1 (WS1) S... 95 6e-19
 emb|AW290614|AW290614 NXNV044B03F Nsf Xylem Normal wood Vertical... 95 6e-19
 emb|AW508849|AW508849 si41b03.y1 Gm-r1030 Glycine max cDNA clone... 59 7e-19
 30 emb|AW569644|AW569644 si89f04.y1 Gm-c1031 Glycine max cDNA clone... 59 7e-19
 emb|AW569636|AW569636 si89e04.y1 Gm-c1031 Glycine max cDNA clone... 59 7e-19
 emb|AW568435|AW568435 si70g06.y1 Gm-c1031 Glycine max cDNA clone... 59 1e-18
 emb|AW567658|AW567658 si77b11.y1 Gm-c1031 Glycine max cDNA clone... 63 1e-18
 emb|AW569747|AW569747 si79h07.y1 Gm-c1031 Glycine max cDNA clone... 59 1e-18
 35 emb|AF089845|AF089845 Funaria hygrometrica cytosolic II small he... 94 1e-18
 emb|X53852|DCHSP179 Carrot gene for a heat shock protein. 61 1e-18
 emb|AW223810|AW223810 EST300621 tomato fruit red ripe, TAMU Lyco... 57 1e-18

40 Query= hsp83_s_at 13285_s_at /id_source genbank /description
 gb|aaa32822.1| (m62984) heat shock protein 83 [arabidopsis thaliana]
 /blast_score 0
 (2411 letters)

45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

50 Score E
 Sequences producing significant alignments: (bits) Value

gb|M99431|PHNHSP83A Pharbitis nil heat shock protein 83 (Hsp83) ... 597 0.0
 gb|M96549|TOMHSC80P Tomato heat shock cognate protein 80 gene, 3... 577 0.0
 55 gb|U55859|TAU55859 Triticum aestivum heat shock protein 80 mRNA,... 575 0.0
 emb|X98582|TAX98582 T.aestivum mRNA for HSP80-2 protein. 572 0.0
 emb|X63195|NTHSP82 N.tabacum mRNA for heat shock protein 82. 601 0.0
 emb|AF123259|AF123259 Lycopersicon esculentum heat shock protein... 483 0.0
 emb|AF165818|AF165818 Guillardia theta nucleomorph 5S ribosomal ... 505 0.0
 60 emb|AF042329|AF042329 Eimeria tenella heat shock protein 90 (hsp... 514 0.0
 gb|M57386|THEHSP90 T.parva heat shock protein 90 (hsp90) mRNA, c... 500 0.0

	emb Z29667 PFHESHP P.falciparum (7) mRNA for heat-shock protein. 507 0.0
	gb U45449 EBU45449 Eimeria bovis heat shock protein 90 (hsp90) m... 495 0.0
	emb AF151114 AF151114 Tetrahymena thermophila strain B2086 hsp82... 486 0.0
	emb AF136649 AF136649 Babesia bovis heat shock protein 90 (HSP90... 487 0.0
5	gb M15346 TRBHSC T.cruzi tandemly repeated gene encoding an 85 k... 457 0.0
	emb X14176 TBHSP83 Trypanosoma brucei HSP83 gene. 452 0.0
	gb M73492 LEIHSP90 Leishmania donovani heat shock protein 90 mRN... 456 0.0
	emb X87770 LIHSP83GN L.infantum hsp83 gene. 454 0.0
	gb M92926 LEIHSP01 Leishmania amazonensis heat shock protein 83 ... 449 0.0
10	gb U92465 AFU92465 Aspergillus fumigatus heat shock protein (Hsp... 458 e-165
	emb AF212996 AF212996 Neurospora crassa heat shock protein 80 ge... 473 e-165
	emb AL110469 SPAC926 S.pombe chromosome I cosmid c926. 460 e-165
	gb L35550 YSPHSP90X Schizosaccharomyces pombe heat shock protein... 460 e-162
	gb U81165 PAU81165 Podospora anserina suppressor of vegetative i... 292 e-161
15	emb Z67751 SC38KCXVI S.cerevisiae DNA (chromosome XVI; 38 kb). 448 e-159
	emb Z73596 SCYPL240C S.cerevisiae chromosome XVI reading frame O... 448 e-159
	gb K01387 YSCHSP82A Yeast (S.cerevisiae) HSP82 (heat shock-induc... 448 e-159
	emb X81025 CAHSP90 C.albicans hsp90 gene. 451 e-159
	emb AF251005 AF251005 Candida tropicalis heat shock protein 90 g... 444 e-158
20	emb Z49808 SC8010 S.cerevisiae chromosome XIII cosmid 8010. 447 e-158
	emb AF221856 AF221856 Euphorbia esula heat-shock protein 80 mRNA... 292 e-158
	gb M26044 YSCHSC82 S. cerevisiae HSC82 gene encoding hsc82, the ... 447 e-157
	emb AW729825 AW729825 GA__Ea0026E04 Gossypium arboreum 7-10 dpa ... 473 e-134
	emb AW727612 AW727612 GA__Ea0015C16 Gossypium arboreum 7-10 dpa ... 454 e-132
25	emb AI489832 AI489832 EST248171 tomato ovary, TAMU Lycopersicon ... 471 e-132
	emb AW982575 AW982575 HVSMEg0003K07f Hordeum vulgare pre-anthesi... 471 e-131
	emb AW774793 AW774793 EST333944 KV3 Medicago truncatula cDNA clo... 459 e-128
	emb AW221746 AW221746 EST298557 tomato fruit red ripe, TAMU Lyco... 350 e-128
	emb AW728021 AW728021 GA__Ea0029G22 Gossypium arboreum 7-10 dpa ... 315 e-127
30	gb BE035845 BE035845 MO11A12 MO Mesembryanthemum crystallinum cD... 455 e-127
	emb AW650299 AW650299 EST328753 tomato germinating seedlings, TA... 455 e-127
	emb AW982497 AW982497 HVSMEg0003G20f Hordeum vulgare pre-anthesi... 439 e-126
	emb AF078070 AF078070 Griffithsia japonica heat-shock protein 90... 245 e-126
	emb AW218188 AW218188 EST303369 tomato radicle, 5 d post-imbibit... 452 e-126
35	emb AW731352 AW731352 GA__Ea0030E22 Gossypium arboreum 7-10 dpa ... 449 e-125
	emb AW621485 AW621485 EST312283 tomato root during/after fruit s... 445 e-124
	emb AW905909 AW905909 EST342082 potato stolon, Cornell Universit... 331 e-124
	emb AW618647 AW618647 EST320633 L. pennellii trichome, Cornell U... 439 e-122
	emb AI730385 AI730385 BNLGHi6770 Six-day Cotton fiber Gossypium ... 439 e-122
40	emb AW931002 AW931002 EST356845 tomato fruit mature green, TAMU ... 436 e-121
	emb AW186517 AW186517 se68g12.y1 Gm-c1019 Glycine max cDNA clone... 432 e-120
	gb BE055051 BE055051 GA__Ea0031H10f Gossypium arboreum 7-10 dpa ... 381 e-118
	emb AW217359 AW217359 EST296010 tomato flower buds 0-3 mm, Corne... 427 e-118
	emb AW216642 AW216642 EST295356 tomato callus, TAMU Lycopersicon... 423 e-117
45	emb AW217696 AW217696 EST296410 tomato flower buds 8 mm to pre-a... 422 e-117
	emb AW011081 AW011081 ST16E03 Pine TriplEx shoot tip library Pin... 421 e-116
	emb AI730419 AI730419 BNLGHi7100 Six-day Cotton fiber Gossypium ... 417 e-115
	emb AW907064 AW907064 EST343096 potato stolon, Cornell Universit... 413 e-114
	emb AW696590 AW696590 NF108G11ST1F1087 Developing stem Medicago ... 413 e-114
50	emb AW738699 AW738699 EST340126 tomato flower buds, anthesis, Co... 412 e-114
	emb AI442468 AI442468 sa27d08.y1 Gm-c1004 Glycine max cDNA clone... 412 e-114
	emb AW684853 AW684853 NF022C08NR1F1000 Nodulated root Medicago t... 403 e-114
	emb AW693965 AW693965 NF071A06ST1F1040 Developing stem Medicago ... 408 e-113
	emb AW690869 AW690869 NF036A07ST1F1000 Developing stem Medicago ... 390 e-113
55	emb AW030608 AW030608 EST273863 tomato callus, TAMU Lycopersicon... 407 e-112
	emb AW983321 AW983321 HVSMEg0010D10f Hordeum vulgare pre-anthesi... 354 e-112
	emb AI726426 AI726426 BNLGHi5602 Six-day Cotton fiber Gossypium ... 407 e-112
	emb AW930252 AW930252 EST340709 tomato fruit mature green, TAMU ... 406 e-112
	emb AW979717 AW979717 EST341337 tomato root deficiency, Cornell ... 404 e-111
60	emb AW695561 AW695561 NF096B09ST1F1076 Developing stem Medicago ... 404 e-111
	emb AW691505 AW691505 NF045G02ST1F1000 Developing stem Medicago ... 361 e-111

- emb|AW735801|AW735801 EST336569 tomato flower buds 0-3 mm, Corne... 402 e-111
 emb|AW737406|AW737406 EST338749 tomato flower buds, anthesis, Co... 402 e-111
 emb|AL112936|CNS01AHC Botrytis cinerea strain T4 cDNA library un... 400 e-110
 emb|AW217697|AW217697 EST296411 tomato flower buds 8 mm to pre-a... 400 e-110
 5 emb|AW218948|AW218948 EST301430 tomato root during/after fruit s... 396 e-110
 emb|AW220869|AW220869 EST297338 tomato fruit mature green, TAMU ... 398 e-109
 emb|AW616417|AW616417 EST322828 L. hirsutum trichome, Cornell Un... 397 e-109
 emb|AW688548|AW688548 NF008H04ST1F1000 Developing stem Medicago ... 396 e-109
 emb|AW738535|AW738535 EST339962 tomato flower buds, anthesis, Co... 242 e-109
 10 emb|AW649397|AW649397 EST327851 tomato germinating seedlings, TA... 394 e-108
 emb|AW693115|AW693115 NF060C10ST1F1081 Developing stem Medicago ... 226 e-107
 emb|AI488065|AI488065 EST246387 tomato ovary, TAMU Lycopersicon ... 390 e-107
 emb|AI726157|AI726157 BNLGHi5098 Six-day Cotton fiber Gossypium ... 226 e-107
 gb|BE060856|BE060856 HVSMeg0013J20f Hordeum vulgare pre-anthesis... 388 e-107
 15 emb|AI781620|AI781620 EST262499 tomato susceptible, Cornell Lyco... 389 e-107
 emb|AL111751|CNS019KF Botrytis cinerea strain T4 cDNA library un... 389 e-107
 emb|AW092845|AW092845 EST286025 tomato mixed elicitor, BTI Lycop... 386 e-106
 emb|AW983154|AW983154 HVSMeg0008G17f Hordeum vulgare pre-anthesi... 224 e-106
 emb|AI780272|AI780272 EST261151 tomato susceptible, Cornell Lyco... 215 e-106
 20 emb|AW651194|AW651194 EST329648 tomato germinating seedlings, TA... 266 e-106
 emb|AW690804|AW690804 NF035B11ST1F1000 Developing stem Medicago ... 375 e-106
 emb|AW154860|AW154860 EST290253 tomato root deficiency, Cornell ... 385 e-105
 emb|AI780075|AI780075 EST260954 tomato susceptible, Cornell Lyco... 383 e-105
 emb|AW928471|AW928471 EST337259 tomato flower buds 8 mm to pre-a... 382 e-105
 25 gb|L34028|PFAHSP86B Plasmodium falciparum (clone HB3) heat shock... 382 e-105
 emb|AF030694|AF030694 Plasmodium falciparum strain Dd2 heat shoc... 382 e-105
 gb|L34027|PFAHSP86A Plasmodium falciparum (clone Dd2) heat shock... 382 e-105
 emb|AW737397|AW737397 EST338740 tomato flower buds, anthesis, Co... 381 e-104
 emb|AW334905|AW334905 S40F8 AGS-1 Pneumocystis carinii f. sp. ca... 381 e-104
 30 emb|AW035244|AW035244 EST280506 tomato callus, TAMU Lycopersicon... 380 e-104

Query= Mloli2_s_at 13685_s_at /id_source genbank /description
 gb|aad25552.1|ac005850_9 (ac005850) highly similar to mlo proteins
 35 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link /ncgi
 (1752 letters)

Database: plantfungal
 40 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	
45	Sequences producing significant alignments:	(bits)	Value
	emb A92838 A92838 Sequence 12 from Patent WO9804586.	258	e-123
	emb Z83834 HVML0 H.vulgare mRNA for Mlo protein.	261	e-116
	emb A92833 A92833 Sequence 7 from Patent WO9804586.	261	e-116
50	emb A92828 A92828 Sequence 2 from Patent WO9804586.	261	e-116
	emb AW216578 AW216578 EST295292 tomato callus, TAMU Lycopersicon...	165	6e-78
	emb AJ005341 LUAJ5341 Linum usitatissimum mRNA for MLO-like prot...	287	2e-76
	emb AW934153 AW934153 EST359996 tomato fruit mature green, TAMU ...	235	4e-74
	emb AW132264 AW132264 sd98f11.y1 Gm-c1013 Glycine max cDNA clone...	128	2e-60
55	emb AI779924 AI779924 EST260803 tomato susceptible, Cornell Lyco...	228	8e-59
	gb BE020055 BE020055 sm38e01.y1 Gm-c1028 Glycine max cDNA clone ...	199	2e-58
	emb AW132268 AW132268 sd98g11.y1 Gm-c1013 Glycine max cDNA clone...	124	5e-58
	emb AI729603 AI729603 BNLGHi13760 Six-day Cotton fiber Gossypium...	202	8e-51
	emb AI054629 AI054629 coau0001J02 Cotton Boll Abscission Zone cD...	133	2e-44
60	emb AV426381 AV426381 AV426381 Lotus japonicus young plants (two...	145	3e-43
	emb AI729043 AI729043 BNLGHi12416 Six-day Cotton fiber Gossypium...	142	6e-42

	emb Y14573 HVCH4H Hordeum vulgare DNA for chromosome 4H.	107 7e-41
	emb A92831 A92831 Sequence 5 from Patent WO9804586.	107 7e-41
	emb AI731933 AI731933 BNLGH11440 Six-day Cotton fiber Gossypium...	136 3e-40
	emb AI440563 AI440563 sa84c07.y1 Gm-cl004 Glycine max cDNA clone...	155 1e-36
5	emb AI166945 AI166945 xylem.est.727 Poplar xylem Lambda ZAPII li...	149 4e-35
	emb A92829 A92829 Sequence 3 from Patent WO9804586.	107 4e-34
	gb BE059771 BE059771 sn36h06.y1 Gm-cl016 Glycine max cDNA clone ...	137 2e-31
	emb AB011444 AB011444 Triticum aestivum WESR3 mRNA, partial cds.	137 2e-31
	emb AW350270 AW350270 GM210007B20B6R Gm-r1021 Glycine max cDNA 3...	127 7e-31
10	emb AI778500 AI778500 EST259379 tomato susceptible, Cornell Lyco...	76 3e-30
	emb AW299018 AW299018 EST305692 KV2 Medicago truncatula cDNA clo...	125 1e-27
	emb AW442776 AW442776 EST307706 tomato mixed elicitor, BTI Lycop...	117 2e-25
	emb AW719459 AW719459 LjNEST4h6r Lotus japonicus nodule library,...	85 4e-25
	emb AW087034 AW087034 gal1d07.y1 Moss EST library CPU Ceratodon ...	83 5e-25
15	emb AW672144 AW672144 LG1_357_A11.b1_A002 Light Grown 1 (LG1) So...	108 1e-22
	emb AT000894 AT000894 AT000894 Brassica rapa guard cell Brassica...	108 2e-22
	emb AW906979 AW906979 EST343206 potato stolon, Cornell Universit...	98 2e-19
	emb Z95496 HVMLOH1 H.vulgare Mlo-h1 gene.	98 2e-19
	emb A92836 A92836 Sequence 10 from Patent WO9804586.	98 2e-19
20	emb A92832 A92832 Sequence 6 from Patent WO9804586.	98 2e-19
	emb AW570038 AW570038 si85h06.y1 Gm-cl031 Glycine max cDNA clone...	96 6e-19
	emb AA660856 AA660856 00751 MtRHE Medicago truncatula cDNA 5', m...	90 4e-17
	emb AT000630 AT000630 AT000630 Brassica rapa guard cell Brassica...	87 5e-16
	gb BE022484 BE022484 sm74e08.y1 Gm-cl015 Glycine max cDNA clone ...	84 3e-15
25	emb AW672173 AW672173 LG1_357_A11.g1_A002 Light Grown 1 (LG1) So...	80 4e-14
	emb AI443125 AI443125 sa84f05.y1 Gm-cl004 Glycine max cDNA clone...	78 3e-13
	emb AW870276 AW870276 NXNV_128_G07_F Nsf Xylem Normal wood Verti...	77 4e-13
	emb AW726816 AW726816 GA_Ea0022N04 Gossypium arboreum 7-10 dpa ...	50 6e-13
	emb AI960937 AI960937 sc92h06.y1 Gm-cl019 Glycine max cDNA clone...	76 1e-12
30	emb AW569990 AW569990 si85c05.y1 Gm-cl031 Glycine max cDNA clone...	75 1e-12
	emb AI484886 AI484886 EST243149 tomato ovary, TAMU Lycopersicon ...	73 7e-12
	emb AW285009 AW285009 LG1_297_B09.g1_A002 Light Grown 1 (LG1) So...	72 1e-11
	emb AW203816 AW203816 sf38e09.y1 Gm-cl028 Glycine max cDNA clone...	62 2e-08
	emb AW719871 AW719871 LjNEST11d10r Lotus japonicus nodule librar...	51 8e-08
35	emb AW757069 AW757069 sl02g02.y1 Gm-cl036 Glycine max cDNA clone...	59 9e-08
	emb AW567653 AW567653 si77b05.y1 Gm-cl031 Glycine max cDNA clone...	55 2e-06
	emb AT000874 AT000874 AT000874 Brassica rapa guard cell Brassica...	46 7e-04
	emb AI563090 AI563090 EST00214 watermelon lambda zap library Cit...	37 0.010
	emb Z74921 BOK8A2 B.oleracea mRNA (unknown).	31 0.26
40	emb AZ221382 AZ221382 Gm_UMb001_002_A13R UMN Soybean BAC Library...	33 0.65
	gb BE035329 BE035329 MM06C12 MM Mesembryanthemum crystallinum cD...	36 0.71
	emb AW186503 AW186503 se68f07.y1 Gm-cl019 Glycine max cDNA clone...	36 0.97
	emb AW218260 AW218260 EST303441 tomato radicle, 5 d post-imbibit...	35 1.3
	emb AW693662 AW693662 NF067A11ST1F1084 Developing stem Medicago ...	35 1.3
45	emb AW688978 AW688978 NF014A05ST1F1000 Developing stem Medicago ...	35 1.3
	emb AI374173 AI374173 T6346 MVAT4 bloodstream form of serodeme W...	35 1.3
	emb AW689953 AW689953 NF027B09ST1F1000 Developing stem Medicago ...	35 1.3
	emb AW218259 AW218259 EST303440 tomato radicle, 5 d post-imbibit...	35 1.3
	emb X96770 SCLACHXVI S.cerevisiae chromosome XVI, left arm DNA.	35 1.8
50	emb X05498 SCSNR17B Yeast SNR17B gene for U3 small nuclear RNA.	35 1.8
	emb Z73500 SCYPL144W S.cerevisiae chromosome XVI reading frame O...	35 1.8
	gb U43703 SCU43703 Saccharomyces cerevisiae chromosome XVI cosmi...	35 1.8
	emb Z73499 SCYPL143W S.cerevisiae chromosome XVI reading frame O...	35 1.8
	emb AJ242498 CCL242498 Candida cloacae mRNA for long chain fatty...	35 1.8
55	emb AQ949106 AQ949106 Sheared DNA-49L9.TR Sheared DNA Trypanosom...	35 2.5
	emb AQ650344 AQ650344 Sheared DNA-28J12.TF Sheared DNA Trypanoso...	35 2.5
	emb AQ657515 AQ657515 Sheared DNA-3K7.TR Sheared DNA Trypanosoma...	35 2.5
	emb Z74965 SCYOR057W S.cerevisiae chromosome XV reading frame OR...	34 3.5
	emb AC007061 AC007061 Leishmania major chromosome 3 clone L1559 ...	34 3.5
60	emb AQ642037 AQ642037 RPCI93-DpnII-29K3.TJ RPCI93-DpnII Trypanos...	34 3.5
	emb AQ445280 AQ445280 GSSTc01558 Trypanosoma cruzi random genomi...	34 3.5

emb|Z70678|SCXV55KB *S.cerevisiae* chromosome XV DNA, 54.7 kb region. 34 3.5
 emb|AQ659145|AQ659145 Sheared DNA-16H2.TF Sheared DNA Trypanosom... 34 3.5
 gb|U88830|SCU88830 *Saccharomyces cerevisiae* Sgt1p (SGT1) gene, c... 34 3.5
 emb|AC005927|AC005927 *Leishmania major* chromosome 3 clone L3561 ... 34 3.5
 5 emb|AQ637975|AQ637975 927P1-6A12.TV 927P1 *Trypanosoma brucei* gen... 34 3.5
 emb|AL031744|PFMAL1P1 *Plasmodium falciparum* chromosome 1 strain ... 29 4.5
 emb|AF091345|AF091345 *Schizosaccharomyces pombe* N-terminal serin... 34 4.7
 emb|AC013353|AC013353 *Trypanosoma brucei* chromosome VI clone RPC... 34 4.7
 emb|AQ948416|AQ948416 Sheared DNA-38M22.TR Sheared DNA Trypanoso... 34 4.7
 10 emb|AW257222|AW257222 EST305359 *Medicago truncatula* cDNA clo... 34 4.7
 emb|Y13973|CACIP1 *Candida* sp. CIP1 gene. 34 4.7
 emb|AL031263|SPBC17F3 *S.pombe* chromosome II cosmid c17F3. 34 4.7
 emb|AF152552|AF152552 *Sorghum bicolor* chalcone synthase 5 (CHS5)... 34 4.7
 emb|AQ655690|AQ655690 Sheared DNA-9G1.TR Sheared DNA *Trypanosoma*... 34 4.7
 15 emb|AZ212373|AZ212373 Sheared DNA-101E1.TF Sheared DNA Trypanoso... 34 4.7
 emb|AJ250726|TBR250726 *Trypanosoma brucei* HSP100 gene, GPI-PLC g... 34 4.7
 gb|M17420|YSTHEP *Saccharomyces cerevisiae* heptapeptide repeat re... 33 6.5
 emb|AI730517|AI730517 BNLGHi6942 Six-day Cotton fiber *Gossypium* ... 33 6.5
 emb|Z49511|SCYJR011C *S.cerevisiae* chromosome X reading frame ORF... 33 6.5
 20 gb|U59312|HVU59312 *Hordeum vulgare* (1,4)-beta-xylan endohydrolas... 33 6.5
 emb|Z74188|SCYDL140C *S.cerevisiae* chromosome IV reading frame OR... 33 6.5
 emb|X87611|SCXCOSM83 *S.cerevisiae* chromosome X DNA (cosmid 83). 33 6.5
 emb|AA003500|AA003500 T3189 MVAT4 bloodstream form of serodeme W... 33 6.5
 emb|AQ951709|AQ951709 Sheared DNA-51E22.TF Sheared DNA Trypanoso... 33 6.5
 25

 Query= NI115_at 13696_at /id_source genbank /description no hits found
 less than or equal to 1e-15. /blast_score /ec_number /family /chip
 30 nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ni115|/ncgi
 http://www.ncgr.org/cgi-bin/ff?ni115
 (640 letters)
 35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

 Searching.....done
 40

 Score E
 Sequences producing significant alignments: (bits) Value

 emb|AI856734|AI856734 sb41e04.y1 Gm-c1014 Glycine max cDNA clone... 110 1e-23
 45 gb|C22284|C22284 C22284 Miyagawa-wase satsuma mandarin orange (M... 103 1e-21
 emb|AW759850|AW759850 sl54h05.y1 Gm-c1027 Glycine max cDNA clone... 89 2e-17
 emb|AW565002|AW565002 LG1_313_B11.b1_A002 Light Grown 1 (LG1) So... 89 2e-17
 emb|AW437881|AW437881 ST73F03 Pine TriplEx shoot tip library Pin... 84 1e-15
 emb|AW760009|AW760009 sl56h04.y1 Gm-c1027 Glycine max cDNA clone... 83 3e-15
 50 emb|AW397963|AW397963 sg70e07.y1 Gm-c1007 Glycine max cDNA clone... 53 2e-06
 emb|AI440799|AI440799 sa48g03.y1 Gm-c1004 Glycine max cDNA clone... 47 1e-04
 emb|AI563168|AI563168 EST00292 watermelon lambda zap library Cit... 47 1e-04
 emb|AI491014|AI491014 EST241723 tomato shoot, Cornell Lycopersic... 44 0.001
 emb|AW034769|AW034769 EST278805 tomato callus, TAMU Lycopersicon... 44 0.001
 55 emb|AI777269|AI777269 EST258234 tomato resistant, Cornell Lycop... 44 0.001
 emb|AQ653339|AQ653339 Sheared DNA-6G13.TF Sheared DNA Trypanosom... 34 1.5
 dbj|D50838|CREACTINA *Chlamydomonas reinhardtii* DNA for actin, co... 33 2.0
 emb|AL109815|PFMAL13PA *Plasmodium falciparum* chromosome 13 strai... 33 2.0
 emb|AW257048|AW257048 EST305185 *Medicago truncatula* cDNA clo... 32 3.8
 60 gb|U52151|APU52151 *Aspergillus parasiticus* polyketide synthase P... 32 3.8
 emb|AQ644937|AQ644937 RPCI93-DpnII-27K24.TV RPCI93-DpnII Trypano... 32 3.8

emb|AB009881|AB009881 Nicotiana tabacum mRNA for myo-inositol 1-... 32 3.8
 emb|AQ643140|AQ643140 RPCI93-EcoRI-6J20.TJ RPCI93-EcoRI Trypanos... 32 3.8
 emb|X56441|GL35 G.lemneiformis plasmid GL3.5 DNA starting at Ec... 28 5.1
 gb|M60208|YSPHSP70 S.pombe mitochondrial heat shock protein (HSP... 32 5.2
 5 emb|AF083468|AF083468 Emericella nidulans putative zinc finger p... 32 5.2
 emb|AU011047|AU011047 AU011047 Schizosaccharomyces pombe late lo... 32 5.2
 emb|AL136235|SPAC664 S.pombe chromosome I cosmid c664. 32 5.2
 emb|AL160493|LMFLCHR26 Leishmania major Friedlin assembled chrom... 31 7.1
 emb|X70810|CLEGCGA Euglena gracilis chloroplast complete genome. 31 7.1
 10 emb|AW923451|AW923451 DG1_52_H09.b1_A002 Dark Grown 1 (DG1) Sorg... 31 7.1
 emb|AQ845394|AQ845394 LMAJFV1_lm24h05.y1 Leishmania major FV1 ra... 31 7.1
 emb|AQ908191|AQ908191 GSSTc08820 Trypanosome cruzi random genomi... 31 7.1
 emb|AV410934|AV410934 AV410934 Lotus japonicus young plants (two... 31 7.1
 emb|Z11874|CHEGZ Euglena gracilis Z Chloroplast DNA. 31 7.1
 15 emb|AL049184|PFMAL13P3 Plasmodium falciparum chromosome 13 strai... 31 9.8
 gb|U33050|SCD8035 Saccharomyces cerevisiae chromosome IV cosmids... 31 9.8
 emb|AC007862|AC007862 Trypanosoma brucei chromosome II clone RPC... 31 9.8
 emb|X74406|HSPSEN102 Hemerocallis sp. mRNA for thiol-protease. 31 9.8
 emb|AF107822|AF107822 Hildenbrandia rubra country Mexico ribulos... 31 9.8
 20 emb|AL031744|PFMAL1P1 Plasmodium falciparum chromosome 1 strain ... 31 9.8
 emb|AQ651798|AQ651798 Sheared DNA-20J13.TR Sheared DNA Trypanoso... 31 9.8
 emb|AQ875345|AQ875345 V123A8 mTn-3xHA/lacZ Insertion Library, st... 31 9.8
 emb|AF245210|AF245210 Thuja plicata clone Tp6 microsatellite seq... 31 9.8
 emb|AC006281|AC006281 Plasmodium falciparum chromosome 12 clone ... 31 9.8
 25 emb|AI897641|AI897641 EST267084 tomato ovary, TAMU Lycopersicon ... 31 9.8
 emb|AF163675|AF163675 Sclerotium cepivorum strain SQ-48 anonymou... 31 9.8
 emb|AF163674|AF163674 Sclerotium cepivorum strain DE-1 anonymous... 31 9.8

 30 Query= NI16_at 13697_at /id_source genbank /description no hits found.
 /blast_score /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ni16|/ncgi
 http://www.ncgr.org/cgi-bin/ff?ni16
 35 (509 letters)

 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

 40 Searching.....done

 Score E
 Sequences producing significant alignments: (bits) Value

 45 emb|AV397290|AV397290 AV397290 Chlamydomonas reinhardtii C9 Chla... 36 0.20
 emb|W35667|W35667 TgESTzy83e02.r1 TgRH Tachyzoite cDNA Toxoplasma... 28 0.49
 emb|AL115822|CNS01CPI Botrytis cinerea strain T4 cDNA library un... 33 1.5
 emb|AL031744|PFMAL1P1 Plasmodium falciparum chromosome 1 strain ... 33 2.0
 emb|AW033792|AW033792 EST277363 tomato callus, TAMU Lycopersicon... 33 2.5
 50 emb|Z49705|SC8520X S.cerevisiae chromosome XIII cosmid 8520. 32 3.8
 emb|AB001684|AB001684 Chlorella vulgaris C-27 chloroplast DNA, c... 32 3.8
 emb|AL049185|PFMAL13P2 Plasmodium falciparum chromosome 13 strai... 32 3.8
 emb|AW101318|AW101318 sd77e03.y1 Gm-c1009 Glycine max cDNA clone... 32 3.8
 emb|AQ909718|AQ909718 GSSTc09185 Trypanosome cruzi random genomi... 31 5.3
 55 emb|AW991095|AW991095 SsS0129 Suaeda salsa ZAP cDNA library Suae... 28 5.9
 emb|AJ273065|AJ273065 AJ273065 Metarhizium anisopliae ARSEF 2575... 31 6.5
 emb|AF057379|AF057379 Nicotiana tabacum clone G8-1 unknown mRNA. 31 6.5
 emb|AB005455|AB005455 Antirrhinum majus DNA, genomic survey sequ... 31 7.3
 gb|BE036743|BE036743 MP04G02 MP Mesembryanthemum crystallinum cD... 31 7.3
 60 emb|AI460510|AI460510 sa80h11.y1 Gm-c1004 Glycine max cDNA clone... 31 7.3
 emb|AI026500|AI026500 TENU0712 T. cruzi epimastigote normalized ... 31 7.3

emb|AW651081|AW651081 EST329535 tomato germinating seedlings, TA... 30 10.0
 emb|Z50113|SPAC31A2 S.pombe chromosome I cosmid c31A2. 30 10.0
 gb|BE053763|BE053763 GA__Ea0032N22f Gossypium arboreum 7-10 dpa ... 30 10.0
 emb|AW728950|AW728950 GA__Ea0018L17 Gossypium arboreum 7-10 dpa ... 30 10.0
 5 gb|L38011|L38011 BNAF0228E Mustard flower buds Brassica rapa cDN... 30 10.0

Query= Novartis127_at 13751_at /id_source
 /description gb|aaf16751.1|ac010155_4 (ac010155) f3m18.8
 10 [arabidopsis thaliana] /blast_score 2.00e-27 /ec_number /family
 /chip nova /gb_link
 (341 letters)

Database: plantfungal
 15 661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	
				(bits) Value
20	Sequences producing significant alignments:			
	emb AV428133 AV428133 AV428133 Lotus japonicus young plants (two...	53	9e-07	
	emb AV412192 AV412192 AV412192 Lotus japonicus young plants (two...	53	9e-07	
	emb AW350135 AW350135 GM210007B10E8R Gm-r1021 Glycine max cDNA 3...	51	2e-06	
25	emb AW349971 AW349971 GM210006B10B12R Gm-r1021 Glycine max cDNA ...	51	2e-06	
	emb AW032575 AW032575 EST276134 tomato callus, TAMU Lycopersicon...	51	2e-06	
	emb AW030108 AW030108 EST273363 tomato callus, TAMU Lycopersicon...	51	2e-06	
	emb AI895822 AI895822 EST265265 tomato callus, TAMU Lycopersicon...	51	2e-06	
	emb AI759855 AI759855 sb65c01.y1 Gm-cl017 Glycine max cDNA clone...	51	2e-06	
30	emb AI777275 AI777275 EST258240 tomato resistant, Cornell Lycope...	51	2e-06	
	emb AW625260 AW625260 EST319263 tomato radicle, 5 d post-imbibit...	51	2e-06	
	emb AW441936 AW441936 EST311332 tomato fruit red ripe, TAMU Lyco...	51	2e-06	
	emb AI441970 AI441970 sa82e02.y1 Gm-cl004 Glycine max cDNA clone...	51	2e-06	
35	emb AW705827 AW705827 sk63d05.y1 Gm-cl016 Glycine max cDNA clone...	51	3e-06	
	emb AV428923 AV428923 AV428923 Lotus japonicus young plants (two...	51	3e-06	
	gb BE124339 BE124339 EST393374 GVN Medicago truncatula cDNA clon...	48	2e-05	
	emb AW442099 AW442099 EST311495 tomato fruit red ripe, TAMU Lyco...	48	3e-05	
	emb AW625258 AW625258 EST319261 tomato radicle, 5 d post-imbibit...	47	4e-05	
	emb AI779024 AI779024 EST259903 tomato susceptible, Cornell Lyco...	46	1e-04	
40	emb AW775746 AW775746 EST334811 DSIL Medicago truncatula cDNA cl...	46	1e-04	
	emb AI960660 AI960660 sc87f03.y1 Gm-cl018 Glycine max cDNA clone...	46	1e-04	
	emb AW278224 AW278224 sf41c11.y1 Gm-cl009 Glycine max cDNA clone...	45	3e-04	
	gb BE059759 BE059759 sn36g02.y1 Gm-cl016 Glycine max cDNA clone ...	45	3e-04	
	emb AW348296 AW348296 GM210001B23C7R Gm-r1021 Glycine max cDNA 3...	44	4e-04	
45	emb AW685445 AW685445 NF029E11NR1F1000 Nodulated root Medicago t...	44	4e-04	
	emb AI442537 AI442537 sa32g06.y1 Gm-cl004 Glycine max cDNA clone...	41	0.004	
	emb Z99164 SPAC29B12 S.pombe chromosome I cosmid c29B12.	41	0.005	
	emb AW099733 AW099733 sd30f03.y2 Gm-cl012 Glycine max cDNA clone...	40	0.005	
	emb AU011832 AU011832 AU011832 Schizosaccharomyces pombe late lo...	40	0.006	
50	emb AW622091 AW622091 EST312889 tomato root during/after fruit s...	39	0.017	
	emb AW152886 AW152886 se32c07.y1 Gm-cl015 Glycine max cDNA clone...	38	0.024	
	emb AW661378 AW661378 833004H08.y1 C. reinhardtii CC-125 -S, Lam...	38	0.033	
	emb AW625785 AW625785 EST319692 tomato radicle, 5 d post-imbibit...	37	0.045	
	emb AQ639212 AQ639212 927P1-10E7.TP 927P1 Trypanosoma brucei gen...	30	0.055	
55	emb X02873 DCEXTG Carrot gene for extensin.	37	0.062	
	emb AW926428 AW926428 HVSMEg0007D04 Hordeum vulgare pre-anthesis...	35	0.063	
	emb AI988320 AI988320 sc99b12.y1 Gm-cl020 Glycine max cDNA clone...	36	0.086	
	emb X55685 LEEXTEN5 Tomato extensin mRNA (clone uG-18).	36	0.12	
	emb X55682 LEEXTEN2 Tomato extensin mRNA (clone wY).	35	0.16	
60	emb X55681 LEEXTEN1 Tomato extensin mRNA (clone w17-1).	35	0.16	
	gb M34310 YSCTSDNAA S.cerevisiae telomeric sequence DNA, clone Y...	27	0.20	

	emb AI780236 AI780236 EST261115 tomato susceptible, Cornell Lyco...	35	0.22
	emb AW101170 AW101170 sd75a05.y1 Gm-c1008 Glycine max cDNA clone...	35	0.22
	emb AW775499 AW775499 EST334564 DSIL Medicago truncatula cDNA cl...	35	0.22
	emb AI780235 AI780235 EST261114 tomato susceptible, Cornell Lyco...	35	0.22
5	emb AI779223 AI779223 EST260102 tomato susceptible, Cornell Lyco...	35	0.22
	emb AW091576 AW091576 EST284852 tomato mixed elicitor, BTI Lycop...	35	0.22
	emb AI900504 AI900504 sc11h04.y1 Gm-c1012 Glycine max cDNA clone...	35	0.22
	emb AF163959 AF163959 Saccharomyces cerevisiae isolate wt-20 tel...	29	0.23
	gb M34311 YSCTSDNAB S.cerevisiae telomeric sequence DNA, clone Y...	27	0.25
10	emb AF163953 AF163953 Saccharomyces cerevisiae isolate wt-2 telo...	29	0.26
	emb X59720 SCCHRIII S.cerevisiae chromosome III complete DNA seq...	28	0.30
	gb M15317 PFAHRPA P.lophurae histidine-rich protein mRNA, 3' end.	35	0.30
	emb AV408422 AV408422 AV408422 Lotus japonicus young plants (two...	35	0.30
	emb AF163955 AF163955 Saccharomyces cerevisiae isolate wt-8 telo...	33	0.34
15	emb AL116033 CNS01CVD Botrytis cinerea strain T4 cDNA library un...	27	0.38
	gb BE034443 BE034443 MH05A01 MH Mesembryanthemum crystallinum cD...	34	0.42
	gb M12922 YSCARSX Yeast (S.cerevisiae) chromosome III L terminal...	28	0.44
	emb AF163958 AF163958 Saccharomyces cerevisiae isolate wt-13 tel...	26	0.56
	emb X91836 VUEXT26GN V.unguiculata Ext26G gene.	34	0.58
20	emb AI667994 AI667994 TENG0819 T. Cruzi epimastigote normalised ...	34	0.58
	emb AW928828 AW928828 EST337616 tomato flower buds 8 mm to pre-a...	34	0.58
	emb X86030 VURNEXT26 V.unguiculata mRNA for extensin-like prote...	34	0.58
	emb AF163960 AF163960 Saccharomyces cerevisiae isolate wt-21 tel...	31	0.58
	emb AF163947 AF163947 Saccharomyces cerevisiae strain yku70Delta...	28	0.60
25	emb AF163957 AF163957 Saccharomyces cerevisiae isolate wt-11 tel...	30	0.60
	emb AW722164 AW722164 a5d01nm.r1 Neurospora crassa morning cDNA ...	34	0.72
	emb AI065410 AI065410 TENU2298 T. cruzi epimastigote normalized ...	33	0.79
	emb Y15372 MTY15372 Medicago truncatula mRNA for MtN4 gene, part...	33	0.79
	emb AV393340 AV393340 AV393340 Chlamydomonas reinhardtii C9 Chla...	33	0.79
30	emb AL117324 LMFL2719 Leishmania major Friedlin chromosome 23 co...	33	0.79
	emb AW926294 AW926294 HVSMeg0006N09 Hordeum vulgare pre-anthesis...	33	0.79
	emb AI895893 AI895893 EST265336 tomato callus, TAMU Lycopersicon...	33	0.79
	emb AW926361 AW926361 HVSMeg0007A04 Hordeum vulgare pre-anthesis...	33	0.79
	emb AW712341 AW712341 glb02ne.fl Neurospora crassa evening cDNA ...	33	0.79
35	emb AI066197 AI066197 TENU2588 T. cruzi epimastigote normalized ...	33	0.79
	gb L16776 LEIGP63Z Leishmania guyanensis (clone Lg63c7) major su...	29	1.0
	gb L07282 CREPETE Chlamydomonas reinhardtii plastocyanin (petE) ...	33	1.1
	emb AW471567 AW471567 si12b01.y1 Gm-c1029 Glycine max cDNA clone...	33	1.1
	emb AI399511 AI399511 NCSP6D11T3 Subtracted Perithecial Neurospo...	33	1.1
40	emb AW696703 AW696703 NF109H07ST1F1063 Developing stem Medicago ...	33	1.1
	emb AW164290 AW164290 se70e09.y1 Gm-c1023 Glycine max cDNA clone...	33	1.1
	emb AV410275 AV410275 AV410275 Lotus japonicus young plants (two...	33	1.1
	emb AW507760 AW507760 si44g05.y1 Gm-r1030 Glycine max cDNA clone...	33	1.1
	emb X74106 NTGRPR N.tabacum gene for glycine-rich protein.	33	1.1
45	emb AW725658 AW725658 GA__Ea0019C15 Gossypium arboreum 7-10 dpa ...	27	1.5
	emb AA660327 AA660327 00198 MtrHE Medicago truncatula cDNA 5', m...	32	1.5
	emb AW690202 AW690202 NF030A02ST1F1000 Developing stem Medicago ...	32	1.5
	gb BE123911 BE123911 EST394036 DSIL Medicago truncatula cDNA clo...	32	1.5
	emb AI496548 AI496548 sb13b10.y1 Gm-c1004 Glycine max cDNA clone...	32	1.5
50	emb AW686104 AW686104 NF034D07NR1F1000 Nodulated root Medicago t...	32	1.5
	gb M76670 TOMEXTENA L.esculentum extensin (class I) gene, comple...	32	1.5
	gb BE034655 BE034655 ML01E08 ML Mesembryanthemum crystallinum cD...	32	1.5
	emb AL161025 L3320Y Leishmania major Friedlin cosmid L3320 t7 en...	32	1.5
	emb AW329194 AW329194 N200406e rootphos(-) Medicago truncatula c...	32	1.5
55	emb AF163952 AF163952 Saccharomyces cerevisiae isolate wt-1 telo...	27	1.5
	emb Z98532 SPAC1B1 S.pombe chromosome I cosmid c1B1.	28	1.6
	emb X01469 PLHRP1 Plasmodium gene fragment for histidine-rich pr...	32	2.0
	gb U66179 SCU66179 Skeletonema costatum fucoxanthin-chlorophyll ...	32	2.0
	emb AC006280 AC006280 Plasmodium falciparum chromosome 12 clone ...	32	2.0
60	emb AW277958 AW277958 sf88a11.y1 Gm-c1019 Glycine max cDNA clone...	32	2.0

Query= Novartis22_at 13764_at/id_source
 /description gb|aad39641.1|ac007591_6 (ac007591) f911.6 [arabidopsis
 thaliana] /blast_score 2.00e-30
 5 (973 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

10 Searching.....done

		Score	E
	Sequences producing significant alignments:	(bits)	Value
15	emb AJ245480 BNA245480 Brassica napus slg gene for S-locus glyco...	260	e-123
	emb AJ245479 BNA245479 Brassica napus SII3, slk, srk, CePP, Fmt,...	260	e-121
	emb AI495914 AI495914 sb17g06.y1 Gm-c1004 Glycine max cDNA clone...	57	4e-10
	emb AW217278 AW217278 EST295992 tomato callus, TAMU Lycopersicon...	50	6e-10
	emb AF179222 AF179222 Brassica rapa subsp. pekinensis floral nec...	43	2e-08
20	emb AW737522 AW737522 EST338949 tomato flower buds, anthesis, Co...	52	5e-06
	emb AW650581 AW650581 EST329035 tomato germinating seedlings, TA...	49	6e-06
	emb AW200887 AW200887 se94g08.y1 Gm-c1027 Glycine max cDNA clone...	50	3e-05
	emb AW774361 AW774361 EST333512 KV3 Medicago truncatula cDNA clo...	48	1e-04
	emb AW033701 AW033701 EST277272 tomato callus, TAMU Lycopersicon...	47	2e-04
25	emb AW738253 AW738253 EST339680 tomato flower buds, anthesis, Co...	46	5e-04
	emb AW285102 AW285102 LG1_300_F04.g1_A002 Light Grown 1 (LG1) So...	40	6e-04
	emb AI896626 AI896626 EST266069 tomato callus, TAMU Lycopersicon...	46	6e-04
	emb AW563740 AW563740 LG1_248_A08.g1_A002 Light Grown 1 (LG1) So...	43	0.004
	emb AW256640 AW256640 EST304777 KV2 Medicago truncatula cDNA clo...	42	0.006
30	emb AF133053 AF133053 Clarkia breweri S-adenosyl-L-methionine:sa...	42	0.006
	emb AI773683 AI773683 EST254783 tomato resistant, Cornell Lycope...	41	0.011
	emb AW563321 AW563321 LG1_235_A01.b1_A002 Light Grown 1 (LG1) So...	40	0.021
	emb AJ234779 HVU234779 Hordeum vulgare genomic DNA fragment; clo...	37	0.26
	emb W66488 W66488 TgESTzy71b04.r1 TgME49 Tachyzoite cDNA Toxopla...	36	0.50
35	emb AW595921 AW595921 si95b09.y1 Gm-c1032 Glycine max cDNA clone...	35	0.94
	emb AW567624 AW567624 si65f05.y1 Gm-r1030 Glycine max cDNA clone...	35	1.3
	emb AQ875548 AQ875548 V126F8 mTn-3xHA/lacZ Insertion Library, st...	35	1.3
	emb AI069155 AI069155 mgae0005da02f Magnaporthe grisea Appressor...	34	1.8
	emb AW734368 AW734368 sk19c07.y1 Gm-c1028 Glycine max cDNA clone...	34	1.8
40	gb T02585 T02585 0228C3 cbsPfHB3.1, Debopam Chakrabarti Plasmodi...	34	2.4
	emb AC005507 AC005507 Plasmodium falciparum chromosome 12 clone ...	34	2.4
	emb AF134688 AF134688 Plasmodium falciparum strain MAI5 from Mal...	34	2.4
	emb AF134683 AF134683 Plasmodium falciparum strain UNK1 CG2 omeg...	34	2.4
	emb AB009111 AB009111 AB009111 Chlamydomonas W80 lambda ZAP II C...	34	2.4
45	emb AL109814 PFMAL13PB Plasmodium falciparum chromosome 13 strai...	34	2.4
	emb AF061282 AF061282 Sorghum bicolor 22 kDa kafirin cluster.	33	3.3
	emb AV397690 AV397690 AV397690 Chlamydomonas reinhardtii C9 Chla...	33	3.3
	emb AW695936 AW695936 NF100B08ST1F1064 Developing stem Medicago ...	33	3.3
	emb AV389414 AV389414 AV389414 Chlamydomonas reinhardtii C9 Chla...	33	3.3
50	emb AF134698 AF134698 Plasmodium falciparum strain COM1 from Com...	33	3.3
	gb U60200 STU60200 Solanum tuberosum lipoxxygenase (POTLX-1) mRNA...	33	4.6
	emb AF039651 AF039651 Solanum tuberosum 5-lipoxxygenase mRNA, com...	33	4.6
	emb AQ447600 AQ447600 mgxb0008I05f CUGI Rice Blast BAC Library P...	33	4.6
	emb Z15131 ASBGLUCAN A.sativa mRNA for beta glucanase.	33	4.6
55	gb BE126052 BE126052 DG1_65_G12.b1_A002 Dark Grown 1 (DG1) Sorgh...	33	4.6
	emb Y18548 STU18548 Solanum tuberosum mRNA for lipoxxygenase.	33	4.6
	emb AF019614 AF019614 Solanum tuberosum lipoxxygenase (plo2) mRN...	33	4.6
	emb X79107 STLOX1 S.tuberosum (Desiree) mRNA for lipoxxygenase.	33	4.6
	emb AQ400078 AQ400078 mgxb0017C10f CUGI Rice Blast BAC Library P...	33	4.6
60	emb X95516 STLIPOT13 S.tuberosum mRNA for lipoxxygenase (clone T13).	33	4.6
	dbj D85900 ASNPDIA Aspergillus oryzae DNA for protein disulfide ...	33	4.6

emb|AQ396525|AQ396525 mgxb0011J08f CUGI Rice Blast BAC Library P... 33 4.6
 gb|U60201|STU60201 Solanum tuberosum lipoxygenase (POTLX-2) mRNA... 33 4.6
 emb|AW759238|AW759238 sl38f10.y1 Gm-cl027 Glycine max cDNA clone... 33 4.6
 emb|AQ399938|AQ399938 mgxb0012O04f CUGI Rice Blast BAC Library P... 33 4.6
 5 emb|AF019613|AF019613 Solanum tuberosum lipoxygenase (plox1) mRN... 33 4.6
 emb|X95512|STLIPOXT6 S.tuberosum mRNA for lipoxygenase (clone T6). 33 4.6
 emb|AW278834|AW278834 sf99c02.y1 Gm-cl019 Glycine max cDNA clone... 32 6.3
 emb|AL160371|LMFLCHR15 Leishmania major Friedlin assembled chrom... 32 6.3
 emb|AB005555|AB005555 Triticum aestivum mRNA for wga20, complete... 32 6.3
 10 emb|AA786508|AA786508 m3a04a1.r1 Aspergillus nidulans 24hr asexu... 32 6.3
 emb|AJ274333|AJ274333 AJ274333 Metarhizium anisopliae ARSEF 2575... 32 6.3
 emb|Y14007|TAY14007 Triticum aestivum mRNA for gibberellin 20-ox... 32 6.3
 emb|AW234216|AW234216 sf22f02.y1 Gm-cl028 Glycine max cDNA clone... 27 6.8
 emb|AC004710|AC004710 Plasmodium falciparum chromosome 12, *** S... 32 8.6
 15 emb|AA273033|AA273033 T4296 MVAT4 bloodstream form of serodeme W... 32 8.6
 emb|AZ215931|AZ215931 Sheared DNA-116D3.TR Sheared DNA Trypanoso... 32 8.6
 emb|AA495648|AA495648 c078 Zhou and Ragan 1993 Gracilaria gracil... 32 8.6
 emb|AL049182|PFMAL13P5 Plasmodium falciparum chromosome 13 strai... 32 8.6
 emb|X56775|HVGLB1 H.vulgare Glb 1 gene for 1-3,1-4-beta-D-glucan... 32 8.6
 20 emb|Z72916|SCYGR131W S.cerevisiae chromosome VII reading frame O... 32 8.6
 emb|Z72915|SCYGR130C S.cerevisiae chromosome VII reading frame O... 32 8.6
 gb|U10083|TGU10083 Toxoplasma gondii RH hypoxanthine-guanine pho... 32 8.6
 emb|AB026835|AB026835 Toxoplasma gondii mRNA for hypoxanthine-gu... 32 8.6
 gb|U09219|TGU09219 Toxoplasma gondii RH hypoxanthine-guanine pho... 32 8.6
 25 gb|U10247|TGU10247 Toxoplasma gondii RH hypoxanthine-xanthine-gu... 32 8.6
 emb|AB012774|AB012774 AB012774 Toxoplasma gondii mRNA (T.Koyama)... 32 8.6
 gb|S73865|S73865 linoleate:oxygen oxidoreductase [Solanum tubero... 32 8.6
 emb|AW761275|AW761275 sl65d12.y1 Gm-cl027 Glycine max cDNA clone... 32 8.6
 emb|AL112245|CNS019Y5 Botrytis cinerea strain T4 cDNA library un... 32 8.6
 30 emb|X56260|HVGLUEND Barley DNA for (1,3;1,4)-beta-glucanase.(EC ... 32 8.6
 emb|AI162017|AI162017 A011P07U Hybrid aspen plasmid library Popu... 30 9.4

Query= Novartis31_at 14141_at /id_source
 35 /description no hits found less than or equal to 1e-15. /blast_score
 /ec_number /family /chip.nova /gb_link /ncgi
 (309 letters)

Database: plantfungal
 40 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 45 Sequences producing significant alignments: (bits) Value

emb|X87143|HACYTB5RN H.annuus mRNA for extraplastidial fusion pr... 34 0.49
 emb|X74782|BNSACPD1 B.napus gene for stearyl-acyl carrier prote... 32 1.3
 emb|AW560462|AW560462 EST315510 DSIR Medicago truncatula cDNA cl... 32 1.3
 50 emb|AW687516|AW687516 NF010D12RT1F1101 Developing root Medicago ... 32 1.3
 emb|AW256825|AW256825 EST304962 KV2 Medicago truncatula cDNA clo... 32 1.3
 emb|X07644|NTALSURA Tobacco acetolactate synthase gene, ALS SuRA... 32 1.7
 emb|AA451568|AA451568 AOB213F Onion seedling leaf cDNA library A... 31 2.4
 emb|AW067623|AW067623 SBcD89 Sugar beet leaf cDNA library Beta v... 31 3.3
 55 emb|AF030694|AF030694 Plasmodium falciparum strain Dd2 heat shoc... 31 3.3
 emb|X12493|SCADR6 Yeast ADR6 gene for transcription factor. 30 4.5
 gb|U14726|SCU14726 Saccharomyces cerevisiae Syg1p (SYG1) gene, c... 30 4.5
 emb|Z46861|SC9905 S.cerevisiae chromosome IX cosmid 9905 and lam... 30 4.5
 gb|L29456|TOBHIC12X Nicotiana tabacum histone H1 (H1C12) mRNA, c... 30 4.5
 60 gb|U33335|U33335 Saccharomyces cerevisiae chromosome XVI, left a... 30 4.5
 emb|AJ290663|PAB290663 Picea abies copia like retroelement parti... 30 6.2

emb|AL115708|CNS01CMC Botrytis cinerea strain T4 cDNA library un... 30 6.2
 emb|Z71630|SCYNR015W S.cerevisiae chromosome XIV reading frame O... 29 8.5
 emb|Z71629|SCYNR014W S.cerevisiae chromosome XIV reading frame O... 29 8.5
 emb|AQ875584|AQ875584 V127B11 mTn-3xHA/lacZ Insertion Library, s... 29 8.5
 5 gb|L16451|YSAAPRP Candida albicans acid proteinase-related prote... 29 8.5
 emb|AW981797|AW981797 PC18H02 Pine TriplEx pollen cone library P... 29 8.5
 emb|AQ644958|AQ644958 RPCI93-DpnII-30N9.TJ RPCI93-DpnII Trypanos... 29 8.5
 emb|AW672524|AW672524 LG1_360_D10.b1_A002 Light Grown 1 (LG1) So... 29 8.5
 emb|AW564851|AW564851 LG1_310_D10.b1_A002 Light Grown 1 (LG1) So... 29 8.5
 10 emb|AI895394|AI895394 EST264837 tomato callus, TAMU Lycopersicon... 27 9.6

Query= Novartis35_at 14145_at /id_source
 /description "dbj|baa22813.1| (d26015) cnd41, chloroplast nucleoid dna
 binding protein [nicotiana tabacum]" /blast_score 8.00e-58 /ec_number
 15 /family /chip nova /gb_link /ncgi
 (783 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters
 20

Searching.....done

	Score	E	
			(bits) Value
25	Sequences producing significant alignments:		
	gb BE053273 BE053273 GA__Ea0035A10f Gossypium arboreum 7-10 dpa ...	149	4e-61
	dbj D26015 D26015 Nicotiana tabacum mRNA for CND41, chloroplast ...	148	9e-56
	emb AI487587 AI487587 EST245909 tomato ovary, TAMU Lycopersicon ...	152	4e-54
	emb AI489151 AI489151 EST247490 tomato ovary, TAMU Lycopersicon ...	152	4e-54
30	emb AI483907 AI483907 EST249778 tomato ovary, TAMU Lycopersicon ...	152	1e-52
	emb AW931514 AW931514 EST357357 tomato fruit mature green, TAMU ...	145	4e-52
	emb AI771546 AI771546 EST252646 tomato ovary, TAMU Lycopersicon ...	144	2e-49
	emb AW736637 AW736637 EST333129 KV3 Medicago truncatula cDNA clo...	142	6e-48
	emb AI166286 AI166286 xylem.est.133 Poplar xylem Lambda ZAPII li...	151	6e-40
35	emb AW693272 AW693272 NF064A05ST1F1000 Developing stem Medicago ...	143	3e-39
	emb AW736636 AW736636 EST333128 KV3 Medicago truncatula cDNA clo...	145	5e-39
	emb AW559446 AW559446 EST314494 DSIR Medicago truncatula cDNA cl...	143	1e-38
	emb AW730900 AW730900 GA__Ea0029G11 Gossypium arboreum 7-10 dpa ...	146	2e-37
	emb AW692307 AW692307 NF049H04ST1F1043 Developing stem Medicago ...	143	1e-36
40	emb AW737187 AW737187 EST338614 tomato flower buds, anthesis, Co...	149	3e-36
	emb AW688595 AW688595 NF009D06ST1F1000 Developing stem Medicago ...	137	8e-35
	emb AI974844 AI974844 T113327e KV2 Medicago truncatula cDNA clon...	143	3e-33
	emb AW773698 AW773698 EST332684 KV3 Medicago truncatula cDNA clo...	129	1e-32
	emb AV408654 AV408654 AV408654 Lotus japonicus young plants (two...	135	6e-32
45	emb AW688941 AW688941 NF013E03ST1F1000 Developing stem Medicago ...	121	4e-30
	emb AI725786 AI725786 BNLGHi12992 Six-day Cotton fiber Gossypium...	66	7e-29
	emb AW677148 AW677148 DG1_5_C02.b1_A002 Dark Grown 1 (DG1) Sorgh...	92	4e-27
	emb AW932074 AW932074 EST357917 tomato fruit mature green, TAMU ...	116	3e-26
	emb AI731300 AI731300 BNLGHi9147 Six-day Cotton fiber Gossypium ...	50	9e-25
50	emb AW933383 AW933383 EST359322 tomato fruit mature green, TAMU ...	57	5e-23
	emb AW034232 AW034232 EST277803 tomato callus, TAMU Lycopersicon...	63	4e-22
	emb AW221352 AW221352 EST297821 tomato fruit mature green, TAMU ...	63	2e-21
	emb AW307535 AW307535 sf58b08.y1 Gm-cl009 Glycine max cDNA clone...	63	2e-21
	emb AI974298 AI974298 T110300e KV0 Medicago truncatula cDNA clon...	90	5e-21
55	emb AI772366 AI772366 EST253466 tomato resistant, Cornell Lycop...	63	7e-21
	emb AV423168 AV423168 AV423168 Lotus japonicus young plants (two...	63	2e-20
	emb AW928704 AW928704 EST337492 tomato flower buds 8 mm to pre-a...	67	8e-20
	emb AW731304 AW731304 GA__Ea0030M17 Gossypium arboreum 7-10 dpa ...	66	1e-19
	emb AW219354 AW219354 EST301836 tomato root during/after fruit s...	64	1e-19
60	emb AW695746 AW695746 NF098B04ST1F1032 Developing stem Medicago ...	60	4e-19
	emb AW729560 AW729560 GA__Ea0025G03 Gossypium arboreum 7-10 dpa ...	64	5e-19

- emb|AW774011|AW774011 EST332997 KV3 *Medicago truncatula* cDNA clo... 63 1e-18
emb|AW691624|AW691624 NF047B12ST1F1000 Developing stem *Medicago* ... 60 1e-18
emb|AW690628|AW690628 NF036F05ST1F1000 Developing stem *Medicago* ... 60 1e-18
emb|AW398635|AW398635 EST309135 *L. pennellii* trichome, Cornell U... 48 1e-18
5 gb|BE033948|BE033948 MG02E01 MG *Mesembryanthemum crystallinum* cD... 68 2e-18
emb|AW980831|AW980831 EST391984 GVN *Medicago truncatula* cDNA clo... 48 2e-17
emb|AW266728|AW266728 L48-63T3 Ice plant Lambda Uni-Zap XR expre... 89 4e-17
emb|AW728833|AW728833 GA_Ea0028L16 *Gossypium arboreum* 7-10 dpa ... 64 5e-17
emb|AI726953|AI726953 BNLGH16948 Six-day Cotton fiber *Gossypium* ... 66 5e-17
10 emb|AW666733|AW666733 GA_Ea0005N06 *Gossypium arboreum* 7-10 dpa ... 64 7e-17
emb|AW693054|AW693054 NF059C10ST1F1081 Developing stem *Medicago* ... 63 1e-16
emb|AW692433|AW692433 NF055F02ST1F1000 Developing stem *Medicago* ... 60 2e-16
emb|AW560983|AW560983 EST316031 DSIR *Medicago truncatula* cDNA cl... 61 3e-16
emb|AW686542|AW686542 NF039C04NR1F1000 Nodulated root *Medicago* t... 60 4e-16
15 emb|AW726749|AW726749 GA_Ea0022J22 *Gossypium arboreum* 7-10 dpa ... 64 6e-16
emb|AW689509|AW689509 NF021E09ST1F1000 Developing stem *Medicago* ... 63 6e-16
emb|AV411180|AV411180 AV411180 *Lotus japonicus* young plants (two... 75 9e-16
emb|AW697936|AW697936 NXNV_072_C04_F Nsf Xylem Normal wood Verti... 42 1e-15
emb|AW692507|AW692507 NF052C09ST1F1000 Developing stem *Medicago* ... 60 2e-15
20 emb|AW685394|AW685394 NF028G11NR1F1000 Nodulated root *Medicago* t... 60 2e-15
emb|AI725103|AI725103 1002 PtIFG2 *Pinus taeda* cDNA clone 8942r, ... 54 3e-15
emb|AW133056|AW133056 se13g09.y1 Gm-c1013 *Glycine max* cDNA clone... 69 4e-15
emb|AW695422|AW695422 NF094F05ST1F1046 Developing stem *Medicago* ... 52 5e-15
emb|AW693273|AW693273 NF064A06ST1F1000 Developing stem *Medicago* ... 60 7e-15
25 emb|AI727564|AI727564 BNLGH18414 Six-day Cotton fiber *Gossypium* ... 66 1e-14
emb|AW254916|AW254916 ML134 peppermint glandular trichome *Mentha*... 67 3e-14
emb|AI166906|AI166906 xylem.est.692 Poplar xylem Lambda ZAPII li... 59 5e-14
emb|AW648535|AW648535 EST326989 tomato germinating seedlings, TA... 64 7e-14
emb|AW691201|AW691201 NF038H04ST1F1000 Developing stem *Medicago* ... 45 2e-13
30 emb|AW691254|AW691254 NF042G01ST1F1000 Developing stem *Medicago* ... 71 6e-13
emb|AI771903|AI771903 EST253003 tomato ovary, TAMU *Lycopersicon* ... 58 2e-12
emb|AW755537|AW755537 sl05b09.y1 Gm-c1036 *Glycine max* cDNA clone... 43 2e-12
emb|AW690391|AW690391 NF030B07ST1F1000 Developing stem *Medicago* ... 49 3e-12
gb|BE125956|BE125956 DG1_60_B12.b1_A002 Dark Grown 1 (DG1) *Sorgh*... 56 2e-11
35 emb|AW933549|AW933549 EST359308 tomato fruit mature green, TAMU ... 46 3e-11
emb|AW573921|AW573921 EST316512 GVN *Medicago truncatula* cDNA clo... 59 6e-11
emb|AV425214|AV425214 AV425214 *Lotus japonicus* young plants (two... 54 6e-11
emb|AW621185|AW621185 EST311983 tomato root during/after fruit s... 62 1e-10
emb|AW720132|AW720132 LjNEST14h12r *Lotus japonicus* nodule librar... 57 1e-10
40 emb|AW697024|AW697024 NF111E05ST1F1038 Developing stem *Medicago* ... 43 1e-10
emb|AI727398|AI727398 BNLGH17916 Six-day Cotton fiber *Gossypium* ... 66 2e-10
emb|AW317889|AW317889 sg58e01.y1 Gm-c1007 *Glycine max* cDNA clone... 64 2e-10
emb|AI773497|AI773497 EST254597 tomato resistant, Cornell *Lycopersicon*... 66 6e-10
emb|AI779047|AI779047 EST259926 tomato susceptible, Cornell *Lycopersicon*... 66 6e-10
45 emb|AW160290|AW160290 EST290148 *L. pennellii* trichome, Cornell U... 66 6e-10
emb|AW690159|AW690159 NF028E04ST1F1000 Developing stem *Medicago* ... 40 9e-10
emb|AW697130|AW697130 NF112E12ST1F1098 Developing stem *Medicago* ... 40 9e-10
emb|AA739537|AA739537 302 PtIFG2 *Pinus taeda* cDNA clone 8497M 3'... 57 9e-10
emb|AW934683|AW934683 EST353575 tomato flower buds 0-3 mm, Corne... 44 1e-09
50 emb|AW217676|AW217676 EST296390 tomato flower buds 8 mm to pre-a... 44 1e-09
gb|L47871|L47871 BNAF1521 Mustard flower buds *Brassica rapa* cDNA... 47 1e-09
emb|AI163871|AI163871 A050p31u Hybrid aspen plasmid library Popu... 59 1e-09
emb|AW728602|AW728602 GA_Ea0017E06 *Gossypium arboreum* 7-10 dpa ... 64 1e-09
emb|AW617945|AW617945 EST314019 *L. pennellii* trichome, Cornell U... 46 2e-09
55 emb|AW647996|AW647996 EST326450 tomato germinating seedlings, TA... 64 2e-09
emb|AW218271|AW218271 EST303452 tomato radicle, 5 d post-imbibit... 64 2e-09
emb|AI776062|AI776062 EST257162 tomato resistant, Cornell *Lycopersicon*... 64 2e-09
emb|AW036254|AW036254 EST278333 tomato seed, TAMU *Lycopersicon* e... 64 2e-09
emb|AW650814|AW650814 EST329268 tomato germinating seedlings, TA... 64 2e-09
60 emb|AI443133|AI443133 sa84g05.y1 Gm-c1004 *Glycine max* cDNA clone... 63 3e-09
emb|AW906997|AW906997 EST343224 potato stolon, Cornell Universit... 63 3e-09

emb|AI495275|AI495275 sb02h04.y1 Gm-c1004 Glycine max cDNA clone... 50 3e-09
 gb|BE053949|BE053949 GA__Ea0031D21f Gossypium arboreum 7-10 dpa ... 48 4e-09
 emb|AW730655|AW730655 GA__Ea0018A01 Gossypium arboreum 7-10 dpa ... 48 4e-09

5

Query= Novartis36_at 14146_at /id_source
 /description gb|aad25550.1|ac005850_7 (ac005850) hypothetical protein
 [arabidopsis thaliana] /blast_score 7.00e-26 /ec_number /family
 /chip nova /gb_link
 (507 letters)

10

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

20

emb|AV427887|AV427887 AV427887 Lotus japonicus young plants (two... 61 6e-17
 emb|AV419761|AV419761 AV419761 Lotus japonicus young plants (two... 56 1e-15
 emb|AI967590|AI967590 Ljimpest06-480-c9 Ljirnp Lambda HybriZap ... 68 2e-14
 emb|AW684644|AW684644 NF019C10NR1F1000 Nodulated root Medicago t... 62 9e-12
 gb|BE036389|BE036389 MO24B03 MO Mesembryanthemum crystallinum cD... 44 2e-06

25

gb|BE034652|BE034652 ML01E04 ML Mesembryanthemum crystallinum cD... 35 0.57
 emb|AC005308|AC005308 Plasmodium falciparum chromosome 12 clone ... 35 0.57
 gb|N60116|N60116 TgESTzy01b10.r1 TgRH Tachyzoite cDNA Toxoplasma... 34 0.78
 emb|AF161334|AF161334 Raphanus raphanistrum subsp. raphanistrum ... 33 1.5
 gb|L37356|PUMPAL3A Petroselinum crispum phenylalanine ammonia-ly... 33 2.0

30

emb|AI974840|AI974840 T113322e KV2 Medicago truncatula cDNA clon... 32 2.8
 gb|U36470|NCU36470 Neurospora crassa vacuolar ATPase 41 kDa subu... 32 2.8
 emb|AI938788|AI938788 sc60a05.y1 Gm-c1016 Glycine max cDNA clone... 32 2.8
 emb|AF114794|AF114794 Porphyra purpurea mitochondrion, complete ... 32 3.8
 emb|AI374339|AI374339 T6652 MVAT4 bloodstream form of serodeme W... 32 3.8

35

emb|AI374387|AI374387 T6725 MVAT4 bloodstream form of serodeme W... 32 3.8
 emb|AI374381|AI374381 T6716 MVAT4 bloodstream form of serodeme W... 32 3.8
 emb|AI894927|AI894927 EST264370 tomato callus, TAMU Lycopersicon... 31 5.2
 emb|AA550548|AA550548 1711m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 31 5.2
 emb|AJ223459|ANAJ3459 Aspergillus nidulans prnA gene. 31 5.2

40

emb|AJ390536|CAL390536 Candida albicans DNA, clone 222g9. 31 5.2
 emb|AW119888|AW119888 sd54b09.y1 Gm-c1016 Glycine max cDNA clone... 31 5.2
 emb|AI431203|AI431203 sa22f12.y2 Gm-c1006 Glycine max cDNA clone... 31 5.2
 emb|AF161331|AF161331 Sinapis arvensis S-locus related 1 (SLR1) ... 31 7.2
 emb|AF137311|AF137311 Miscanthus sinensis phytochrome B (PHYB) g... 31 7.2

45

gb|T36711|T36711 EST101701 S. cerevisiae strain X2180-1A Sacchar... 31 7.2
 emb|AW781868|AW781868 sl97g02.y1 Gm-c1027 Glycine max cDNA clone... 31 7.2
 emb|AW755482|AW755482 sl04e07.y1 Gm-c1036 Glycine max cDNA clone... 30 9.9
 emb|AW694935|AW694935 NF081F05ST1F1046 Developing stem Medicago ... 30 9.9
 emb|AZ215370|AZ215370 Sheared DNA-56C1.TF Sheared DNA Trypanosom... 30 9.9

50

emb|AQ945786|AQ945786 Sheared DNA-30C5.TR Sheared DNA Trypanosom... 30 9.9
 emb|AA739646|AA739646 411 PtIFG2 Pinus taeda cDNA clone 8694M 3'... 30 9.9
 emb|AL034353|SPBC1271 S.pombe chromosome II cosmid c1271. 30 9.9
 gb|N69599|N69599 TgESTzy41b11.r1 TgRH Tachyzoite cDNA Toxoplasma... 30 9.9

55

Query= Novartis38_at 14148_at /id_source
 /description gb|aaf34713.1|af224762_1 (af224762) siga binding protein
 [arabidopsis thaliana] /blast_score 4.00e-53 /ec_number /family
 /chip nova /gb_link
 (770 letters)

60

Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E
Sequences producing significant alignments: (bits) Value

	emb AW266797 AW266797 L48-136T3 Ice plant Lambda Uni-Zap XR expr...	59	5e-08
10	emb AI776331 AI776331 EST257431 tomato resistant, Cornell Lycopersicon...	51	8e-06
	emb AI938454 AI938454 sc45e10.y1 Gm-c1015 Glycine max cDNA clone...	44	0.001
	emb AF086822 AF086822 Candida boidinii dihydroxyacetone synthase...	36	0.38
	emb AV406828 AV406828 AV406828 Lotus japonicus young plants (two...	31	0.49
	emb AI731942 AI731942 BNLGH11450 Six-day Cotton fiber Gossypium...	35	0.71
15	emb AQ255443 AQ255443 mgxb0014I21r CUGI Rice Blast BAC Library P...	35	0.71
	emb AQ940346 AQ940346 Sheared DNA-33M2.TF Sheared DNA Trypanosoma...	34	1.3
	emb AI210373 AI210373 i0e05a1.r1 Aspergillus nidulans 24hr asexu...	34	1.8
	emb AQ935542 AQ935542 CpG2525A CpIOWAgDNA1 Cryptosporidium parvu...	33	2.5
	gb T18147 T18147 0722c3 czapPFd2.1, Debopam Chakrabarti Plasmodium...	33	2.5
20	emb AW651276 AW651276 EST329730 tomato germinating seedlings, TA...	33	3.5
	emb AI392128 AI392128 NCSM1B1T7 Subtracted Mycelial Neurospora c...	32	4.8
	emb AW330094 AW330094 TENU4840 T.cruzi epimastigote normalized c...	32	4.8
	emb AF055296 AF055296 Zantedeschia aethiopica geranylgeranyl red...	32	4.8
	emb AI725804 AI725804 BNLGH113200 Six-day Cotton fiber Gossypium...	32	4.8
25	emb AW686984 AW686984 NF004F11RT1F1094 Developing root Medicago ...	32	6.6
	emb AJ273808 AJ273808 AJ273808 Metarhizium anisopliae ARSEF 2575...	32	6.6
	emb AQ943530 AQ943530 Sheared DNA-42D24.TR Sheared DNA Trypanoso...	31	9.0
	emb AQ941987 AQ941987 Sheared DNA-42F7.TR Sheared DNA Trypanoso...	31	9.0
	emb AW620371 AW620371 sj04d01.y1 Gm-c1032 Glycine max cDNA clone...	31	9.0
30	emb AI973930 AI973930 sd13g08.y1 Gm-c1020 Glycine max cDNA clone...	31	9.0
	emb AF069470 AF069470 Phleum pratense group V allergen Phl p 5.0...	31	9.0
	emb AL160716 P406R Leishmania major Friedlin PAC P406 right end...	31	9.0
	emb AQ851400 AQ851400 LMAJFV1_lm40b04.y1 Leishmania major FV1 ra...	31	9.0
	emb AF061068 AF061068 Phleum pratense clone 10029 major allergen...	31	9.0
35	emb AQ953188 AQ953188 Sheared DNA-50B12.TF Sheared DNA Trypanoso...	31	9.0
	emb AW719942 AW719942 LjNEST12c6r Lotus japonicus nodule library...	31	9.0
	emb X74735 PPHLP5 P. pratense mRNA for PhlpV.	31	9.0
	emb AW396374 AW396374 sh27d05.y1 Gm-c1016 Glycine max cDNA clone...	31	9.0
	gb N60997 N60997 TgESTzy23f10.r1 TgRH Tachyzoite cDNA Toxoplasma...	31	9.0
40	emb AI164737 AI164737 A068P10U Hybrid aspen plasmid library Popu...	31	9.0
	emb AW348348 AW348348 GM210002A13A5R Gm-r1021 Glycine max cDNA 3...	26	9.5
	emb AW309665 AW309665 sf22g06.x1 Gm-c1028 Glycine max cDNA clone...	26	9.5
	emb AW310247 AW310247 sf33d01.x1 Gm-c1028 Glycine max cDNA clone...	26	9.5
	emb AW508196 AW508196 si50d10.y1 Gm-r1030 Glycine max cDNA clone...	27	9.6
45	emb AW102012 AW102012 sd81h10.y1 Gm-c1009 Glycine max cDNA clone...	26	9.8
	emb AW309166 AW309166 sg05b01.y1 Gm-c1019 Glycine max cDNA clone...	26	9.8
	emb AW598779 AW598779 sj46h06.y1 Gm-c1033 Glycine max cDNA clone...	26	9.8
	emb AW311252 AW311252 sg34d09.y1 Gm-c1025 Glycine max cDNA clone...	26	9.8

50

Query= Novartis73_at 14201_at /id_source
/description no hits found less than or equal to 1e-15. /blast_score
/ec_number /family /chip nova /gb_link
(430 letters)

55

Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

60

Score E

	Sequences producing significant alignments:	(bits)	Value
	emb AQ952678 AQ952678 Sheared DNA-48H20.TF Sheared DNA Trypanoso...	35	0.32
	emb AW698685 AW698685 R125 non-glandular-haired subtracted cDNA ...	32	1.4
5	emb AF061282 AF061282 Sorghum bicolor 22 kDa kafirin cluster.	31	5.6
	emb AL031854 SPBC337 S.pombe chromosome II cosmid c337.	31	5.6
	emb AC004709 AC004709 Plasmodium falciparum chromosome 12, *** S...	31	5.6
	emb AC006280 AC006280 Plasmodium falciparum chromosome 12 clone ...	31	5.6
	gb M74062 YSPCDC27A Schizosaccharomyces pombe cdc27+ gene, compl...	31	5.6
10	emb AQ947500 AQ947500 Sheared DNA-39L12.TF Sheared DNA Trypanoso...	31	5.6
	gb M83307 YSPCDC27B Schizosaccharomyces pombe cdc27+ mRNA, compl...	31	5.6
	emb AL031856 SPBC1734 S.pombe chromosome II cosmid c1734.	31	5.6
	emb AC073246 AC073246 Trypanosoma brucei chromosome II clone RPC...	30	7.7
	emb AL031535 SPCC16C4 S.pombe chromosome III cosmid c16C4.	30	7.7
15	emb AC012647 AC012647 Trypanosoma brucei chromosome II clone RPC...	30	7.7
	gb L28038 TRBKINCSBA Trypanosoma rangeli kinetoplast DNA sequenc...	30	7.7
	emb AB004322 AB004322 Nicotiana sylvestris NsPMT1 gene for putre...	30	7.7
	emb AQ941496 AQ941496 Sheared DNA-44O18.TF Sheared DNA Trypanoso...	30	7.7
	emb AQ946940 AQ946940 Sheared DNA-36C7.TF Sheared DNA Trypanosom...	30	7.7
20	emb AQ942433 AQ942433 Sheared DNA-45G7.TR Sheared DNA Trypanosom...	30	7.7
	emb AF133529 AF133529 Candida albicans mRNA cap methyltransferas...	30	7.7

25 Query= Novartis73_RC_at 14202_at /id_source
/description no hits found less than or equal to 1e-15.
/blast_score /ec_number /family /chip nova /gb_link
(430 letters)

30 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

	Sequences producing significant alignments:	Score	E	(bits)	Value
35	emb AQ952678 AQ952678 Sheared DNA-48H20.TF Sheared DNA Trypanoso...	35	0.32		
	emb AW698685 AW698685 R125 non-glandular-haired subtracted cDNA ...	32	1.4		
	emb AF061282 AF061282 Sorghum bicolor 22 kDa kafirin cluster.	31	5.6		
40	emb AL031854 SPBC337 S.pombe chromosome II cosmid c337.	31	5.6		
	emb AC004709 AC004709 Plasmodium falciparum chromosome 12, *** S...	31	5.6		
	emb AC006280 AC006280 Plasmodium falciparum chromosome 12 clone ...	31	5.6		
	gb M74062 YSPCDC27A Schizosaccharomyces pombe cdc27+ gene, compl...	31	5.6		
	emb AQ947500 AQ947500 Sheared DNA-39L12.TF Sheared DNA Trypanoso...	31	5.6		
45	gb M83307 YSPCDC27B Schizosaccharomyces pombe cdc27+ mRNA, compl...	31	5.6		
	emb AL031856 SPBC1734 S.pombe chromosome II cosmid c1734.	31	5.6		
	emb AC073246 AC073246 Trypanosoma brucei chromosome II clone RPC...	30	7.7		
	emb AL031535 SPCC16C4 S.pombe chromosome III cosmid c16C4.	30	7.7		
	emb AC012647 AC012647 Trypanosoma brucei chromosome II clone RPC...	30	7.7		
50	gb L28038 TRBKINCSBA Trypanosoma rangeli kinetoplast DNA sequenc...	30	7.7		
	emb AB004322 AB004322 Nicotiana sylvestris NsPMT1 gene for putre...	30	7.7		
	emb AQ941496 AQ941496 Sheared DNA-44O18.TF Sheared DNA Trypanoso...	30	7.7		
	emb AQ946940 AQ946940 Sheared DNA-36C7.TF Sheared DNA Trypanosom...	30	7.7		
	emb AQ942433 AQ942433 Sheared DNA-45G7.TR Sheared DNA Trypanosom...	30	7.7		
55	emb AF133529 AF133529 Candida albicans mRNA cap methyltransferas...	30	7.7		

60 Query= Novartis9_at 14223_at /id_source
/description emb|caa19683.1| (al024486) putative protein [arabidopsis
thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
(1761 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5 Searching.....done

		Score	E
	Sequences producing significant alignments:	(bits)	Value
10	emb AW745943 AW745943 WS1_38_H06.b1_A002 Water-stressed 1 (WS1) ...	240	3e-62
	gb BE023215 BE023215 sm70a04.y1 Gm-c1028 Glycine max cDNA clone ...	236	5e-61
	emb AW399343 AW399343 EST309843 L. pennellii trichome, Cornell U...	234	2e-60
	emb AW618318 AW618318 EST320304 L. pennellii trichome, Cornell U...	177	1e-53
	emb AW310982 AW310982 sg31b02.x1 Gm-c1024 Glycine max cDNA clone...	97	1e-51
15	emb AI442277 AI442277 sa66a04.y1 Gm-c1004 Glycine max cDNA clone...	200	2e-50
	emb AW687759 AW687759 NF013B05RT1F1044 Developing root Medicago ...	160	1e-46
	emb AW684122 AW684122 NF012F06NR1F1000 Nodulated root Medicago t...	83	2e-44
	emb AW309867 AW309867 sf25g10.x1 Gm-c1028 Glycine max cDNA clone...	89	5e-43
	gb BE020423 BE020423 sm40e08.y1 Gm-c1028 Glycine max cDNA clone ...	88	2e-39
20	emb AW691118 AW691118 NF041D08ST1F1000 Developing stem Medicago ...	78	2e-35
	emb AW160235 AW160235 EST290093 L. pennellii trichome, Cornell U...	120	6e-32
	emb AI960862 AI960862 sc91f07.y1 Gm-c1019 Glycine max cDNA clone...	74	5e-30
	emb AW349633 AW349633 GM210006A11B3R Gm-r1021 Glycine max cDNA 3...	89	8e-29
	emb AW775076 AW775076 EST334227 KV3 Medicago truncatula cDNA clo...	81	6e-26
25	gb BE020331 BE020331 sm40d08.y1 Gm-c1028 Glycine max cDNA clone ...	69	4e-23
	emb AW746031 AW746031 WS1_39_A03.b1_A002 Water-stressed 1 (WS1) ...	74	8e-23
	emb AW621546 AW621546 EST312344 tomato root during/after fruit s...	64	1e-13
	emb AW622846 AW622846 EST306916 tomato flower buds 3-8 mm, Come...	54	2e-12
	gb L43984 BLYBD Hordeum vulgare (clone ABG377) chromosome 3H STS...	69	8e-11
30	emb AW774216 AW774216 EST333367 KV3 Medicago truncatula cDNA clo...	69	1e-10
	emb AW774324 AW774324 EST333475 KV3 Medicago truncatula cDNA clo...	69	1e-10
	emb AW686169 AW686169 NF038H07NR1F1000 Nodulated root Medicago t...	68	2e-10
	emb AW160234 AW160234 EST290092 L. pennellii trichome, Cornell U...	46	2e-08
	emb AW685496 AW685496 NF030G02NR1F1000 Nodulated root Medicago t...	45	2e-07
35	emb AW684082 AW684082 NF011H08NR1F1000 Nodulated root Medicago t...	55	2e-06
	emb AW693839 AW693839 NF069F08ST1F1074 Developing stem Medicago ...	53	6e-06
	emb AI163659 AI163659 A046p04u Hybrid aspen plasmid library Popu...	53	6e-06
	emb AW033404 AW033404 EST276975 tomato callus, TAMU Lycopersicon...	49	1e-04
	emb AI054662 AI054662 coau0001K11 Cotton Boll Abscission Zone cD...	37	2e-04
40	emb AW758414 AW758414 874008A01.y1 C. reinhardtii CC-1690, Lambd...	41	0.022
	emb AW746188 AW746188 WS1_39_A03.g1_A002 Water-stressed 1 (WS1) ...	41	0.022
	emb Z99126 SPAC26H5 S.pombe chromosome I cosmid c26H5.	41	0.022
	emb AJ225805 EDKCHALPH Egeria densa mRNA for inward potassium ch...	39	0.14
	emb AI488725 AI488725 EST247064 tomato ovary, TAMU Lycopersicon ...	38	0.20
45	emb Z69731 SPAC6C3 S.pombe chromosome I cosmid c6C3.	36	0.71
	emb Z38061 SC9168 S.cerevisiae chromosome IX cosmid 9168.	36	0.71
	emb AW925349 AW925349 HVSMEG0001B12 Hordeum vulgare pre-anthesis...	36	0.71
	emb AW671585 AW671585 LG1_348_H11.b1_A002 Light Grown 1 (LG1) So...	36	0.97
	gb BE024935 BE024935 894007A03.x1 C. reinhardtii CC-1690, normal...	36	0.97
50	emb AW216501 AW216501 EST295215 tomato callus, TAMU Lycopersicon...	36	0.97
	emb AW680841 AW680841 WS1_7_E11.g1_A002 Water-stressed 1 (WS1) S...	35	1.3
	emb AQ911629 AQ911629 LMAJFV1_lm96c04.y1 Leishmania major FV1 ra...	35	1.3
	emb AW100578 AW100578 sd57b08.y1 Gm-c1008 Glycine max cDNA clone...	35	1.3
	emb AW010724 AW010724 ST11E02 Pine TriplEx shoot tip library Pin...	35	1.8
55	emb AL138854 SPAC23G3 S.pombe chromosome I cosmid c23G3.	35	2.5
	emb AW934681 AW934681 EST353573 tomato flower buds 0-3 mm, Come...	34	3.5
	emb Z98975 SPAC19E9 S.pombe chromosome I cosmid c19E9.	34	3.5
	emb AW690479 AW690479 NF035A03ST1F1000 Developing stem Medicago ...	34	3.5
	emb Z50142 SPAC2F7 S.pombe chromosome I cosmid c2F7.	34	3.5
60	emb AA728334 AA728334 LmLv39p7/70M Leishmania major promastigote...	34	4.8
	emb AI779448 AI779448 EST260327 tomato susceptible, Cornell Lyco...	34	4.8

	emb AQ639314 AQ639314 927P1-2A10.TV 927P1 Trypanosoma brucei gen...	34	4.8
	emb AW725460 AW725460 GA__Ea0018B02 Gossypium arboreum 7-10 dpa ...	34	4.8
	emb AW256577 AW256577 EST304714 KV2 Medicago truncatula cDNA clo...	34	4.8
	emb AW234006 AW234006 sf33a07.y1 Gm-c1028 Glycine max cDNA clone...	34	4.8
5	emb AW727061 AW727061 GA__Ea0011B08 Gossypium arboreum 7-10 dpa ...	34	4.8
	emb AZ221057 AZ221057 Sheared DNA-64F1.TR Sheared DNA Trypanosom...	34	4.8
	emb AI781303 AI781303 EST262182 tomato susceptible, Cornell Lyco...	34	4.8
	emb AA898817 AA898817 NCP3G4T7 Perithecial Neurospora crassa cDN...	34	4.8
	emb AI329539 AI329539 b6b04ne.fl Neurospora crassa evening cDNA ...	33	6.6
10	emb AW754602 AW754602 PC04B10 Pine TriplEx pollen cone library P...	33	6.6
	emb AL049181 PFMAL13P4 Plasmodium falciparum chromosome 13 strai...	33	6.6
	emb AW756307 AW756307 sl19a02.y1 Gm-c1036 Glycine max cDNA clone...	33	6.6
	emb AC004145 AC004145 Leishmania major chromosome 3 clone L5801 ...	33	6.6
	emb AI778201 AI778201 EST259080 tomato susceptible, Cornell Lyco...	33	9.0
15	emb AZ215585 AZ215585 Sheared DNA-74E7.TR Sheared DNA Trypanosom...	33	9.0
	emb AF216960 AF216960 Pichia pastoris strain GS115 Sec12 (SEC12)...	33	9.0
	emb AI896488 AI896488 EST265931 tomato callus, TAMU Lycopersicon...	33	9.0
	emb AW670919 AW670919 LG1_266_B11.b1_A002 Light Grown 1 (LG1) So...	33	9.0
	emb AQ842680 AQ842680 CpG1185B CpIOWAgDNA1 Cryptosporidium parvu...	33	9.0
20	emb AW982007 AW982007 PC23H10 Pine TriplEx pollen cone library P...	33	9.0
	gb U51030 YSCD9954 Saccharomyces cerevisiae chromosome IV cosmid...	33	9.0
	emb AQ988815 AQ988815 11E1D03NE.R1 C. parvum Lambda Zap Express ...	33	9.0
	emb AV419655 AV419655 AV419655 Lotus japonicus young plants (two...	33	9.0
	emb AQ023613 AQ023613 CpGR0073A Cryptosporidium parvum genomic r...	33	9.0
25	gb BE024936 BE024936 894007A03.y1 C. reinhardtii CC-1690, normal...	33	9.0
	gb L31407 YSCAKR Saccharomyces cerevisiae ankyrin repeat-contain...	33	9.0
	emb AQ648055 AQ648055 RPCI93-DpnII-30G1.TJ RPCI93-DpnII Trypanos...	33	9.0
	emb AQ641411 AQ641411 RPCI93-DpnII-28C15.TJ RPCI93-DpnII Trypano...	33	9.0
	emb AZ215288 AZ215288 Sheared DNA-83F7.TR Sheared DNA Trypanosom...	33	9.0
30	emb AW282605 AW282605 LG1_310_E08.gl_A002 Light Grown 1 (LG1) So...	29	9.8

Query= Novartis95_at 14232_at /id_source
/description gb|aaf16756.1|ac010155_9 (ac010155) f3m18.20 [arabidopsis
35 thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova
/gb_link /ncgi
(447 letters)

Database: plantfungal
40 661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	
45	Sequences producing significant alignments:	(bits)	Value	
	emb AV417327 AV417327 AV417327 Lotus japonicus young plants (two...	28	0.003	
	emb AV411846 AV411846 AV411846 Lotus japonicus young plants (two...	28	0.005	
	emb AV423458 AV423458 AV423458 Lotus japonicus young plants (two...	28	0.005	
50	emb AV422547 AV422547 AV422547 Lotus japonicus young plants (two...	28	0.006	
	emb AW706554 AW706554 sj58h12.y1 Gm-c1033 Glycine max cDNA clone...	28	0.010	
	emb AW508852 AW508852 si41b07.y1 Gm-r1030 Glycine max cDNA clone...	28	0.015	
	emb AW432586 AW432586 sh76d11.y1 Gm-c1015 Glycine max cDNA clone...	28	0.016	
	emb AI965714 AI965714 sc77f01.y1 Gm-c1018 Glycine max cDNA clone...	28	0.021	
55	emb AI930916 AI930916 sb44d12.y1 Gm-c1015 Glycine max cDNA clone...	28	0.031	
	emb AW100187 AW100187 sd26g01.y1 Gm-c1012 Glycine max cDNA clone...	26	0.031	
	emb AW153030 AW153030 se34a10.y1 Gm-c1015 Glycine max cDNA clone...	30	0.13	
	gb BE055645 BE055645 GA__Ea0021E15f Gossypium arboreum 7-10 dpa ...	33	0.19	
	gb U91857 SHU91857 Stylosanthes hamata ethylene-responsive eleme...	28	0.29	
60	emb AW329270 AW329270 N200490e rootphos(-) Medicago truncatula c...	29	0.33	
	emb X02873 DCEXTG Carrot gene for extensin.	35	0.34	

	gb M11221 DAREXTA Carrot (<i>D.carota</i>) extensin mRNA, partial cds.	35	0.47
	emb AW306694 AW306694 sf47b08.y1 Gm-c1009 Glycine max cDNA clone...	27	0.54
	emb AW035648 AW035648 EST281480 tomato callus, TAMU Lycopersicon...	28	0.57
	emb AW559374 AW559374 EST314422 DSIR Medicago truncatula cDNA cl...	27	0.59
5	emb AV411578 AV411578 AV411578 Lotus japonicus young plants (two...	26	0.68
	emb AW618112 AW618112 EST314162 L. pennellii trichome, Cornell U...	28	0.72
	emb AW164515 AW164515 se74g06.y1 Gm-c1023 Glycine max cDNA clone...	27	0.74
	emb AI900852 AI900852 sb95c05.y1 Gm-c1012 Glycine max cDNA clone...	27	0.75
	emb AW328989 AW328989 N200181e rootphos(-) Medicago truncatula c...	27	0.81
10	emb AV425804 AV425804 AV425804 Lotus japonicus young plants (two...	34	0.89
	emb AV427232 AV427232 AV427232 Lotus japonicus young plants (two...	34	0.89
	emb AI775562 AI775562 EST256662 tomato resistant, Cornell Lycopersicon...	28	1.2
	emb AW647824 AW647824 EST326278 tomato germinating seedlings, TA...	28	1.2
	emb AI486798 AI486798 EST245120 tomato ovary, TAMU Lycopersicon ...	28	1.3
15	emb AW568194 AW568194 si57g03.y1 Gm-r1030 Glycine max cDNA clone...	29	1.3
	emb AW031184 AW031184 EST274722 tomato callus, TAMU Lycopersicon...	28	1.3
	emb AW622531 AW622531 EST313331 tomato root during/after fruit s...	28	1.3
	dbj D38124 TOBBY4B Tobacco mRNA for EREBP-3, complete cds.	28	1.4
	emb AW695699 AW695699 NF097F03ST1F1029 Developing stem Medicago ...	31	1.4
20	emb AW186005 AW186005 se62d09.y1 Gm-c1019 Glycine max cDNA clone...	29	1.5
	emb AW306715 AW306715 sf47d10.y1 Gm-c1009 Glycine max cDNA clone...	28	1.6
	dbj D86853 D86853 Catharanthus roseus cyc15 mRNA for extensin, c...	33	1.7
	emb AW650803 AW650803 EST329257 tomato germinating seedlings, TA...	33	1.7
	emb X63339 SRENOD2 S.rostrata Enod2 gene for nodulin.	32	2.3
25	gb C95684 C95684 C95684 Marchantia polymorpha immature sex organ...	32	2.3
	gb M12865 YSCRSCATC Yeast (<i>S.cerevisiae</i>) CAT repetitive element,...	27	2.7
	emb AW040234 AW040234 EST282740 tomato mixed elicitor, BTI Lycopersicon...	28	3.0
	emb AW720424 AW720424 LjNEST22g2r Lotus japonicus nodule library...	32	3.2
	emb AW686730 AW686730 NF041H01NR1F1000 Nodulated root Medicago t...	32	3.2
30	emb AV412432 AV412432 AV412432 Lotus japonicus young plants (two...	26	3.2
	emb AV407890 AV407890 AV407890 Lotus japonicus young plants (two...	26	3.4
	gb U91982 SHU91982 Stylosanthes hamata EREBP-3 homolog mRNA, com...	28	3.5
	emb AV413265 AV413265 AV413265 Lotus japonicus young plants (two...	26	3.6
	gb U10398 YSCH9315 Saccharomyces cerevisiae chromosome VIII cosm...	27	3.6
35	emb AV412856 AV412856 AV412856 Lotus japonicus young plants (two...	26	3.7
	emb AV420682 AV420682 AV420682 Lotus japonicus young plants (two...	26	3.9
	emb AW099863 AW099863 sd17e06.y2 Gm-c1012 Glycine max cDNA clone...	27	3.9
	emb AV419065 AV419065 AV419065 Lotus japonicus young plants (two...	26	4.0
	emb AV413080 AV413080 AV413080 Lotus japonicus young plants (two...	26	4.0
40	emb AV425734 AV425734 AV425734 Lotus japonicus young plants (two...	26	4.3
	emb AV413154 AV413154 AV413154 Lotus japonicus young plants (two...	28	4.3
	emb AQ944381 AQ944381 Sheared DNA-53H12.TF Sheared DNA Trypanoso...	31	4.3
	emb AI166472 AI166472 xylem.est.300 Poplar xylem Lambda ZAPII li...	31	4.3
	emb AI495395 AI495395 sa97d11.y1 Gm-c1004 Glycine max cDNA clone...	25	4.9
45	emb AW278410 AW278410 sf43g05.y1 Gm-c1009 Glycine max cDNA clone...	25	5.0
	emb AV425829 AV425829 AV425829 Lotus japonicus young plants (two...	28	5.2
	emb AV414990 AV414990 AV414990 Lotus japonicus young plants (two...	28	5.2
	emb AV426605 AV426605 AV426605 Lotus japonicus young plants (two...	28	5.9
	emb AW722435 AW722435 b3b06nm.r1 Neurospora crassa morning cDNA ...	31	6.0
50	emb AW724180 AW724180 f4c08nm.r1 Neurospora crassa morning cDNA ...	31	6.0
	emb AV396007 AV396007 AV396007 Chlamydomonas reinhardtii C9 Chla...	31	6.0
	emb AA660373 AA660373 00246 MtRHE Medicago truncatula cDNA 5', m...	31	6.0
	emb AV395215 AV395215 AV395215 Chlamydomonas reinhardtii C9 Chla...	31	6.0
	emb AW720526 AW720526 LjNEST18f4r Lotus japonicus nodule library...	31	6.0
55	emb AW717057 AW717057 h6e06nm.r1 Neurospora crassa morning cDNA ...	31	6.0
	emb AW038232 AW038232 EST279889 tomato mixed elicitor, BTI Lycopersicon...	31	6.0
	emb AW234792 AW234792 sf19c08.y1 Gm-c1028 Glycine max cDNA clone...	31	6.0
	emb AV406499 AV406499 AV406499 Lotus japonicus young plants (two...	31	6.0
	emb AI900301 AI900301 sc03g01.y1 Gm-c1012 Glycine max cDNA clone...	31	6.0
60	emb AI487770 AI487770 EST246092 tomato ovary, TAMU Lycopersicon ...	28	6.6
	emb AA840807 AA840807 CFB53 Floral bud cDNA library of Hot peppe...	23	6.8

emb|AF056182|AF056182 Emericella nidulans G-protein beta subunit... 30 8.2
 emb|AC007862|AC007862 Trypanosoma brucei chromosome II clone RPC... 30 8.2
 emb|AC010851|AC010851 Leishmania major chromosome 22 clone L4134... 30 8.2
 emb|AW707173|AW707173 sk10f12.y1 Gm-c1023 Glycine max cDNA clone... 30 8.2
 5 emb|AW686992|AW686992 NF004G07RT1F1055 Developing root Medicago ... 30 8.2
 emb|AW618891|AW618891 EST320877 L. pennellii trichome, Cornell U... 30 8.2
 emb|AW507786|AW507786 si45a10.y1 Gm-r1030 Glycine max cDNA clone... 30 8.2
 emb|AQ910557|AQ910557 GSSTc05793 Trypanosome cruzi random genomi... 28 8.5
 emb|AW032140|AW032140 EST275594 tomato callus, TAMU Lycopersicon... 26 8.7
 10 emb|AW932239|AW932239 EST358082 tomato fruit mature green, TAMU ... 26 8.7
 emb|AW933044|AW933044 EST358887 tomato fruit mature green, TAMU ... 26 8.7
 emb|AW030545|AW030545 EST273800 tomato callus, TAMU Lycopersicon... 26 8.8
 emb|AW932961|AW932961 EST358804 tomato fruit mature green, TAMU ... 26 8.8

15
 Query= PAD3_at 14248_at /id_source genbank /description
 "gb|aad31062.1|ac007357_11 (ac007357) strong similarity to gb|x97864
 cytochrome p450 from arabidopsis thaliana and is a member of the
 pf|00067 cytochrome p450 family. ests gb|n65665, gb|t14112,
 20 gb|t76255, gb|t20906 and gb|ai100027 come from this gene."
 /blast_score 0 /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|pad3| /ncgi
 http://www.ncgr.org/cgi-bin/ff?pad3
 25 (1635 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

30 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

35 emb|AF029858|AF029858 Sorghum bicolor cytochrome P450 CYP71E1 (C... 220 e-104
 gb|M32885|AVOCYP Avocado cytochrome P-450LXXIA1 (cyp71A1) mRNA, ... 173 3e-89
 gb|BE054146|BE054146 GA__Ea0034H12f Gossypium arboreum 7-10 dpa ... 167 7e-50
 gb|L24438|THLCYP450A Thlaspi arvense germline cytochrome P450 mR... 144 2e-48
 emb|Z22545|PHFLAHYDB P.hybrida flavonoid 3',5'-hydroxylase mRNA. 77 9e-47
 40 dbj|D14588|PETHF1 Petunia hybrida Hfl mRNA for flavonoid-3',5'-h... 77 9e-47
 emb|Z22544|PHFLAHYDA P.hybrida flavonoid 3',5'-hydroxylase mRNA. 71 2e-44
 dbj|D85184|D85184 Gentiana triflora mRNA for flavonoid 3',5'-hyd... 85 8e-44
 emb|AW234222|AW234222 sf22f08.y1 Gm-c1028 Glycine max cDNA clone... 147 5e-43
 emb|Y09423|NRCYP71A5 Nepeta racemosa mRNA for cytochrome P450, C... 126 8e-40
 45 emb|AF122821|AF122821 Capsicum annuum cytochrome P450 (PepCYP) m... 127 2e-39
 gb|U48435|SCU48435 Solanum chacoense putative cytochrome P450 ge... 136 3e-39
 emb|AJ238612|CRO238612 Catharanthus roseus mRNA for cytochrome P... 135 3e-39
 emb|AF124815|AF124815 Mentha spicata cytochrome p450 mRNA, compl... 134 4e-39
 emb|AW053855|AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp... 130 9e-39
 50 gb|U48434|SCU48434 Solanum chacoense cytochrome P450 mRNA, compl... 124 2e-38
 emb|AW255799|AW255799 ML868 peppermint glandular trichome Mentha... 116 2e-38
 emb|AF124816|AF124816 Mentha x piperita cytochrome p450 isoform ... 123 1e-37
 emb|AF022460|AF022460 Glycine max cytochrome P450 monooxygenase ... 116 3e-37
 emb|AW349428|AW349428 GM210007A20E11R Gm-r1021 Glycine max cDNA ... 69 8e-37
 55 emb|X71658|SMCYPEG8 S.melongena CYP76A1 mRNA. 130 2e-36
 emb|AW830233|AW830233 sm24f03.y1 Gm-c1028 Glycine max cDNA clone... 110 2e-36
 emb|AW668053|AW668053 GA__Ea0012G23 Gossypium arboreum 7-10 dpa ... 129 3e-36
 emb|Z33875|CYMPCP450 M.piperita gene for cytochrome P-450 oxidase. 126 3e-36
 emb|AW690420|AW690420 NF033B04ST1F1000 Developing stem Medicago ... 79 5e-36
 60 emb|AF134590|AF134590 Papaver somniferum (S)-N-methylcoclaurine ... 140 2e-35
 emb|AW774664|AW774664 EST333815 KV3 Medicago truncatula cDNA clo... 144 6e-35

- emb|AF191772|AF191772 *Papaver somniferum* (S)-N-methylcoclaurine ... 138 8e-35
- emb|AW832405|AW832405 sm09e01.y1 Gm-c1027 Glycine max cDNA clone... 147 2e-34
- emb|AW432372|AW432372 sh73b04.y1 Gm-c1015 Glycine max cDNA clone... 147 3e-34
- emb|AF029856|AF029856 *Sorghum bicolor* cytochrome P450 CYP98A1 (C... 122 4e-34
- 5 emb|X70981|SMCYPEG2 *S.melongena* CYP71A1 mRNA for P450 hydroxylase. 119 7e-34
- emb|AF022157|AF022157 Glycine max cytochrome P450 monooxygenase ... 145 1e-33
- emb|AW156616|AW156616 se27f06.y1 Gm-c1015 Glycine max cDNA clone... 90 1e-33
- emb|AF107765|AF107765 *Prunus dulcis* cytochrome P450 (P450) gene,... 144 1e-33
- emb|Y09920|HT7EC0DET *Helianthus tuberosus* mRNA for 7-ethoxycouma... 117 2e-33
- 10 emb|Y10098|HTCYP76B1 *H.tuberosus* mRNA for 7-ethoxycoumarin O-dee... 117 2e-33
- emb|X71130|PHPET1 *P.hybrida* mRNA for P450 hydroxylase. 77 2e-33
- emb|AF166332|AF166332 *Nicotiana tabacum* cytochrome P450 gene, co... 127 2e-33
- emb|Y09424|NRCYP71A6 *N.racemosa* mRNA for cytochrome P450, CYP71A... 117 2e-33
- emb|AI895521|AI895521 EST264964 tomato callus, TAMU *Lycopersicon*... 142 7e-33
- 15 emb|AQ917284|AQ917284 T233265b *Medicago truncatula* BAC library M... 142 9e-33
- emb|AF022458|AF022458 Glycine max cytochrome P450 monooxygenase ... 115 2e-32
- emb|AF029857|AF029857 *Sorghum bicolor* cytochrome P450 CYP99A1 (C... 78 2e-32
- emb|X71654|SMCYP71B3 *S.melongena* CYP71A2 mRNA for hydroxylase. 115 3e-32
- dbj|D14990|POTCPEG4 Eggplant mRNA for cytochrome P-450EG4, compl... 115 3e-32
- 20 emb|AW310655|AW310655 sg22h01.x1 Gm-c1024 Glycine max cDNA clone... 140 3e-32
- emb|AF022459|AF022459 Glycine max cytochrome P450 monooxygenase ... 139 4e-32
- emb|AB028151|AB028151 *Antirrhinum majus* AFNS2 mRNA for cytochrom... 66 7e-32
- emb|AF150881|AF150881 *Lycopersicon esculentum* x *Lycopersicon per*... 78 3e-31
- emb|Y10493|GMC450CP7 *G.max* mRNA for putative cytochrome P450, cl... 137 3e-31
- 25 emb|AW569661|AW569661 si89h01.y1 Gm-c1031 Glycine max cDNA clone... 137 3e-31
- emb|AW569417|AW569417 si86h05.y1 Gm-c1031 Glycine max cDNA clone... 137 3e-31
- emb|AW676782|AW676782 DG1_14_D06.g1_A002 Dark Grown 1 (DG1) *Sorg*... 135 4e-31
- emb|AW677294|AW677294 DG1_5_H08.g1_A002 Dark Grown 1 (DG1) *Sorgh*... 136 4e-31
- emb|AW623139|AW623139 EST321084 tomato flower buds 3-8 mm, Corne... 117 5e-31
- 30 emb|AW256491|AW256491 EST304628 KV2 *Medicago truncatula* cDNA clo... 136 6e-31
- dbj|D86351|D86351 Glycine max CYP93A2 mRNA for cytochrome P-450,... 66 6e-31
- emb|AW922446|AW922446 DG1_19_F10.g1_A002 Dark Grown 1 (DG1) *Sorg*... 135 1e-30
- gb|U09610|U09610 *Berberis stolonifera* cytochrome P-450 CYP80 mRN... 125 2e-30
- emb|AW031613|AW031613 EST275067 tomato callus, TAMU *Lycopersicon*... 73 2e-30
- 35 emb|Y10490|GMC450CP3 *G.max* mRNA for putative cytochrome P450, cl... 133 3e-30
- emb|AF156976|AF156976 *Gerbera hybrida* flavone synthase II (CYP93... 63 3e-30
- emb|AW218579|AW218579 EST303762 tomato radicle, 5 d post-imbibit... 133 4e-30
- emb|AB028152|AB028152 *Torenia hybrida* TFNS5 mRNA for cytochrome ... 64 4e-30
- emb|AI489371|AI489371 EST247722 tomato ovary, TAMU *Lycopersicon* ... 111 6e-30
- 40 emb|AF000403|AF000403 *Lotus japonicus* putative cytochorome P450 ... 131 2e-29
- emb|AW394303|AW394303 sh31c01.y1 Gm-c1017 Glycine max cDNA clone... 130 3e-29
- emb|AW560246|AW560246 EST315294 DSIR *Medicago truncatula* cDNA cl... 130 3e-29
- emb|AW458764|AW458764 sh82d02.y1 Gm-c1016 Glycine max cDNA clone... 130 3e-29
- emb|AF135485|AF135485 Glycine max cytochrome P450 monooxygenaseC... 73 4e-29
- 45 emb|AF014800|AF014800 *Eschscholzia californica* (S)-N-methylcocla... 105 5e-29
- emb|AW923050|AW923050 DG1_48_G09.g1_A002 Dark Grown 1 (DG1) *Sorg*... 129 7e-29
- emb|AJ249799|CAR249799 *Cicer arietinum* partial mRNA for cytochro... 115 8e-29
- emb|AI938505|AI938505 sb46e03.y1 Gm-c1015 Glycine max cDNA clone... 128 9e-29
- emb|AW728587|AW728587 GA_Ea0017C12 *Gossypium arboreum* 7-10 dpa ... 101 1e-28
- 50 emb|AW922486|AW922486 DG1_19_B12.g1_A002 Dark Grown 1 (DG1) *Sorg*... 128 1e-28
- emb|AW759717|AW759717 sl47a12.y1 Gm-c1027 Glycine max cDNA clone... 127 2e-28
- emb|AF014801|AF014801 *Eschscholzia californica* (S)-N-methylcocla... 104 3e-28
- emb|AW278861|AW278861 sf99f08.y1 Gm-c1019 Glycine max cDNA clone... 126 4e-28
- emb|AF014802|AF014802 *Eschscholzia californica* (S)-N-methylcocla... 72 4e-28
- 55 emb|AI776223|AI776223 EST257323 tomato resistant, Cornell *Lycopersicon*... 126 6e-28
- emb|AW255421|AW255421 ML442 peppermint glandular trichome *Mentha*... 125 8e-28
- emb|AW256010|AW256010 MW364 peppermint glandular trichome *Mentha*... 125 8e-28
- emb|AW156752|AW156752 se30c09.y1 Gm-c1015 Glycine max cDNA clone... 125 8e-28
- emb|X70824|SMPEG1 *S.melongena* pEG1 mRNA for hydroxylase P450. 72 1e-27
- 60 dbj|E05111|E05111 cDNA encoding solanum flavonoid 3',5'-hydroxyg... 72 1e-27
- emb|AB006790|AB006790 *Petunia x hybrida* IMT-2 mRNA for cytochrom... 75 1e-27

emb|AW255848|AW255848 ML931 peppermint glandular trichome Mentha... 124 2e-27
emb|AW255619|AW255619 ML666 peppermint glandular trichome Mentha... 124 2e-27
emb|AW255274|AW255274 ML276 peppermint glandular trichome Mentha... 124 2e-27
emb|AF124817|AF124817 Mentha x piperita cytochrome p450 isoform ... 124 2e-27
5 emb|AW032343|AW032343 EST275797 tomato callus, TAMU Lycopersicon... 123 2e-27
emb|AI779370|AI779370 EST260249 tomato susceptible, Cornell Lyco... 105 2e-27
emb|AW255953|AW255953 MW299 peppermint glandular trichome Mentha... 123 3e-27
emb|AI988440|AI988440 sd02b09.y1 Gm-c1020 Glycine max cDNA clone... 123 3e-27
emb|AW038144|AW038144 EST279801 tomato mixed elicitor, BTI Lycop... 123 3e-27
10 emb|Y10489|GMC450CP1 G.max mRNA for putative cytochrome P450, cl... 123 3e-27
emb|AW255346|AW255346 ML357 peppermint glandular trichome Mentha... 123 4e-27
emb|AF139532|AF139532 Liquidambar styraciflua aldehyde 5-hydroxy... 78 5e-27

15 Query= PAD4_i_at 14249_i_at /id_source genbank /description
emb|cab43438.1| (al050300) putative protein [arabidopsis thaliana]
/blast_score 0 /ec_number /family /chip nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|pad4| /ncgi
20 http://www.ncgr.org/cgi-bin/ff?pad4
(1732 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

25 Searching.....done

Score E
Sequences producing significant alignments: (bits) Value

30 emb|AW981483|AW981483 EST392636 DSIL Medicago truncatula cDNA cl... 126 8e-59
emb|AW684289|AW684289 NF015A11NR1F1000 Nodulated root Medicago t... 124 5e-37
emb|AW032082|AW032082 EST275536 tomato callus, TAMU Lycopersicon... 112 2e-29
emb|AI781175|AI781175 EST262054 tomato susceptible, Cornell Lyco... 62 4e-24
35 emb|AW011208|AW011208 ST18A05 Pine TriplEx shoot tip library Pin... 107 2e-23
emb|AW225676|AW225676 ST70B12 Pine TriplEx shoot tip library Pin... 95 2e-20
emb|AV423915|AV423915 AV423915 Lotus japonicus young plants (two... 98 6e-20
emb|AI778594|AI778594 EST259473 tomato susceptible, Cornell Lyco... 95 2e-19
emb|AW032676|AW032676 EST276235 tomato callus, TAMU Lycopersicon... 95 2e-19
40 emb|AW559251|AW559251 EST306087 DSIR Medicago truncatula cDNA cl... 97 4e-19
emb|AW774727|AW774727 EST333878 KV3 Medicago truncatula cDNA clo... 97 4e-19
emb|AW707128|AW707128 sk10a03.y1 Gm-c1023 Glycine max cDNA clone... 58 4e-17
emb|AW560897|AW560897 EST315945 DSIR Medicago truncatula cDNA cl... 73 1e-16
emb|AW257406|AW257406 EST305543 KV2 Medicago truncatula cDNA clo... 73 1e-16
45 emb|AW685948|AW685948 NF036G07NR1F1000 Nodulated root Medicago t... 73 1e-16
emb|AW698315|AW698315 NXNV_071_G01_F Nsf Xylem Normal wood Verti... 75 3e-16
emb|AZ051219|AZ051219 Gm_UMb001_062_F16R UMN Soybean BAC Library... 55 2e-15
emb|AW587665|AW587665 ST63B10 Pine TriplEx shoot tip library Pin... 78 2e-15
emb|AW217058|AW217058 EST295772 tomato callus, TAMU Lycopersicon... 71 2e-15
50 emb|AW888098|AW888098 NXNV_108_F09_F Nsf Xylem Normal wood Verti... 72 1e-14
emb|AW560122|AW560122 EST315170 DSIR Medicago truncatula cDNA cl... 51 4e-14
emb|AW980840|AW980840 EST391993 GVN Medicago truncatula cDNA clo... 51 4e-14
emb|AW560121|AW560121 EST315169 DSIR Medicago truncatula cDNA cl... 51 7e-14
emb|AI920196|AI920196 1726 Pine Lambda Zap Xylem library Pinus t... 59 1e-13
55 emb|AW559836|AW559836 EST314884 DSIR Medicago truncatula cDNA cl... 78 2e-13
emb|AW290408|AW290408 NXNV019H08F Nsf Xylem Normal wood Vertical... 73 3e-13
gb|BE049795|BE049795 NXNV_144_C08_F Nsf Xylem Normal wood Vertic... 52 7e-13
emb|AW687647|AW687647 NF011F10RT1F1090 Developing root Medicago ... 51 9e-13
emb|AW687408|AW687408 NF009C08RT1F1065 Developing root Medicago ... 49 2e-10
60 emb|AW870069|AW870069 NXNV_123_G03_F Nsf Xylem Normal wood Verti... 58 2e-10
emb|AI855891|AI855891 sc30h08.y1 Gm-c1014 Glycine max cDNA clone... 58 1e-09

	emb AW349142 AW349142 GM210003B22H5R Gm-r1021 Glycine max cDNA 3...	57	3e-09
	emb AW065112 AW065112 ST39G09 Pine TriplEx shoot tip library Pin...	62	1e-08
	emb AW736866 AW736866 NXNV_083_H05_F Nsf Xylem Normal wood Verti...	52	2e-08
	emb AW685287 AW685287 NF027B11NR1F1000 Nodulated root Medicago t...	46	4e-08
5	emb AW031593 AW031593 EST275047 tomato callus, TAMU Lycopersicon...	35	2e-07
	emb AW560074 AW560074 EST315122 DSIR Medicago truncatula cDNA cl...	48	5e-07
	emb AW773999 AW773999 EST332985 KV3 Medicago truncatula cDNA clo...	51	5e-07
	emb AW704685 AW704685 sk39c02.y1 Gm-cl028 Glycine max cDNA clone...	39	5e-07
	gb BE123705 BE123705 NXNV_151_H02_F Nsf Xylem Normal wood Vertic...	53	1e-06
10	emb AW349364 AW349364 GM210004B12G1R Gm-r1021 Glycine max cDNA 3...	56	1e-06
	emb AW560073 AW560073 EST315121 DSIR Medicago truncatula cDNA cl...	46	1e-06
	emb AW432244 AW432244 sh71a11.y1 Gm-cl015 Glycine max cDNA clone...	52	2e-06
	emb AW773847 AW773847 EST332833 KV3 Medicago truncatula cDNA clo...	39	4e-06
	emb AW694970 AW694970 NF082B02ST1F1015 Developing stem Medicago ...	37	8e-06
15	emb AW687653 AW687653 NF011G04RT1F1035 Developing root Medicago ...	49	1e-04
	emb AI416889 AI416889 sa19d09.x1 Gm-cl005 Glycine max cDNA clone...	49	1e-04
	emb AW438038 AW438038 ST83G07 Pine TriplEx shoot tip library Pin...	49	1e-04
	emb AI780239 AI780239 EST261118 tomato susceptible, Cornell Lyco...	34	4e-04
	emb AW985058 AW985058 NXNV_130_D03_F Nsf Xylem Normal wood Verti...	31	7e-04
20	emb AZ214023 AZ214023 Sheared DNA-77H11.TF Sheared DNA Trypanoso...	46	9e-04
	emb AZ214029 AZ214029 Sheared DNA-77H12.TF Sheared DNA Trypanoso...	46	0.001
	emb AW933515 AW933515 EST359274 tomato fruit mature green, TAMU ...	32	0.003
	emb AZ213147 AZ213147 Sheared DNA-96E11.TR Sheared DNA Trypanoso...	36	0.003
	emb AW616497 AW616497 EST322908 L. hirsutum trichome, Cornell Un...	35	0.004
25	emb AW870252 AW870252 NXNV_128_C06_F Nsf Xylem Normal wood Verti...	44	0.004
	emb AW687535 AW687535 NF010F08RT1F1074 Developing root Medicago ...	43	0.006
	gb BE123796 BE123796 NXNV_156_E06_F Nsf Xylem Normal wood Vertic...	31	0.006
	emb AW618666 AW618666 EST320652 L. pennellii trichome, Cornell U...	33	0.009
	emb AW317531 AW317531 sg51e11.y1 Gm-cl025 Glycine max cDNA clone...	41	0.013
30	emb AW686129 AW686129 NF033H12NR1F1000 Nodulated root Medicago t...	32	0.023
	emb AV417662 AV417662 AV417662 Lotus japonicus young plants (two...	30	0.025
	emb AW010126 AW010126 ST02C06 Pine TriplEx shoot tip library Pin...	41	0.029
	emb AW686977 AW686977 NF004F04RT1F1042 Developing root Medicago ...	33	0.031
	emb AW329638 AW329638 N200899e rootphos(-) Medicago truncatula c...	40	0.075
35	emb AW687805 AW687805 NF013F08RT1F1074 Developing root Medicago ...	32	0.14
	emb AW775153 AW775153 EST334304 KV3 Medicago truncatula cDNA clo...	29	0.14
	emb AI812757 AI812757 18G10 Pine Lambda Zap Xylem library Pinus ...	39	0.14
	emb AW774485 AW774485 EST333636 KV3 Medicago truncatula cDNA clo...	39	0.14
	emb AW693919 AW693919 NF070E05ST1F1038 Developing stem Medicago ...	39	0.14
40	emb AW685575 AW685575 NF029B05NR1F1000 Nodulated root Medicago t...	39	0.14
	emb AW705444 AW705444 sk49b08.y1 Gm-cl019 Glycine max cDNA clone...	39	0.14
	emb AW695353 AW695353 NF094C07ST1F1053 Developing stem Medicago ...	39	0.14
	emb AW257266 AW257266 EST305403 KV2 Medicago truncatula cDNA clo...	39	0.14
	emb AW934555 AW934555 EST353447 tomato flower buds 0-3 mm, Corne...	38	0.27
45	emb AW307176 AW307176 sf53g04.y1 Gm-cl009 Glycine max cDNA clone...	31	0.36
	emb AL031525 SPCC1682 S.pombe chromosome III cosmid c1682.	37	0.51
	emb AW698283 AW698283 NXNV_071_C12_F Nsf Xylem Normal wood Verti...	28	0.66
	emb AW698011 AW698011 NXNV_079_E11_F Nsf Xylem Normal wood Verti...	29	0.88
	emb AW693913 AW693913 NF070E02ST1F1017 Developing stem Medicago ...	36	0.96
50	emb AW686305 AW686305 NF036D07NR1F1000 Nodulated root Medicago t...	36	0.96
	emb AW685079 AW685079 NF024H05NR1F1000 Nodulated root Medicago t...	36	0.96
	emb AW043221 AW043221 ST30G04 Pine TriplEx shoot tip library Pin...	36	0.96
	emb AF127256 AF127256 Laureliopsis philippiana rpl16 gene, chlor...	35	1.8
	emb AF127255 AF127255 Laurelia sempervirens rpl16 gene, chloropl...	35	1.8
55	emb AF127257 AF127257 Nemuaron vieillardii rpl16 gene, chloropla...	35	1.8
	emb AW508953 AW508953 si38d01.y1 Gm-r1030 Glycine max cDNA clone...	28	2.1
	emb AW719424 AW719424 LjNEST4d11r Lotus japonicus nodule library...	28	2.1
	emb AW032864 AW032864 EST276423 tomato callus, TAMU Lycopersicon...	29	2.1
	emb AW306559 AW306559 se52d10.y1 Gm-cl017 Glycine max cDNA clone...	35	2.5
60	emb AI399344 AI399344 NCW01D11T7 Westergaards Neurospora crassa ...	35	2.5
	emb AI485040 AI485040 EST243320 tomato ovary, TAMU Lycopersicon ...	34	3.4

emb|Z49212|SC9952X *S.cerevisiae* chromosome XIII cosmid 9952. 34 3.4
emb|AA741585|AA741585 *LmLv39p3/132B* *Leishmania major* promastigot... 34 3.4
emb|X81715|SCMDYGENE *S.cerevisiae* partial MDY gene. 34 3.4
emb|X73956|TBMAP292 *T.brucei* Tb-292 mRNA for membrane associated... 34 3.4
5 emb|AZ212769|AZ212769 Sheared DNA-66C3.TR Sheared DNA *Trypanosom...* 34 3.4
emb|X82612|SCATM1 *S.cerevisiae* ATM1 gene. 34 3.4
emb|AC005139|AC005139 *Plasmodium falciparum* chromosome 12, *** S... 34 4.7
emb|AA649446|AA649446 T4369 MVAT4 bloodstream form of serodeme W... 34 4.7

10
Query= PAD4_r_at 14250_r_at /id_source genbank /description
emb|cab43438.1| (al050300) putative protein [*arabidopsis thaliana*]
/blast_score 0 /ec_number /family /chip nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-
15 post/entrez/query?db=n&form=6&dopt=g&uid=gb|pad4|/ncgi
http://www.ncgr.org/cgi-bin/ff?pad4
(1732 letters)

20 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
25 Sequences producing significant alignments: (bits) Value

emb|AW981483|AW981483 EST392636 *DSIL* *Medicago truncatula* cDNA cl... 126 8e-59
emb|AW684289|AW684289 NF015A11NR1F1000 *Nodulated root* *Medicago t...* 124 5e-37
emb|AW032082|AW032082 EST275536 tomato callus, TAMU *Lycopersicon...* 112 2e-29
30 emb|AI781175|AI781175 EST262054 tomato susceptible, Cornell Lyco... 62 4e-24
emb|AW011208|AW011208 ST18A05 Pine TriplEx shoot tip library Pin... 107 2e-23
emb|AW225676|AW225676 ST70B12 Pine TriplEx shoot tip library Pin... 95 2e-20
emb|AV423915|AV423915 AV423915 *Lotus japonicus* young plants (two... 98 6e-20
emb|AI778594|AI778594 EST259473 tomato susceptible, Cornell Lyco... 95 2e-19
35 emb|AW032676|AW032676 EST276235 tomato callus, TAMU *Lycopersicon...* 95 2e-19
emb|AW559251|AW559251 EST306087 *DSIR* *Medicago truncatula* cDNA cl... 97 4e-19
emb|AW774727|AW774727 EST333878 KV3 *Medicago truncatula* cDNA clo... 97 4e-19
emb|AW707128|AW707128 sk10a03.y1 *Gm-c1023* *Glycine max* cDNA clone... 58 4e-17
emb|AW560897|AW560897 EST315945 *DSIR* *Medicago truncatula* cDNA cl... 73 1e-16
40 emb|AW257406|AW257406 EST305543 KV2 *Medicago truncatula* cDNA clo... 73 1e-16
emb|AW685948|AW685948 NF036G07NR1F1000 *Nodulated root* *Medicago t...* 73 1e-16
emb|AW698315|AW698315 NXNV_071_G01_F Nsf Xylem Normal wood Verti... 75 3e-16
emb|AZ051219|AZ051219 *Gm_UMb001_062_F16R* *UMN Soybean BAC Library...* 55 2e-15
emb|AW587665|AW587665 ST63B10 Pine TriplEx shoot tip library Pin... 78 2e-15
45 emb|AW217058|AW217058 EST295772 tomato callus, TAMU *Lycopersicon...* 71 2e-15
emb|AW888098|AW888098 NXNV_108_F09_F Nsf Xylem Normal wood Verti... 72 1e-14
emb|AW560122|AW560122 EST315170 *DSIR* *Medicago truncatula* cDNA cl... 51 4e-14
emb|AW980840|AW980840 EST391993 GVN *Medicago truncatula* cDNA clo... 51 4e-14
emb|AW560121|AW560121 EST315169 *DSIR* *Medicago truncatula* cDNA cl... 51 7e-14
50 emb|AI920196|AI920196 1726 Pine Lambda Zap Xylem library *Pinus t...* 59 1e-13
emb|AW559836|AW559836 EST314884 *DSIR* *Medicago truncatula* cDNA cl... 78 2e-13
emb|AW290408|AW290408 NXNV019H08F Nsf Xylem Normal wood Vertical... 73 3e-13
gb|BE049795|BE049795 NXNV_144_C08_F Nsf Xylem Normal wood Vertic... 52 7e-13
emb|AW687647|AW687647 NF011F10RT1F1090 Developing root *Medicago ...* 51 9e-13
55 emb|AW687408|AW687408 NF009C08RT1F1065 Developing root *Medicago ...* 49 2e-10
emb|AW870069|AW870069 NXNV_123_G03_F Nsf Xylem Normal wood Verti... 58 2e-10
emb|AI855891|AI855891 sc30h08.y1 *Gm-c1014* *Glycine max* cDNA clone... 58 1e-09
emb|AW349142|AW349142 GM210003B22H5R *Gm-r1021* *Glycine max* cDNA 3... 57 3e-09
emb|AW065112|AW065112 ST39G09 Pine TriplEx shoot tip library Pin... 62 1e-08
60 emb|AW736866|AW736866 NXNV_083_H05_F Nsf Xylem Normal wood Verti... 52 2e-08
emb|AW685287|AW685287 NF027B11NR1F1000 *Nodulated root* *Medicago t...* 46 4e-08

	emb AW031593 AW031593 EST275047 tomato callus, TAMU Lycopersicon...	35	2e-07
	emb AW560074 AW560074 EST315122 DSIR Medicago truncatula cDNA cl...	48	5e-07
	emb AW773999 AW773999 EST332985 KV3 Medicago truncatula cDNA clo...	51	5e-07
	emb AW704685 AW704685 sk39c02.y1 Gm-c1028 Glycine max cDNA clone...	39	5e-07
5	gb BE123705 BE123705 NXNV_151_H02_F Nsf Xylem Normal wood Vertic...	53	1e-06
	emb AW349364 AW349364 GM210004B12G1R Gm-r1021 Glycine max cDNA 3...	56	1e-06
	emb AW560073 AW560073 EST315121 DSIR Medicago truncatula cDNA cl...	46	1e-06
	emb AW432244 AW432244 sh71a11.y1 Gm-c1015 Glycine max cDNA clone...	52	2e-06
	emb AW773847 AW773847 EST332833 KV3 Medicago truncatula cDNA clo...	39	4e-06
10	emb AW694970 AW694970 NF082B02ST1F1015 Developing stem Medicago ...	37	8e-06
	emb AW687653 AW687653 NF011G04RT1F1035 Developing root Medicago ...	49	1e-04
	emb AI416889 AI416889 sa19d09.x1 Gm-c1005 Glycine max cDNA clone...	49	1e-04
	emb AW438038 AW438038 ST83G07 Pine TriplEx shoot tip library Pin...	49	1e-04
	emb AI780239 AI780239 EST261118 tomato susceptible, Cornell Lyco...	34	4e-04
15	emb AW985058 AW985058 NXNV_130_D03_F Nsf Xylem Normal wood Verti...	31	7e-04
	emb AZ214023 AZ214023 Sheared DNA-77H11.TF Sheared DNA Trypanoso...	46	9e-04
	emb AZ214029 AZ214029 Sheared DNA-77H12.TF Sheared DNA Trypanoso...	46	0.001
	emb AW933515 AW933515 EST359274 tomato fruit mature green, TAMU ...	32	0.003
	emb AZ213147 AZ213147 Sheared DNA-96E11.TR Sheared DNA Trypanoso...	36	0.003
20	emb AW616497 AW616497 EST322908 L. hirsutum trichome, Cornell Un...	35	0.004
	emb AW870252 AW870252 NXNV_128_C06_F Nsf Xylem Normal wood Verti...	44	0.004
	emb AW687535 AW687535 NF010F08RT1F1074 Developing root Medicago ...	43	0.006
	gb BE123796 BE123796 NXNV_156_E06_F Nsf Xylem Normal wood Vertic...	31	0.006
	emb AW618666 AW618666 EST320652 L. pennellii trichome, Cornell U...	33	0.009
25	emb AW317531 AW317531 sg51e11.y1 Gm-c1025 Glycine max cDNA clone...	41	0.013
	emb AW686129 AW686129 NF033H12NR1F1000 Nodulated root Medicago t...	32	0.023
	emb AV417662 AV417662 AV417662 Lotus japonicus young plants (two...	30	0.025
	emb AW010126 AW010126 ST02C06 Pine TriplEx shoot tip library Pin...	41	0.029
	emb AW686977 AW686977 NF004F04RT1F1042 Developing root Medicago ...	33	0.031
30	emb AW329638 AW329638 N200899e rootphos(-) Medicago truncatula c...	40	0.075
	emb AW687805 AW687805 NF013F08RT1F1074 Developing root Medicago ...	32	0.14
	emb AW775153 AW775153 EST334304 KV3 Medicago truncatula cDNA clo...	29	0.14
	emb AI812757 AI812757 18G10 Pine Lambda Zap Xylem library Pinus ...	39	0.14
	emb AW774485 AW774485 EST333636 KV3 Medicago truncatula cDNA clo...	39	0.14
35	emb AW693919 AW693919 NF070E05ST1F1038 Developing stem Medicago ...	39	0.14
	emb AW685575 AW685575 NF029B05NR1F1000 Nodulated root Medicago t...	39	0.14
	emb AW705444 AW705444 sk49b08.y1 Gm-c1019 Glycine max cDNA clone...	39	0.14
	emb AW695353 AW695353 NF094C07ST1F1053 Developing stem Medicago ...	39	0.14
	emb AW257266 AW257266 EST305403 KV2 Medicago truncatula cDNA clo...	39	0.14
40	emb AW934555 AW934555 EST353447 tomato flower buds 0-3 mm, Corne...	38	0.27
	emb AW307176 AW307176 sf53g04.y1 Gm-c1009 Glycine max cDNA clone...	31	0.36
	emb AL031525 SPCC1682 S.pombe chromosome III cosmid c1682.	37	0.51
	emb AW698283 AW698283 NXNV_071_C12_F Nsf Xylem Normal wood Verti...	28	0.66
	emb AW698011 AW698011 NXNV_079_E11_F Nsf Xylem Normal wood Verti...	29	0.88
45	emb AW693913 AW693913 NF070E02ST1F1017 Developing stem Medicago ...	36	0.96
	emb AW686305 AW686305 NF036D07NR1F1000 Nodulated root Medicago t...	36	0.96
	emb AW685079 AW685079 NF024H05NR1F1000 Nodulated root Medicago t...	36	0.96
	emb AW043221 AW043221 ST30G04 Pine TriplEx shoot tip library Pin...	36	0.96
	emb AF127256 AF127256 Laureliopsis philippiana rpl16 gene, chlor...	35	1.8
50	emb AF127255 AF127255 Laurelia sempervirens rpl16 gene, chloropl...	35	1.8
	emb AF127257 AF127257 Nemuaron vieillardii rpl16 gene, chloropla...	35	1.8
	emb AW508953 AW508953 si38d01.y1 Gm-r1030 Glycine max cDNA clone...	28	2.1
	emb AW719424 AW719424 LjNEST4d11r Lotus japonicus nodule library...	28	2.1
	emb AW032864 AW032864 EST276423 tomato callus, TAMU Lycopersicon...	29	2.1
55	emb AW306559 AW306559 se52d10.y1 Gm-c1017 Glycine max cDNA clone...	35	2.5
	emb AI399344 AI399344 NCW01D11T7 Westergaards Neurospora crassa ...	35	2.5
	emb AI485040 AI485040 EST243320 tomato ovary, TAMU Lycopersicon ...	34	3.4
	emb Z49212 SC9952X S.cerevisiae chromosome XIII cosmid 9952.	34	3.4
	emb AA741585 AA741585 LmLv39p3/132B Leishmania major promastigot...	34	3.4
60	emb X81715 SCMDYGENE S.cerevisiae partial MDY gene.	34	3.4
	emb X73956 TBMAP292 T.brucei Tb-292 mRNA for membrane associated...	34	3.4

emb|AZ212769|AZ212769 Sheared DNA-66C3.TR Sheared DNA Trypanosom... 34 3.4
 emb|X82612|SCATM1 S.cerevisiae ATM1 gene. 34 3.4
 emb|AC005139|AC005139 Plasmodium falciparum chromosome 12, *** S... 34 4.7
 emb|AA649446|AA649446 T4369 MVAT4 bloodstream form of serodeme W... 34 4.7

5

Query= PAL1-mRNA_s_at 14254_s_at /id_source genbank /description
 gb|aad18156.2| (ac006260) phenylalanine ammonia lyase (pal1)
 [arabidopsis /blast_score 1.00e-134 /ec_number /family /chip nova
 /gb_link /ncgi
 (848 letters)

10

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

20

emb|AF036948|AF036948 Prunus avium phenylalanine ammonia-lyase (... 419 e-115
 emb|AJ002221|DLJ002221 Digitalis lanata mRNA for phenylalanine a... 412 e-113
 dbj|D83076|D83076 Lithospermum erythrorhizon mRNA for phenylalan... 411 e-113
 dbj|D83075|D83075 Lithospermum erythrorhizon mRNA for phenylalan... 408 e-112
 25 emb|Y12461|HAPHAMLY Helianthus annuus mRNA for phenylalanine amm... 331 e-112
 emb|AF237955|AF237955 Rubus idaeus phenylalanine ammonia-lyase 2... 407 e-112
 gb|M29232|IPBPAL Sweet potato phenylalanine ammonia-lyase mRNA (... 407 e-112
 emb|AB042520|AB042520 Catharanthus roseus mRNA for phenylalanine... 328 e-111
 gb|L36822|SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas... 403 e-111
 30 dbj|D26596|CMEPAL Camellia sinensis mRNA for phenylalanine ammon... 403 e-111
 emb|X58180|MSPAL M.sativa PAL mRNA for phenylalanine ammonia-lyase. 398 e-109
 gb|L11747|POPPALGA Populus tricarpha X Populus deltoides (hybri... 318 e-109
 gb|U43338|CLU43338 Citrus limon phenylalanine ammonia-lyase (pal... 396 e-109
 emb|AF237954|AF237954 Rubus idaeus phenylalanine ammonia-lyase 1... 395 e-108
 35 emb|X17462|PCPAL4 P.crispum RNA for PAL4, phenylalanine ammonia-... 319 e-108
 emb|X78269|NTPHEAL N.tabacum (Samsun NN) mRNA for phenylalanine ... 312 e-106
 dbj|D17467|TOBPAL1 Tobacco mRNA for phenylalanine ammonia-lyase,... 312 e-105
 emb|AJ250836|CAR250836 Cicer arietinum mRNA for phenylalanine am... 373 e-102
 emb|X81159|PCPAL3 P.crispum mRNA for phenylalanine ammonia-lyase 3. 174 e-102
 40 emb|X81158|PCPAL2 P.crispum mRNA for phenylalanine ammonia-lyase 2. 173 e-101
 emb|X99997|BFPAL B.finlaysoniana mRNA for phenylalanine ammonia-... 214 2e-95
 emb|AW667320|AW667320 GA__Ea0008P06 Gossypium arboreum 7-10 dpa ... 349 8e-95
 dbj|E04042|E04042 cDNA sequence coding for pea phenylalanine amm... 347 3e-94
 dbj|D10001|PEAPAL P.sativum mRNA for phenylalanine ammonia-lyase... 347 3e-94
 45 dbj|D78640|IPBPALA Ipomoea batatas mRNA for phenylalanine ammoni... 291 3e-94
 emb|AJ238754|CCL238754 Citrus clementina X Citrus reticulata mRN... 314 3e-91
 emb|AW220322|AW220322 EST302805 tomato root during/after fruit s... 326 6e-88
 emb|AW725857|AW725857 GA__Ea0019022 Gossypium arboreum 7-10 dpa ... 319 9e-86
 emb|AJ238753|CCL238753 Citrus clementina X Citrus reticulata mRN... 319 1e-85
 50 dbj|D10003|PEAPAL2 P.sativum gene for phenylalanine ammonia-lyas... 220 2e-85
 emb|Z49147|HVPAL7RM H.vulgare partial PAL mRNA for phenylalanine... 154 5e-85
 gb|U16130|PAU16130 Persea americana phenylalanine ammonia lyase ... 296 9e-81
 emb|AW774460|AW774460 EST333611 KV3 Medicago truncatula cDNA clo... 302 1e-80
 emb|X63103|STPAL1 S.tuberosum PAL-1 gene for phenylalanine ammon... 196 6e-79
 55 emb|AW685111|AW685111 NF026A05NR1F1000 Nodulated root Medicago t... 292 8e-78
 emb|AF165998|AF165998 Vigna unguiculata phenylalanine ammonia-ly... 292 1e-77
 emb|AI899906|AI899906 sb96a02.y1 Gm-c1012 Glycine max cDNA clone... 287 3e-76
 emb|AW691458|AW691458 NF045B11ST1F1000 Developing stem Medicago ... 286 6e-76
 emb|AW696215|AW696215 NF103G12ST1F1099 Developing stem Medicago ... 283 7e-76
 60 emb|AW688208|AW688208 NF004F12ST1F1000 Developing stem Medicago ... 278 1e-73
 emb|AF218453|AF218453 Coffea arabica clone 369.1.6r phenylalanin... 275 9e-73

- emb|AF218454|AF218454 *Coffea arabica* clone 430.4 phenylalanine a... 275 2e-72
emb|AW560722|AW560722 EST315770 *DSIR Medicago truncatula* cDNA cl... 269 7e-71
emb|X76130|CMPAL C.melo (cantaloupe) pal mRNA. 262 1e-68
emb|AV407891|AV407891 AV407891 *Lotus japonicus* young plants (two... 260 3e-68
5 emb|AI729040|AI729040 BNLGHI12413 Six-day Cotton fiber *Gossypium*... 258 1e-67
emb|AI780119|AI780119 EST260998 tomato susceptible, Cornell Lyco... 237 3e-66
emb|X99705|TAPALGEN1 *T.aestivum* PAL gene. 156 2e-65
emb|AW694081|AW694081 NF072E06ST1F1050 Developing stem *Medicago* ... 225 8e-65
emb|AW688761|AW688761 NF011C12ST1F1000 Developing stem *Medicago* ... 246 7e-64
10 emb|AW684895|AW684895 NF022G07NR1F1000 Nodulated root *Medicago* t... 237 3e-63
emb|AW267882|AW267882 EST306160 *DSIR Medicago truncatula* cDNA cl... 240 4e-62
emb|AW685144|AW685144 NF025D11NR1F1000 Nodulated root *Medicago* t... 232 5e-61
emb|AW686498|AW686498 NF042A10NR1F1000 Nodulated root *Medicago* t... 168 2e-60
gb|U39792|PTU39792 *Pinus taeda* phenylalanine ammonia-lyase (lpPA... 129 5e-60
15 dbj|D10002|PEAPAL1 *P.sativum* gene for phenylalanine ammonia-lyas... 231 2e-59
emb|AW720528|AW720528 LjNEST18f8r *Lotus japonicus* nodule library... 146 7e-58
emb|AI563248|AI563248 EST00372 watermelon lambda zap library Cit... 222 7e-57
emb|AJ289609|BPE289609 *Betula pendula* partial pal gene for pheny... 133 3e-56
emb|AW685192|AW685192 NF027D11NR1F1000 Nodulated root *Medicago* t... 219 6e-56
20 emb|AJ278116|BPE278116 *Betula pendula* partial pal gene for phen... 131 9e-56
emb|AW033848|AW033848 EST277419 tomato callus, TAMU *Lycopersicon*... 218 1e-55
emb|AW039368|AW039368 EST281625 tomato mixed elicitor, BTI *Lycop*... 218 1e-55
emb|AB015871|AB015871 *Vitis vinifera* gene for phenylalanine ammo... 215 8e-55
emb|AW031670|AW031670 EST275124 tomato callus, TAMU *Lycopersicon*... 215 8e-55
25 emb|AW650661|AW650661 EST329115 tomato germinating seedlings, TA... 213 4e-54
emb|AB015870|AB015870 *Vitis vinifera* gene for phenylalanine ammo... 213 4e-54
emb|X52953|DMPAL1 *Glycine max* PAL1 gene for phenylalanine ammoni... 213 5e-54
emb|AW219754|AW219754 EST302236 tomato root during/after fruit s... 211 2e-53
emb|AW690758|AW690758 NF033B06ST1F1000 Developing stem *Medicago* ... 210 3e-53
30 dbj|D30656|POPPALA *Populus kitakamiensis* gene for phenylalanine ... 208 1e-52
dbj|D43802|POPPALG2BA *Populus kitakamiensis* gene for phenylalani... 208 2e-52
emb|AW689402|AW689402 NF018G12ST1F1000 Developing stem *Medicago* ... 207 2e-52
gb|M91192|TFRPAL1X *Trifolium subterraneum* phenylalanine ammonia-... 197 3e-52
emb|AW034358|AW034358 EST277929 tomato callus, TAMU *Lycopersicon*... 190 1e-51
35 emb|AB008200|AB008200 *Nicotiana tabacum* palB gene for phenylalan... 204 2e-51
gb|M84466|TOBTPA1A Tobacco phenylalanine ammonia-lyase (tpal) gen... 204 2e-51
gb|M90692|TOMPAL5A *Lycopersicon esculentum* phenylalanine ammonia... 203 5e-51
emb|Y07654|PCPAL1 *P.crispum* pal gene. 173 6e-51
dbj|D43803|POPPALG4B *Populus kitakamiensis* gene for phenylalanin... 201 2e-50
40 emb|AI495627|AI495627 sb11c09.y1 Gm-cl004 *Glycine max* cDNA clone... 140 4e-50
gb|M83314|TOMPHEAMLY *Lycopersicon esculentum* phenylalanine ammon... 199 7e-50
dbj|D85850|D85850 *Daucus carota* gDcPAL1 gene for phenylalanine a... 198 1e-49
emb|AW034782|AW034782 EST278818 tomato callus, TAMU *Lycopersicon*... 141 1e-49
emb|AW689099|AW689099 NF015D05ST1F1000 Developing stem *Medicago* ... 197 3e-49
45 emb|AB008199|AB008199 *Nicotiana tabacum* palA gene for phenylalan... 195 6e-49
emb|X15473|PCPAL1GN *P.crispum* PAL-1 gene for phenylalanine ammon... 120 6e-49
emb|X63104|STPAL2 *S.tuberosum* PAL-2 gene for phenylalanine ammon... 193 5e-48
emb|AI974372|AI974372 T110225e KVO *Medicago truncatula* cDNA clon... 191 2e-47
dbj|D30657|POPPALB *Populus kitakamiensis* gene for phenylalanine ... 185 9e-46
50 emb|AF019965|AF019965 *Pinus monticola* phenylalanine ammonia lyas... 130 4e-45
emb|AI778115|AI778115 EST258994 tomato susceptible, Cornell Lyco... 166 1e-44
emb|AW031859|AW031859 EST275313 tomato callus, TAMU *Lycopersicon*... 165 4e-44
emb|X16772|PCPAL1EX2 *P.crispum* PAL-1 gene for phenylalanine ammo... 173 1e-42
emb|AW757191|AW757191 sl30c12.y1 Gm-cl027 *Glycine max* cDNA clone... 174 2e-42
55 emb|AI484637|AI484637 EST242898 tomato ovary, TAMU *Lycopersicon* ... 174 2e-42
emb|AW683457|AW683457 NF012E02LF1F1017 Developing leaf *Medicago* ... 173 3e-42
emb|AI495119|AI495119 sb03f10.y1 Gm-cl004 *Glycine max* cDNA clone... 169 7e-41
emb|AW922611|AW922611 DG1_46_C11.b1_A002 Dark Grown 1 (DG1) *Sorg*... 102 1e-40
emb|AV409143|AV409143 AV409143 *Lotus japonicus* young plants (two... 166 3e-40
60

Query= pal1-intron_f_at 14256_f_at /id_source genbank /description
 gb|aad18156.2| (ac006260) phenylalanine ammonia lyase (pal1)
 [arabidopsis thaliana] /blast_score 7.00e-77 /ec_number /family
 /chip nova /gb_link /ncgi
 5 (3115 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

10 Searching.....done

		Score	E
	Sequences producing significant alignments:	(bits)	Value
15	dbj E04042 E04042 cDNA sequence coding for pea phenylalanine amm...	232	9e-60
	dbj D10001 PEAPAL P.sativum mRNA for phenylalanine ammonia-lyase...	232	9e-60
	dbj D10002 PEAPAL1 P.sativum gene for phenylalanine ammonia-lyas...	231	2e-59
	emb AW774460 AW774460 EST333611 KV3 Medicago truncatula cDNA clo...	228	2e-58
	emb AW688761 AW688761 NF011C12ST1F1000 Developing stem Medicago ...	226	5e-58
20	emb AW694081 AW694081 NF072E06ST1F1050 Developing stem Medicago ...	225	1e-57
	emb AW684895 AW684895 NF022G07NR1F1000 Nodulated root Medicago t...	222	9e-57
	emb AI899906 AI899906 sb96a02.y1 Gm-c1012 Glycine max cDNA clone...	220	5e-56
	emb AF036948 AF036948 Prunus avium phenylalanine ammonia-lyase (...)	220	6e-56
	emb AF237955 AF237955 Rubus idaeus phenylalanine ammonia-lyase 2...	220	6e-56
25	dbj D10003 PEAPAL2 P.sativum gene for phenylalanine ammonia-lyas...	219	9e-56
	emb X58180 MSPAL M.sativa PAL mRNA for phenylalanine ammonia-lyase.	219	9e-56
	emb AB015871 AB015871 Vitis vinifera gene for phenylalanine ammo...	215	1e-54
	dbj D26596 CMEPAL Camellia sinensis mRNA for phenylalanine ammon...	215	2e-54
	emb AJ002221 DLJ002221 Digitalis lanata mRNA for phenylalanine a...	214	4e-54
30	emb AW667320 AW667320 GA__Ea0008P06 Gossypium arboreum 7-10 dpa ...	214	4e-54
	emb AB015870 AB015870 Vitis vinifera gene for phenylalanine ammo...	213	5e-54
	emb AW725857 AW725857 GA__Ea0019O22 Gossypium arboreum 7-10 dpa ...	212	1e-53
	emb AW696215 AW696215 NF103G12ST1F1099 Developing stem Medicago ...	211	2e-53
	emb AW691458 AW691458 NF045B11ST1F1000 Developing stem Medicago ...	211	2e-53
35	dbj D83076 D83076 Lithospermum erythrorhizon mRNA for phenylalan...	211	2e-53
	gb M29232 IPBPAL Sweet potato phenylalanine ammonia-lyase mRNA (...)	211	3e-53
	emb X52953 DMPAL1 Glycine max PAL1 gene for phenylalanine ammoni...	210	5e-53
	emb Y12461 HAPHAMLY Helianthus annuus mRNA for phenylalanine amm...	205	7e-53
	emb AW267882 AW267882 EST306160 DSIR Medicago truncatula cDNA cl...	209	9e-53
40	gb L36822 SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas...	209	9e-53
	dbj D83075 D83075 Lithospermum erythrorhizon mRNA for phenylalan...	209	1e-52
	emb AW685192 AW685192 NF027D11NR1F1000 Nodulated root Medicago t...	209	1e-52
	emb AW690758 AW690758 NF033B06ST1F1000 Developing stem Medicago ...	209	1e-52
	emb AW688208 AW688208 NF004F12ST1F1000 Developing stem Medicago ...	209	1e-52
45	emb AF237954 AF237954 Rubus idaeus phenylalanine ammonia-lyase 1...	208	2e-52
	emb AW689402 AW689402 NF018G12ST1F1000 Developing stem Medicago ...	207	3e-52
	dbj D43802 POPPALG2BA Populus kitakamiensis gene for phenylalani...	207	3e-52
	gb M91192 TFRPAL1X Trifolium subterraneum phenylalanine ammonia-...	197	3e-52
	dbj D30656 POPPALA Populus kitakamiensis gene for phenylalanine ...	207	5e-52
50	emb AB042520 AB042520 Catharanthus roseus mRNA for phenylalanine...	207	5e-52
	gb M90692 TOMPAL5A Lycopersicon esculentum phenylalanine ammonia...	207	5e-52
	emb AI729040 AI729040 BNLGHi12413 Six-day Cotton fiber Gossypium...	206	6e-52
	emb AW686498 AW686498 NF042A10NR1F1000 Nodulated root Medicago t...	153	9e-52
	gb L11747 POPPALGA Populus tricarpha X Populus deltoides (hybri...	205	2e-51
55	emb AB008200 AB008200 Nicotiana tabacum palB gene for phenylalan...	204	2e-51
	gb M84466 TOBTPA1A Tobacco phenylalanine ammonialyase (tpal) gen...	204	2e-51
	gb U43338 CLU43338 Citrus limon phenylalanine ammonia-lyase (pal...	204	3e-51
	emb AW033848 AW033848 EST277419 tomato callus, TAMU Lycopersicon...	203	8e-51
	emb AW650661 AW650661 EST329115 tomato germinating seedlings, TA...	203	8e-51
60	emb AW219754 AW219754 EST302236 tomato root during/after fruit s...	203	8e-51
	emb AW220322 AW220322 EST302805 tomato root during/after fruit s...	203	8e-51

- emb|AW039368|AW039368 EST281625 tomato mixed elicitor, BTI Lycop... 203 8e-51
 dbj|D78640|IPBPALA Ipomoea batatas mRNA for phenylalanine ammoni... 202 1e-50
 emb|AI563248|AI563248 EST00372 watermelon lambda zap library Cit... 202 2e-50
 emb|AW031670|AW031670 EST275124 tomato callus, TAMU Lycopersicon... 202 2e-50
 5 emb|Y07654|PCPAL1 P.crispum pal1 gene. 173 2e-50
 dbj|D43803|POPPALG4B Populus kitakamiensis gene for phenylalanin... 201 3e-50
 emb|X81159|PCPAL3 P.crispum mRNA for phenylalanine ammonia-lyase 3. 174 4e-50
 emb|X17462|PCPAL4 P.crispum RNA for PAL4, phenylalanine ammonia-... 199 4e-50
 emb|X81158|PCPAL2 P.crispum mRNA for phenylalanine ammonia-lyase 2. 173 7e-50
 10 emb|AJ238754|CCL238754 Citrus clementina X Citrus reticulata mRN... 199 7e-50
 emb|X78269|NTPHEAL N.tabacum (Samsun NN) mRNA for phenylalanine ... 195 1e-49
 gb|M83314|TOMPHEAMLY Lycopersicon esculentum phenylalanine ammon... 199 1e-49
 emb|AJ238753|CCL238753 Citrus clementina X Citrus reticulata mRN... 199 1e-49
 dbj|D85850|D85850 Daucus carota gDcPAL1 gene for phenylalanine a... 198 2e-49
 15 dbj|D17467|TOBPAL1 Tobacco mRNA for phenylalanine ammonia-lyase,... 195 3e-49
 emb|AW685111|AW685111 NF026A05NR1F1000 Nodulated root Medicago t... 197 4e-49
 emb|AW720528|AW720528 LjNEST18f8r Lotus japonicus nodule library... 116 5e-49
 emb|AW689099|AW689099 NF015D05ST1F1000 Developing stem Medicago ... 197 5e-49
 emb|X63103|STPAL1 S.tuberosum PAL-1 gene for phenylalanine ammon... 197 5e-49
 20 emb|AF218453|AF218453 Coffea arabica clone 369.1.6r phenylalanin... 196 7e-49
 emb|AB008199|AB008199 Nicotiana tabacum palA gene for phenylalan... 195 9e-49
 emb|X15473|PCPAL1GN P.crispum PAL-1 gene for phenylalanine ammon... 120 9e-49
 emb|AF218454|AF218454 Coffea arabica clone 430.4 phenylalanine a... 195 2e-48
 emb|X99997|BFPAL B.finlaysoniana mRNA for phenylalanine ammonia-... 194 2e-48
 25 emb|AF165998|AF165998 Vigna unguiculata phenylalanine ammonia-ly... 194 2e-48
 emb|AW560722|AW560722 EST315770 DSIR Medicago truncatula cDNA cl... 194 2e-48
 emb|AV407891|AV407891 AV407891 Lotus japonicus young plants (two... 193 9e-48
 emb|X63104|STPAL2 S.tuberosum PAL-2 gene for phenylalanine ammon... 193 9e-48
 emb|AJ250836|CAR250836 Cicer arietinum mRNA for phenylalanine am... 191 3e-47
 30 dbj|D30657|POPPALB Populus kitakamiensis gene for phenylalanine ... 185 1e-45
 emb|AI974372|AI974372 T110225e KV0 Medicago truncatula cDNA clon... 185 2e-45
 emb|AW034782|AW034782 EST278818 tomato callus, TAMU Lycopersicon... 141 3e-45
 emb|AW685144|AW685144 NF025D11NR1F1000 Nodulated root Medicago t... 179 5e-45
 gb|U16130|PAU16130 Persea americana phenylalanine ammonia lyase ... 183 7e-45
 35 emb|X76130|CMPAL C.melo (cantaloupe) pal mRNA. 181 3e-44
 emb|X16772|PCPAL1EX2 P.crispum PAL-1 gene for phenylalanine ammo... 173 2e-42
 emb|AI484637|AI484637 EST242898 tomato ovary, TAMU Lycopersicon ... 174 3e-42
 emb|AW683457|AW683457 NF012E02LF1F1017 Developing leaf Medicago ... 173 5e-42
 emb|Z49147|HVPAL7RM H.vulgare partial PAL mRNA for phenylalanine... 154 1e-40
 40 emb|AI495119|AI495119 sb03f10.y1 Gm-c1004 Glycine max cDNA clone... 169 1e-40
 emb|AW757191|AW757191 sl30cl2.y1 Gm-c1027 Glycine max cDNA clone... 168 2e-40
 emb|AW929506|AW929506 EST338294 tomato flower buds 8 mm to pre-a... 96 4e-40
 emb|AV409143|AV409143 AV409143 Lotus japonicus young plants (two... 166 6e-40
 emb|AW694394|AW694394 NF075F09ST1F1078 Developing stem Medicago ... 114 3e-38
 45 emb|AI495627|AI495627 sb11c09.y1 Gm-c1004 Glycine max cDNA clone... 100 3e-38
 emb|AW979905|AW979905 EST341554 tomato root deficiency, Cornell ... 157 4e-37
 emb|X99705|TAPALGEN1 T.aestivum PAL gene. 156 4e-37
 emb|AW694606|AW694606 NF078C03ST1F1020 Developing stem Medicago ... 151 6e-36
 emb|AW922611|AW922611 DG1_46_C11.b1_A002 Dark Grown 1 (DG1) Sorg... 87 9e-36
 50 emb|AI780119|AI780119 EST260998 tomato susceptible, Cornell Lyco... 130 1e-35
 emb|AI778115|AI778115 EST258994 tomato susceptible, Cornell Lyco... 130 1e-35
 emb|AI773582|AI773582 EST254682 tomato resistant, Cornell Lycopes... 130 1e-35
 emb|AW034358|AW034358 EST277929 tomato callus, TAMU Lycopersicon... 130 4e-35

55

Query= PAT1_s_at 14620_s_at /id_source genbank /description
 gb|aaa32835.1| (m96073) phosphoribosylanthranilate transferase
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link /ncgi

60

(1602 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments: (bits) Value

	emb AW687938 AW687938 NF001B11ST1F1000 Developing stem Medicago ...	393	e-108
10	emb AW039382 AW039382 EST281639 tomato mixed elicitor, BTI Lycop...	369	e-101
	emb AW096850 AW096850 EST46F4 potato shoot cDNA library Solanum ...	263	2e-69
	emb AW688778 AW688778 NF011E05ST1F1000 Developing stem Medicago ...	244	1e-65
	emb AW906002 AW906002 EST342043 potato stolon, Cornell Universit...	234	6e-63
	emb AI855689 AI855689 sc23a07.y1 Gm-cl013 Glycine max cDNA clone...	191	1e-47
15	emb AW622744 AW622744 EST306881 tomato flower buds 3-8 mm, Corne...	171	2e-41
	emb AW041025 AW041025 EST283889 tomato mixed elicitor, BTI Lycop...	171	2e-41
	emb AL023554 SPBC16G5 S.pombe chromosome II cosmid cl6G5.	81	1e-31
	gb BE053060 BE053060 GA__Ea0020N16f Gossypium arboreum 7-10 dpa ...	132	7e-30
	gb BE035432 BE035432 MO05D07 MO Mesembryanthemum crystallinum cD...	111	1e-23
20	emb AJ273068 AJ273068 AJ273068 Metarhizium anisopliae ARSEF 2575...	54	2e-16
	emb AV412566 AV412566 AV412566 Lotus japonicus young plants (two...	78	2e-16
	emb AV421776 AV421776 AV421776 Lotus japonicus young plants (two...	72	4e-13
	gb U28372 YSCD9476 Saccharomyces cerevisiae chromosome IV cosmid...	49	8e-09
	emb X04273 SCTRP4 Yeast TRP4 gene for anthranilate phosphoribosy...	49	9e-09
25	emb AQ874893 AQ874893 V118C3 mTn-3xHA/lacZ Insertion Library, st...	49	1e-07
	emb AJ228925 AJ228925 AJ228925 Barley leaf, 8 day old seedling H...	57	4e-07
	emb AW220409 AW220409 EST302892 tomato root during/after fruit s...	53	5e-06
	emb AW737074 AW737074 CAF50 Peronospora parasitica cDNA-AFLP fra...	46	8e-04
	emb X73297 SCSETRP4 S.cerevisiae spacer element.	29	0.002
30	gb U10274 SCU10274 Saccharomyces cerevisiae thioredoxin reductas...	44	0.004
	emb AW933535 AW933535 EST359294 tomato fruit mature green, TAMU ...	38	0.016
	emb AW922212 AW922212 DG1_17_B11.b1_A002 Dark Grown 1 (DG1) Sorg...	41	0.027
	gb BE125449 BE125449 DG1_25_B11.b1_A002 Dark Grown 1 (DG1) Sorgh...	41	0.027
	emb AV407038 AV407038 AV407038 Lotus japonicus young plants (two...	40	0.037
35	emb AI730383 AI730383 BNLGHi6768 Six-day Cotton fiber Gossypium ...	40	0.037
	emb AW201070 AW201070 se97e05.y1 Gm-cl027 Glycine max cDNA clone...	40	0.050
	dbj E08275 E08275 cDNA encoding cystathionine gamma-lyase.	37	0.46
	dbj E08276 E08276 gDNA encoding cystathionine gamma-lyase.	37	0.46
	emb AL113519 CNS01AXJ Botrytis cinerea strain T4 cDNA library un...	36	0.88
40	emb Z31724 PCREPELEM P.chrysosporium DNA for repetitive element.	36	0.88
	emb AW695815 AW695815 NF099E03ST1F1021 Developing stem Medicago ...	34	1.4
	emb A46806 A46806 Sequence 3 from Patent EP0684312.	35	1.7
	emb Z37978 NTCYCMRN Nicotiana tabacum mRNA for cyclin B1 (cycB1 ...	35	1.7
	emb AW729618 AW729618 GA__Ea0025J01 Gossypium arboreum 7-10 dpa ...	35	1.7
45	emb A46810 A46810 Sequence 7 from Patent EP0684312.	35	2.3
	emb AL354572 LMFL5808 Leishmania major Friedlin chromosome 19 co...	35	2.3
	gb BE052827 BE052827 GA__Ea0033G24f Gossypium arboreum 7-10 dpa ...	29	2.5
	emb AW661030 AW661030 832009F12.x1 C. reinhardtii CC-125 nutrien...	34	3.1
	emb AQ447557 AQ447557 mgxb0008C17f CUGI Rice Blast BAC Library P...	34	3.1
50	emb AW257438 AW257438 EST305575 KV2 Medicago truncatula cDNA clo...	34	3.1
	emb AW563834 AW563834 LG1_272_A11.b1_A002 Light Grown 1 (LG1) So...	34	3.1
	emb AQ654417 AQ654417 Sheared DNA-20C20.TF Sheared DNA Trypanoso...	34	4.3
	emb AW756224 AW756224 sl17f04.y1 Gm-cl036 Glycine max cDNA clone...	34	4.3
	emb X89715 SCAOGENES S.cerevisiae AOB567, AOF1001, AOE110, AOE26...	34	4.3
55	emb AF134853 AF134853 Cuphea hookeriana acyl-ACP carrier protein...	34	4.3
	emb Z74896 SCYOL154W S.cerevisiae chromosome XV reading frame OR...	34	4.3
	gb U15935 CWKAS3A Cuphea wrightii beta-ketoacyl-ACP synthase III...	34	4.3
	gb BE033595 BE033595 MF04D10 MF Mesembryanthemum crystallinum cD...	34	4.3
	emb AQ952764 AQ952764 Sheared DNA-43G7.TR Sheared DNA Trypanosom...	33	5.9
60	emb X61281 PBPOLII9 P.berghei RNA polymerase largest subunit.	33	5.9
	emb Z36097 SCYBR228W S.cerevisiae chromosome II reading frame OR...	33	5.9

	emb AL113095 CNS01ALR Botrytis cinerea strain T4 cDNA library un...	33	5.9
	gb U36470 NCU36470 Neurospora crassa vacuolar ATPase 41 kDa subu...	33	5.9
	emb Z78011 ANAXHA A.niger CBS 120.49 axhA gene.	33	5.9
	gb BE023153 BE023153 sm79a01.y1 Gm-c1015 Glycine max cDNA clone ...	33	5.9
5	emb X71807 ANUAPA A.nidulans uapA gene for uric acid-xanthine pe...	33	5.9
	emb AI213031 AI213031 y6f05a1.r1 Aspergillus nidulans 24hr asexu...	33	5.9
	emb AQ874871 AQ874871 V117H8 mTn-3xHA/lacZ Insertion Library, st...	26	6.5
	gb U18839 SCE9747 Saccharomyces cerevisiae chromosome V cosmids ...	33	8.1
	emb AF006304 AF006304 Saccharomyces cerevisiae protein tyrosine ...	33	8.1
10	gb U18814 SCE3612 Saccharomyces cerevisiae chromosome V lambda c...	33	8.1
	emb AW719293 AW719293 LjNEST_C6r Lotus japonicus nodule library,...	33	8.1
	emb AI441951 AI441951 sa83b07.y1 Gm-c1004 Glycine max cDNA clone...	33	8.1
	emb AI443684 AI443684 sa50b09.y1 Gm-c1004 Glycine max cDNA clone...	33	8.1
	emb AW932067 AW932067 EST357910 tomato fruit mature green, TAMU ...	33	8.1
15	emb AW720549 AW720549 LjNEST10b1rc Lotus japonicus nodule librar...	33	8.1
	emb AW706285 AW706285 sj54d11.y1 Gm-c1033 Glycine max cDNA clone...	33	8.1
	emb Z69368 SPAC27F1 S.pombe chromosome I cosmid c27F1.	33	8.1
	emb X55664 SVPEPCA Sorghum vulgare mRNA for phosphoenolpyruvate ...	33	8.1
	emb AW299016 AW299016 EST305690 KV2 Medicago truncatula cDNA clo...	33	8.1
20	emb AW171746 AW171746 N100640e rootphos(-) Medicago truncatula c...	33	8.1
	emb AI960269 AI960269 sc81b07.y1 Gm-c1018 Glycine max cDNA clone...	27	9.1
25	Query= PDF1.2_at 14621_at /id_source genbank /description gb aac31244.1 (ac004747) putative antifungal protein [arabidopsis thaliana] /blast_score 1.00e-31 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb pdf1 /ncgi http://www.ncgr.org/cgi-bin/ff?pdf1 (400 letters)		
30	Database: plantfungal 661,018 sequences; 426,114,510 total letters		
35	Searching.....done		
	Score	E	
	Sequences producing significant alignments:	(bits)	Value
40	emb A26875 A26875 R.sativus AFP1 gene.	160	5e-39
	gb U18557 RSU18557 Raphanus sativus antifungal protein 1 preprot...	159	1e-38
	gb U59459 BNU59459 Brassica napus antifungal protein mRNA, compl...	127	6e-37
	gb U18556 RSU18556 Raphanus sativus antifungal protein 2 preprot...	138	1e-35
	emb X97318 RSAFP4 R.sativus mRNA for antifungal protein 4.	145	3e-34
45	emb X97319 RSEFP3 R.sativus mRNA for antifungal protein 3.	127	2e-31
	emb A26963 A26963 D.merkii AMP1 sequence.	76	2e-13
	emb X53375 HASF18 Sunflower anther-specific mRNA SF18.	75	3e-13
	emb A27062 A27062 C.benedictus AMP2 sequence.	74	4e-13
	emb A26906 A26906 C.benedictus AMP1 sequence.	73	7e-13
50	gb L47901 L47901 BNAF1712 Mustard flower buds Brassica rapa cDNA...	65	2e-10
	emb AT001728 AT001728 AT001728 Flower bud cDNA Brassica rapa sub...	65	3e-10
	emb A27064 A27064 C.tematea AMP1 sequence.	58	7e-09
	emb AT001738 AT001738 AT001738 Flower bud cDNA Brassica rapa sub...	52	2e-06
	emb AW870017 AW870017 NXNV_122_A10_F Nsf Xylem Normal wood Verti...	35	7e-06
55	emb AW064751 AW064751 ST35D04 Pine, TripleEx shoot tip library Pin...	36	7e-06
	emb X91487 PASPI1GEN P.abies mRNA for gamma-thionin protein (put...	40	1e-05
	emb AW621708 AW621708 EST312506 tomato root during/after fruit s...	43	9e-05
	emb AW220215 AW220215 EST302698 tomato root during/after fruit s...	43	1e-04
	emb AW220231 AW220231 EST302714 tomato root during/after fruit s...	43	1e-04
60	emb AW219164 AW219164 EST301646 tomato root during/after fruit s...	43	1e-04
	emb AW219793 AW219793 EST302275 tomato root during/after fruit s...	43	1e-04

	emb AW621529 AW621529 EST312327 tomato root during/after fruit s...	41	3e-04
	emb AW622375 AW622375 EST313174 tomato root during/after fruit s...	41	4e-04
	emb AW622390 AW622390 EST313189 tomato root during/after fruit s...	41	4e-04
	emb AW621171 AW621171 EST311969 tomato root during/after fruit s...	40	7e-04
5	dbj D29679 TOBPIT1A Tobacco pit1 mRNA (which expression is induc...	44	7e-04
	emb AW622051 AW622051 EST312849 tomato root during/after fruit s...	40	7e-04
	emb AW622079 AW622079 EST312877 tomato root during/after fruit s...	40	9e-04
	emb AW621330 AW621330 EST312128 tomato root during/after fruit s...	40	9e-04
	emb AW219347 AW219347 EST301829 tomato root during/after fruit s...	40	0.001
10	emb AW220086 AW220086 EST302569 tomato root during/after fruit s...	40	0.001
	emb AW621962 AW621962 EST312760 tomato root during/after fruit s...	40	0.001
	emb AW621634 AW621634 EST312432 tomato root during/after fruit s...	37	0.005
	emb AW623112 AW623112 EST321057 tomato flower buds 3-8 mm, Corne...	40	0.006
	emb AW683448 AW683448 NF012D04LF1F1041 Developing leaf Medicago ...	40	0.006
15	emb AI487824 AI487824 EST246146 tomato ovary, TAMU Lycopersicon ...	40	0.006
	emb AI483999 AI483999 EST249870 tomato ovary, TAMU Lycopersicon ...	40	0.007
	gb U20591 SLU20591 Solanum lycopersicum flower-specific gamma-th...	40	0.007
	emb AW622923 AW622923 EST306993 tomato flower buds 3-8 mm, Corne...	40	0.007
	emb AW929929 AW929929 EST354199 tomato flower buds 8 mm to pre-a...	40	0.007
20	emb AW929939 AW929939 EST354209 tomato flower buds 8 mm to pre-a...	40	0.007
	emb AI897392 AI897392 EST266835 tomato ovary, TAMU Lycopersicon ...	40	0.008
	emb AI490243 AI490243 EST248569 tomato ovary, TAMU Lycopersicon ...	40	0.008
	emb AI487859 AI487859 EST246181 tomato ovary, TAMU Lycopersicon ...	40	0.009
	emb AW217552 AW217552 EST296266 tomato flower buds 3-8 mm, Corne...	40	0.009
25	emb AI489818 AI489818 EST248157 tomato ovary, TAMU Lycopersicon ...	40	0.009
	emb AI487398 AI487398 EST245720 tomato ovary, TAMU Lycopersicon ...	40	0.009
	emb AW217379 AW217379 EST296063 tomato flower buds 0-3 mm, Corne...	40	0.010
	emb AI898009 AI898009 EST267452 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI897456 AI897456 EST266899 tomato ovary, TAMU Lycopersicon ...	40	0.010
30	emb AI483612 AI483612 EST249462 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI485550 AI485550 EST243871 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI484887 AI484887 EST243150 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI484497 AI484497 EST242507 tomato ovary, TAMU Lycopersicon ...	40	0.012
	emb AI490062 AI490062 EST248401 tomato ovary, TAMU Lycopersicon ...	40	0.012
35	emb AW775186 AW775186 EST331908 GVN Medicago truncatula cDNA clo...	39	0.016
	emb AI486656 AI486656 EST244977 tomato ovary, TAMU Lycopersicon ...	38	0.024
	emb AI485044 AI485044 EST243324 tomato ovary, TAMU Lycopersicon ...	37	0.041
	emb AW399651 AW399651 EST310151 L. pennellii trichome, Cornell U...	38	0.042
	emb A26964 A26964 D.merkii AMP2 sequence.	37	0.080
40	emb X77993 HASF18A H.annuus SF18 gene.	31	0.14
	emb A27063 A27063 L.cicera AFP sequence.	34	0.74
	emb AI757757 AI757757 EtESTea34d02.y1 Eimeria S5-2 Sporozoite st...	34	0.74
	emb AW217119 AW217119 EST295833 tomato callus, TAMU Lycopersicon...	27	0.90
	emb X95363 CAGT C.annuum gamma thionin gene.	33	1.0
45	emb X95730 CAGTHIOGN Capsicum annuum defensin gene.	33	1.0
	emb AL035477 PFMAL4P4 Plasmodium falciparum chromosome 4 strain ...	33	1.0
	emb AL117384 LMFL5883 Leishmania major Friedlin chromosome 23 co...	29	1.3
	emb Z74387 SCYDR262W S.cerevisiae chromosome IV reading frame OR...	33	1.4
	emb Z68329 SC9320A S.cerevisiae chromosome IV cosmid 9320A.	33	1.4
50	emb Z70202 SC9320X S.cerevisiae chromosome IV cosmid 9320X.	33	1.4
	emb AQ846121 AQ846121 LMAJFV1_lml4f01.y1 Leishmania major FV1 ra...	29	1.7
	emb AW725876 AW725876 GA_Ea0020A08 Gossypium arboreum 7-10 dpa ...	32	1.9
	emb AV387503 AV387503 AV387503 Chlamydomonas reinhardtii C9 Chla...	32	2.6
	emb AQ947439 AQ947439 Sheared DNA-50L12.TF Sheared DNA Trypanoso...	31	3.6
55	emb AA836739 AA836739 L30-187T3 Ice plant Lambda Uni-Zap XR expr...	31	3.6
	gb M65164 PAR51C P.tetraulera 51C surface protein gene, complet...	31	3.6
	emb X16877 VUSTORED Vigna unguiculata cDNA for stored cotyledon ...	31	3.6
	emb AW736134 AW736134 EST332130 KV3 Medicago truncatula cDNA clo...	25	4.8
	emb AL034381 SPCC61 S.pombe chromosome III cosmid c61.	31	5.0
60	emb AQ642382 AQ642382 RPCI93-DpnII-29C10.TV RPCI93-DpnII Trypano...	31	5.0
	gb L01579 PEADRR230B Pea (pi39) disease resistance response prot...	31	5.0

emb|AW186932|AW186932 BNLGHi7476 Six-day Cotton fiber Gossypium ... 31 5.0
emb|AI727997|AI727997 BNLGHi9540 Six-day Cotton fiber Gossypium ... 31 5.0
emb|AI728914|AI728914 BNLGHi12020 Six-day Cotton fiber Gossypium... 31 5.0
gb|B07260|B07260 G236T7 MVAT4 sheared genomic library Trypanosom... 31 5.0
5 emb|AI728815|AI728815 BNLGHi11757 Six-day Cotton fiber Gossypium... 31 5.0
emb|AI726605|AI726605 BNLGHi6250 Six-day Cotton fiber Gossypium ... 31 5.0
gb|BE033595|BE033595 MF04D10 MF Mesembryanthemum crystallinum cD... 30 6.8
emb|AW508408|AW508408 si40e08.y1 Gm-r1030 Glycine max cDNA clone... 30 6.8
emb|AW830659|AW830659 sm05b06.y1 Gm-cl027 Glycine max cDNA clone... 30 6.8
10 emb|AW266371|AW266371 L30-3125T3 Ice plant Lambda Uni-Zap XR exp... 30 6.8
emb|AW266222|AW266222 L30-2930T3 Ice plant Lambda Uni-Zap XR exp... 30 6.8
emb|AW093819|AW093819 EST286999 tomato mixed elicitor, BTI Lycop... 30 6.8
emb|AI774224|AI774224 EST255419 tomato resistant, Cornell Lycopersicon... 30 6.8
emb|AA962873|AA962873 L30-403T3 Ice plant Lambda Uni-Zap XR expr... 30 6.8
15 emb|AL034557|PFMAL4P1 Plasmodium falciparum chromosome 4 strain ... 30 6.8
emb|AQ905826|AQ905826 GSSTc010408 Trypanosome cruzi random genom... 30 6.8
emb|AW053406|AW053406 L30-1317T3 Ice plant Lambda Uni-Zap XR exp... 30 6.8

20 Query= PR.1_s_at 14635_s_at /id_source genbank /description
gb|aac69381.1| (ac005398) pathogenesis-related pr-1-like protein
[arabidopsis thaliana] /blast_score 1.00e-94 /ec_number /family
/chip nova /gb_link /ncgi
(738 letters)

25 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

30

Score E
Sequences producing significant alignments: (bits) Value

35 gb|U70666|BNU70666 Brassica napus pathogenesis-related protein P... 323 3e-88
gb|U21849|BNU21849 Brassica napus PR-1a (LSC94) mRNA, complete cds. 323 3e-88
gb|U64806|BNU64806 Brassica napus pathogenesis-related protein P... 209 4e-85
emb|AI352851|AI352851 MB69-8A PZ204.BNlib Brassica napus cDNA cl... 311 4e-84
emb|AI352893|AI352893 MB72-6D PZ204.BNlib Brassica napus cDNA cl... 165 3e-62
emb|AW217013|AW217013 EST295727 tomato callus, TAMU Lycopersicon... 152 4e-60
40 emb|AW219671|AW219671 EST302153 tomato root during/after fruit s... 151 1e-59
emb|AW092403|AW092403 EST285583 tomato mixed elicitor, BTI Lycop... 151 1e-59
emb|AI895090|AI895090 EST264533 tomato callus, TAMU Lycopersicon... 151 1e-59
emb|AW625930|AW625930 EST319825 tomato radicle, 5 d post-imbibit... 151 1e-59
emb|AW032514|AW032514 EST276073 tomato callus, TAMU Lycopersicon... 151 1e-59
45 emb|AW034260|AW034260 EST277831 tomato callus, TAMU Lycopersicon... 151 1e-59
emb|AW040983|AW040983 EST283847 tomato mixed elicitor, BTI Lycop... 151 1e-59
emb|AW034206|AW034206 EST277777 tomato callus, TAMU Lycopersicon... 151 1e-59
emb|AW219480|AW219480 EST301878 tomato root during/after fruit s... 151 1e-59
emb|AW092623|AW092623 EST285803 tomato mixed elicitor, BTI Lycop... 151 1e-59
50 emb|AW040954|AW040954 EST283818 tomato mixed elicitor, BTI Lycop... 151 1e-59
emb|AW034454|AW034454 EST278025 tomato callus, TAMU Lycopersicon... 151 1e-59
emb|AW032723|AW032723 EST276282 tomato callus, TAMU Lycopersicon... 151 1e-59
emb|AW033873|AW033873 EST277444 tomato callus, TAMU Lycopersicon... 151 1e-59
emb|AI894650|AI894650 EST264093 tomato callus, TAMU Lycopersicon... 151 1e-59
55 emb|AW033593|AW033593 EST277164 tomato callus, TAMU Lycopersicon... 151 3e-59
emb|AW034724|AW034724 EST278526 tomato callus, TAMU Lycopersicon... 148 7e-59
emb|AW041033|AW041033 EST283897 tomato mixed elicitor, BTI Lycop... 148 7e-59
emb|X66942|NTPRB1B N.tabacum prb-1b gene. 146 9e-59
emb|AW559895|AW559895 EST314943 DSIR Medicago truncatula cDNA cl... 160 1e-58
60 emb|AW329241|AW329241 N200453e rootphos(-) Medicago truncatula c... 160 1e-58
emb|AW559894|AW559894 EST314942 DSIR Medicago truncatula cDNA cl... 159 5e-58

- emb|AW035820|AW035820 EST281974 tomato callus, TAMU Lycopersicon... 145 6e-58
emb|AW032139|AW032139 EST275593 tomato callus, TAMU Lycopersicon... 145 6e-58
emb|AW034330|AW034330 EST277901 tomato callus, TAMU Lycopersicon... 144 2e-57
emb|AW622143|AW622143 EST312941 tomato root during/after fruit s... 149 2e-57
5 emb|AI352771|AI352771 MB58-5G PZ204.BNlib Brassica napus cDNA cl... 220 2e-57
emb|AW032749|AW032749 EST276308 tomato callus, TAMU Lycopersicon... 149 3e-57
emb|AI894391|AI894391 EST263846 tomato callus, TAMU Lycopersicon... 142 4e-57
emb|AI896249|AI896249 EST265692 tomato callus, TAMU Lycopersicon... 142 5e-57
emb|AI782621|AI782621 EST263500 tomato susceptible, Cornell Lyco... 144 7e-57
10 emb|AW126362|AW126362 N100469e rootphos(-) Medicago truncatula c... 160 3e-56
emb|AW981257|AW981257 EST392410 DSIL Medicago truncatula cDNA cl... 128 9e-56
emb|AW033687|AW033687 EST277258 tomato callus, TAMU Lycopersicon... 149 2e-55
emb|AI352783|AI352783 MB59-12D PZ204.BNlib Brassica napus cDNA c... 198 3e-55
emb|X14065|NTPRP1 Nicotiana tabacum gene for basic form of patho... 140 4e-55
15 emb|AW625666|AW625666 EST319573 tomato radicle, 5 d post-imbibit... 135 6e-55
emb|AW032727|AW032727 EST276286 tomato callus, TAMU Lycopersicon... 147 1e-53
emb|X52555|NTW381 Tobacco W38/1 gene for PR-1 pathogenesis-relat... 116 1e-52
gb|BE034214|BE034214 MH01C07 MH Mesembryanthemum crystallinum cD... 112 4e-52
emb|AW053720|AW053720 L30-1612T3 Ice plant Lambda Uni-Zap XR exp... 112 4e-52
20 emb|AW559969|AW559969 EST315017 DSIR Medicago truncatula cDNA cl... 81 4e-52
emb|AI352801|AI352801 MB61-9C PZ204.BNlib Brassica napus cDNA cl... 194 1e-51
emb|X17681|NTPR1CA Tobacco gene for pathogenesis-related protein... 111 2e-51
emb|X05454|NTPR1CR Nicotiana tabacum mRNA for PR-1c protein. 111 2e-51
emb|X12487|NTPR1C Tobacco mRNA fragment for pathogenesis-related... 111 2e-51
25 emb|AJ011520|LES011520 Lycopersicon esculentum pr1a (P4) gene. 98 1e-50
gb|M69247|TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat... 98 1e-50
emb|A22634|LEPI4GENE L.esculentum P14 gene. 98 1e-50
emb|AJ250136|STU250136 Solanum tuberosum mRNA for pathogenesis r... 99 2e-50
emb|AW218808|AW218808 EST301288 tomato root during/after fruit s... 116 3e-50
30 emb|AI896011|AI896011 EST265454 tomato callus, TAMU Lycopersicon... 116 3e-50
emb|AW094536|AW094536 EST287716 tomato mixed elicitor, BTI Lycop... 116 3e-50
emb|AW038553|AW038553 EST280236 tomato mixed elicitor, BTI Lycop... 116 3e-50
dbj|D90196|TOBPR1A Nicotiana tabacum mRNA for PR1a protein precu... 104 3e-50
emb|X05959|NTPR1AG Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
35 emb|X12737|NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
emb|X06361|NTPR1AG1 Nicotiana tabacum gene for pathogenesis-rela... 104 4e-50
emb|X12485|NTPR1A Tobacco mRNA fragment for pathogenesis-related... 104 4e-50
emb|AW033469|AW033469 EST277040 tomato callus, TAMU Lycopersicon... 116 5e-50
emb|X06930|NTPR1AG2 Tobacco PR-1a gene for pathogenesis-related ... 104 7e-50
40 emb|AI352858|AI352858 MB70-10D PZ204.BNlib Brassica napus cDNA c... 197 7e-50
emb|AI782416|AI782416 EST263295 tomato susceptible, Cornell Lyco... 95 7e-50
emb|AW034882|AW034882 EST279111 tomato callus, TAMU Lycopersicon... 95 1e-49
emb|AW031086|AW031086 EST274393 tomato callus, TAMU Lycopersicon... 116 1e-49
emb|X74939|HVPRIAR H.vulgare HvPR-1a mRNA for a basic PR-1-type... 114 2e-49
45 emb|AF136636|AF136636 Glycine max PR1a precursor (PR1a) mRNA, co... 110 2e-49
emb|AW034167|AW034167 EST277738 tomato callus, TAMU Lycopersicon... 94 2e-49
emb|X17680|NTPR1BA Tobacco gene for pathogenesis-related protein... 103 3e-49
emb|X03465|NTPRPR Nicotiana tabacum mRNA for pathogenesis-relate... 103 3e-49
dbj|D90197|TOBPR1B1 Nicotiana tabacum mRNA for PR1b protein. 103 3e-49
50 emb|Y08804|LEPR1B1 L.esculentum mRNA for PR protein. 92 6e-49
gb|M69248|TOMPRP6 Lycopersicon esculentum PR (pathogenesis relat... 92 6e-49
emb|X68738|LEP1P14A L.esculentum mRNA for ethylene-induced P1(pl... 92 6e-49
emb|AI781499|AI781499 EST262378 tomato susceptible, Cornell Lyco... 92 6e-49
emb|AI779424|AI779424 EST260303 tomato susceptible, Cornell Lyco... 92 6e-49
55 emb|AW031093|AW031093 EST274400 tomato callus, TAMU Lycopersicon... 92 6e-49
emb|AI779425|AI779425 EST260304 tomato susceptible, Cornell Lyco... 92 6e-49
emb|AI782545|AI782545 EST263424 tomato susceptible, Cornell Lyco... 92 6e-49
emb|AI782822|AI782822 EST263701 tomato susceptible, Cornell Lyco... 92 6e-49
emb|AI778686|AI778686 EST259565 tomato susceptible, Cornell Lyco... 92 6e-49
60 emb|AI778680|AI778680 EST259559 tomato susceptible, Cornell Lyco... 92 6e-49
emb|AI899514|AI899514 EST268957 tomato susceptible, Cornell Lyco... 92 6e-49

emb|AI779287|AI779287 EST260166 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI773130|AI773130 EST254230 tomato resistant, Cornell Lycope... 92 6e-49
 emb|AI778790|AI778790 EST259669 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI778791|AI778791 EST259670 tomato susceptible, Cornell Lyco... 92 6e-49
 5 emb|AI778985|AI778985 EST259864 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AW032026|AW032026 EST275480 tomato callus, TAMU Lycopersicon... 92 6e-49
 emb|AI782288|AI782288 EST263167 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI779013|AI779013 EST259892 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI781431|AI781431 EST262298 tomato susceptible, Cornell Lyco... 92 6e-49
 10 emb|AI780973|AI780973 EST261852 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI895236|AI895236 EST264679 tomato callus, TAMU Lycopersicon... 92 6e-49

Query= PRXcb_s_at 14638_s_at /id_source genbank /description
 15 emb|caa50677.1|(x71794) peroxidase [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
 (1236 letters)

Database: plantfungal
 20 661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	
25	Sequences producing significant alignments:			(bits) Value
	gb M60729 HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge...	744	0.0	
	emb A00741 A00741 A.rusticana synthetic gene (reverse complement...	692	0.0	
	emb A00740 A00740 A.rusticana synthetic gene for peroxidase.	692	0.0	
30	dbj E01651 E01651 cDNA encoding horseradish peroxidase.	692	0.0	
	gb M37157 HRAHRPCB A.rusticana peroxidase isoenzyme C (HPR C) ge...	371	e-133	
	emb X97349 PTPXP2PER P.trichocarpa mRNA for anionic peroxidase P...	473	e-132	
	emb X97350 PTPXP3PER P.trichocarpa mRNA for anionic peroxidase P...	469	e-131	
	dbj D83224 POPP01 Populus nigra mRNA for peroxidase, complete cds.	468	e-131	
35	gb M37156 HRAHRPCA A.rusticana peroxidase isoenzyme C (HPR C) ge...	363	e-130	
	emb X97348 PTPXP1PER P.trichocarpa mRNA for anionic peroxidase P...	463	e-129	
	dbj D30652 POPPA Populus kitakamiensis mRNA for peroxidase, part...	441	e-123	
	emb X97351 PTPXP4PER P.trichocarpa mRNA for anionic peroxidase P...	383	e-120	
	dbj D30653 POPPB Populus kitakamiensis mRNA for peroxidase, part...	356	e-112	
40	emb AF149277 AF149277 Phaseolus vulgaris peroxidase 1 precursor ...	227	e-107	
	gb L36157 ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple...	229	e-107	
	emb AF007211 AF007211 Glycine max peroxidase precursor (GMIPER1)...	229	e-106	
	gb L07554 LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA...	381	e-105	
	emb X90692 MSRNAPE1A M.sativa mRNA for peroxidase 1A.	211	e-105	
45	dbj D90115 HRAPRXC2 Horseradish prxC2 gene encoding peroxidase i...	296	e-103	
	emb AJ242742 IBA242742 Ipomoea batatas mRNA for peroxidase (pod ...	138	2e-97	
	emb AF149280 AF149280 Phaseolus vulgaris peroxidase 5 precursor ...	142	4e-97	
	emb X90693 MSRNAPE1B M.sativa mRNA for peroxidase 1B.	231	1e-95	
	emb X90694 MSRNAPE1C M.sativa mRNA for peroxidase 1C.	226	7e-94	
50	gb L36111 SSNPEROXIB Stylosanthes humilis peroxidase mRNA.	210	2e-89	
	emb AI959837 AI959837 sc94h07.y1 Gm-cl019 Glycine max cDNA clone...	228	6e-89	
	emb AF244924 AF244924 Spinacia oleracea peroxidase prx15 precurs...	208	9e-88	
	emb AW559660 AW559660 EST314772 DSIR Medicago truncatula cDNA cl...	236	1e-87	
	emb AW774581 AW774581 EST333732 KV3 Medicago truncatula cDNA clo...	236	7e-87	
55	emb AF155124 AF155124 Gossypium hirsutum bacterial-induced perox...	215	2e-86	
	emb AW981426 AW981426 EST392579 DSIL Medicago truncatula cDNA cl...	236	2e-85	
	emb AB042103 AB042103 Asparagus officinalis AspPOX1 mRNA for per...	209	2e-85	
	emb AF244923 AF244923 Spinacia oleracea peroxidase prx14 precurs...	205	9e-85	
	emb AJ250121 PAB250121 Picea abies mRNA for SPI2 protein (spi2 g...	253	1e-83	
60	emb AW775762 AW775762 EST334827 DSIL Medicago truncatula cDNA cl...	236	6e-83	
	emb Y10466 SOPR XR5 S.oleracea mRNA for peroxidase, clone PC18.	218	3e-82	

- emb|AW775425|AW775425 EST334490 *DSIL Medicago truncatula* cDNA cl... 208 1e-81
 emb|AW685437|AW685437 NF029D09NR1F1000 *Nodulated root Medicago t...* 230 9e-80
 emb|AB024439|AB024439 *Scutellaria baicalensis* mRNA for peroxidas... 209 2e-79
 emb|AF244922|AF244922 *Spinacia oleracea* peroxidase prx13 precurs... 212 3e-79
 5 emb|X57564|ARNEUPERO *A.rusticana* mRNA for neutral peroxidase. 115 6e-78
 emb|AW776273|AW776273 EST335338 *DSIL Medicago truncatula* cDNA cl... 222 1e-77
 emb|AW267813|AW267813 EST305941 *DSIR Medicago truncatula* cDNA cl... 200 1e-76
 emb|X91232|MARNAPRX *M.annua* mRNA for peroxidase. 196 5e-76
 emb|AF049881|AF049881 *Linum usitatissimum* peroxidase FLXPER4 (PE... 207 7e-76
 10 emb|AW256487|AW256487 EST304624 KV2 *Medicago truncatula* cDNA clo... 200 9e-76
 emb|AW775890|AW775890 EST334955 *DSIL Medicago truncatula* cDNA cl... 200 3e-74
 emb|AW257195|AW257195 EST305332 KV2 *Medicago truncatula* cDNA clo... 214 5e-74
 gb|M91373|CUSPREPER *Cucumis sativus* peroxidase mRNA, complete cds. 86 2e-73
 gb|U41657|GMU41657 *Glycine max* seed coat peroxidase isozyme (SPO... 159 3e-73
 15 emb|AB027752|AB027752 *Nicotiana tabacum* mRNA for peroxidase, com... 197 5e-73
 gb|L36110|SSNPEROXIA *Stylosanthes humilis* peroxidase mRNA. 199 5e-73
 gb|M37636|ARCPNC1 *Arachis hypogaea* cationic peroxidase (PNC1) mR... 204 7e-73
 emb|AW685235|AW685235 NF027H10NR1F1000 *Nodulated root Medicago t...* 236 9e-73
 emb|AW278775|AW278775 sf97d02.y1 *Gm-c1019 Glycine max* cDNA clone... 155 1e-72
 20 emb|X71593|LECEVI1A *L.esculentum* CEVI-1 mRNA. 99 2e-72
 gb|J02979|TOBPXDLF *Nicotiana tabacum* lignin-forming peroxidase m... 100 2e-72
 emb|AW559945|AW559945 EST314993 *DSIR Medicago truncatula* cDNA cl... 233 2e-72
 emb|AW980744|AW980744 EST391897 *GVN Medicago truncatula* cDNA clo... 235 5e-70
 emb|Y10467|SOPRXR6 *S.oleracea* mRNA for peroxidase, clone PC23. 105 1e-69
 25 dbj|D83225|POPP02 *Populus nigra* peroxidase gene, complete cds. 196 2e-69
 gb|M74103|TOBANPER *Nicotiana sylvestris* anionic peroxidase mRNA,... 205 6e-69
 emb|AF043234|AF043234 *Striga asiatica* ferriprotein porphyrin-con... 211 1e-68
 gb|BE034991|BE034991 MM01A12 *MM Mesembryanthemum crystallinum* cD... 202 6e-68
 emb|AW574244|AW574244 EST316835 *GVN Medicago truncatula* cDNA clo... 202 1e-67
 30 emb|Y10465|SOPRXR4 *S.oleracea* mRNA for peroxidase, clone PC44. 98 3e-67
 emb|AW686084|AW686084 NF038B07NR1F1000 *Nodulated root Medicago t...* 236 5e-67
 emb|AW561032|AW561032 EST316080 *DSIR Medicago truncatula* cDNA cl... 203 7e-67
 emb|X56011|TAPERO *Wheat* mRNA for peroxidase. 111 2e-66
 emb|AW185769|AW185769 se59d08.y1 *Gm-c1019 Glycine max* cDNA clone... 219 4e-65
 35 emb|Y17192|CPY17192 *Cucurbita pepo* mRNA for peroxidase. 96 2e-64
 gb|BE033422|BE033422 ME01E09 *ME Mesembryanthemum crystallinum* cD... 184 4e-64
 emb|AB024438|AB024438 *Scutellaria baicalensis* mRNA for peroxidas... 205 7e-64
 gb|M91374|CUSPREPERA *Cucumis sativus* peroxidase mRNA, complete cds. 76 2e-63
 gb|L24120|LINFLXP *Linum usitatissimum* peroxidase precursor (FLXP... 167 2e-63
 40 gb|M91372|CUSPREPERB *Cucumis sativus* peroxidase mRNA, complete cds. 134 2e-63
 emb|AF043235|AF043235 *Striga asiatica* ferriprotein porphyrin-con... 199 3e-63
 emb|AW288002|AW288002 N100846e rootphos(-) *Medicago truncatula* c... 182 7e-63
 emb|AW126121|AW126121 N100318e rootphos(-) *Medicago truncatula* c... 216 1e-62
 gb|L36093|BLYPRX *Barley* peroxidase mRNA, complete cds. 133 5e-62
 45 emb|AW687443|AW687443 NF009F07RT1F1062 *Developing root Medicago ...* 235 1e-61
 emb|AW687957|AW687957 NF001D11ST1F1000 *Developing stem Medicago ...* 236 3e-61
 emb|AB024437|AB024437 *Scutellaria baicalensis* mRNA for peroxidas... 163 3e-61
 emb|X58396|HVPEROXI *Barley* mRNA for peroxidase (EC=1.11.1.7). 133 5e-61
 emb|AI496388|AI496388 sb04a11.y1 *Gm-c1004 Glycine max* cDNA clone... 224 6e-61
 50 emb|AW686765|AW686765 NF042E07NR1F1000 *Nodulated root Medicago t...* 222 8e-61
 dbj|D38050|POPP1 *Aspen* prxA3a gene for peroxidase, complete cds. 121 9e-61
 emb|AW704659|AW704659 sk54h10.y1 *Gm-c1019 Glycine max* cDNA clone... 149 9e-61
 emb|Y10464|SOPRXR3 *S.oleracea* mRNA for peroxidase, clone PC42. 80 3e-60
 emb|AW705730|AW705730 sk51b02.y1 *Gm-c1019 Glycine max* cDNA clone... 149 8e-60
 55 gb|U51191|GMU51191 *Glycine max* peroxidase precursor (sEPa1) mRNA... 100 9e-60
 gb|U12314|CCU12314 *Cenchrus ciliaris* clone PX7 peroxidase mRNA, ... 105 9e-60
 emb|AI938533|AI938533 sb46h09.y1 *Gm-c1015 Glycine max* cDNA clone... 145 1e-59
 emb|AW705617|AW705617 sk50d03.y1 *Gm-c1019 Glycine max* cDNA clone... 149 2e-59
 emb|AI781859|AI781859 EST262738 *tomato susceptible, Cornell Lyco...* 102 2e-59
 60 emb|AF149278|AF149278 *Phaseolus vulgaris* peroxidase 3 precursor ... 90 3e-59
 gb|U51192|GMU51192 *Glycine max* peroxidase precursor (sEPa2) mRNA... 102 4e-59

emb|AW441632|AW441632 EST311028 tomato fruit red ripe, TAMU Lyco... 105 7e-59
 emb|AF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 156 8e-59
 gb|M32742|CUSCUPER C.sativus peroxidase (put.) (CuPer2) mRNA, 3'... 107 2e-58
 emb|AW705946|AW705946 sk52h07.y1 Gm-c1019 Glycine max cDNA clone... 224 6e-58

5

Query= TSA1_s_at 14672_s_at /id_source genbank /description
 gb|aac49117.1| (u18993) tryptophan synthase alpha chain [arabidopsis
 thaliana] /blast_score 1.00e-158 /ec_number /family /chip nova
 /gb_link /ncgi
 (939 letters)

10

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

20

emb|AW730233|AW730233 GA_Ea0014B16 Gossypium arboreum 7-10 dpa ... 352 5e-98
 emb|AW649960|AW649960 EST328414 tomato germinating seedlings, TA... 308 4e-83
 emb|AW621664|AW621664 EST312462 tomato root during/after fruit s... 290 1e-77
 emb|AW031327|AW031327 EST274781 tomato callus, TAMU Lycopersicon... 282 3e-75
 25 gb|U38804|PPU38804 Porphyra purpurea chloroplast, complete genome. 271 4e-72
 emb|AW775853|AW775853 EST334918 DSIL Medicago truncatula cDNA cl... 264 9e-70
 emb|Z21642|CHASTRNAA Antithamnion sp. Chloroplast trnK, trnE, trpA... 255 4e-67
 gb|BE124387|BE124387 EST393422 GVN Medicago truncatula cDNA clon... 227 9e-59
 gb|BE121873|BE121873 894015F07.y1 C. reinhardtii CC-1690, normal... 227 1e-58
 30 emb|AF022186|AF022186 Cyanidium caldarium strain RK1 chloroplast... 220 1e-56
 emb|AI782364|AI782364 EST263243 tomato susceptible, Cornell Lyco... 210 1e-53
 emb|AW691298|AW691298 NF040B01ST1F1000 Developing stem Medicago ... 193 1e-49
 dbj|D63675|D63675 Cyanidioschyzon merolae trnK, trpA, trnT, rps4... 130 1e-49
 emb|AV392084|AV392084 AV392084 Chlamydomonas reinhardtii C9 Chla... 195 5e-49
 35 emb|AA660642|AA660642 00530 MtRHE Medicago truncatula cDNA 5' si... 190 1e-47
 dbj|D17791|CYNPLTRNK C.caldarium chloroplast gene for trnK and g... 121 1e-46
 emb|AW034248|AW034248 EST277819 tomato callus, TAMU Lycopersicon... 184 9e-46
 dbj|D63676|D63676 Cyanidium caldarium trnK, trpA, trnT, rps4, tr... 122 1e-45
 gb|L38526|L38526 BNAF0168E Mustard flower buds Brassica rapa cDN... 177 1e-43
 40 emb|V01342|SCTRP5A Yeast gene (trp5) for tryptophan synthetase. 86 9e-42
 emb|Z72548|SCYGL026C S.cerevisiae chromosome VII reading frame O... 86 9e-42
 emb|AW398861|AW398861 EST309361 L. pennellii trichome, Cornell U... 158 5e-38
 emb|AU090244|AU090244 AU090244 Hordeum vulgare subsp. vulgare Up... 149 7e-38
 emb|AW650911|AW650911 EST329365 tomato germinating seedlings, TA... 141 1e-32
 45 emb|AI773494|AI773494 EST254594 tomato resistant, Cornell Lycopersicon... 138 5e-32
 emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8. 74 3e-30
 emb|V01343|SCTRP5B Part of the yeast gene for tryptophan synthet... 86 2e-26
 emb|AI165371|AI165371 A082p39u Hybrid aspen plasmid library Popu... 81 1e-21
 emb|AU090028|AU090028 AU090028 Hordeum vulgare subsp. vulgare Up... 97 2e-19
 50 gb|J04594|NEUTRP3A N.crassa tryptophan synthetase (trp3) alpha-2... 78 1e-17
 emb|AF084886|AF084886 Neurospora crassa 314-448A mutant tryptoph... 68 9e-11
 emb|AF084890|AF084890 Neurospora crassa TD 554-6A mutant tryptop... 53 4e-10
 emb|AF084880|AF084880 Neurospora crassa EMSG9-9A mutant tryptoph... 66 5e-10
 emb|AF084885|AF084885 Neurospora crassa NG61-6A mutant tryptoph... 64 1e-09
 55 emb|AF084884|AF084884 Neurospora crassa 314-722A mutant tryptoph... 64 1e-09
 emb|AF084883|AF084883 Neurospora crassa 314-709A mutant tryptoph... 64 1e-09
 emb|AF084882|AF084882 Neurospora crassa 314-682A mutant tryptoph... 64 1e-09
 emb|AF084881|AF084881 Neurospora crassa 314-693A mutant tryptoph... 64 2e-09
 emb|AF084889|AF084889 Neurospora crassa 314-492-2A mutant trypto... 53 3e-09
 60 gb|M29094|CCITRP01 Mushroom (C.cinereus) tryptophan synthetase (... 59 4e-08
 emb|AU011013|AU011013 AU011013 Schizosaccharomyces pombe late lo... 54 2e-06

	emb AW693052 AW693052 NF059C08ST1F1065 Developing stem Medicago ...	51	1e-05
	emb AV390244 AV390244 AV390244 Chlamydomonas reinhardtii C9 Chla...	49	4e-05
	emb AW616467 AW616467 EST322878 L. hirsutum trichome, Cornell Un...	48	7e-05
	emb AL354022 P761R Leishmania major Friedlin PAC P761 right end-...	44	0.002
5	gb M91656 CCITRP05 Coprinus cinereus tryptophan synthetase (TRP1...	43	0.005
	emb AQ903789 AQ903789 GSSTc04230 Trypanosome cruzi random genomi...	35	0.24
	emb AW727215 AW727215 GA__Ea0023N23 Gossypium arboreum 7-10 dpa ...	36	0.52
	gb M91654 CCITRP03 Coprinus cinereus tryptophan synthetase (TRP1...	36	0.52
	emb AW728975 AW728975 GA__Ea0018P19 Gossypium arboreum 7-10 dpa ...	35	0.64
10	emb AL139794 LMFP1105 Leishmania major Friedlin chromosome 4 PAC...	35	0.87
	emb AW926438 AW926438 HVSMeg0007D14 Hordeum vulgare pre-anthesis...	34	1.2
	emb AA965348 AA965348 e9d04a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
	gb U12630 ENU12630 Emericella nidulans R153 core histone H3 (H3)...	34	1.3
	emb AI007494 AI007494 e9c09a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
15	emb AA787433 AA787433 n3d04a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
	emb X55548 ANH3GENE A.nidulans gene for core histone for H3.	34	1.3
	emb AQ396426 AQ396426 mgxb0013C24f CUGI Rice Blast BAC Library P...	34	1.6
	emb AF262997 AF262997 Ricinus communis NADP-dependent malic prot...	34	1.6
	gb M19025 CFUCPOR C.fumago cpo gene encoding chloroperoxidase, c...	34	1.6
20	emb AF084888 AF084888 Neurospora crassa 656-2A mutant tryptophan...	31	1.7
	emb AF084887 AF084887 Neurospora crassa TDA78(1-A)9A(TD201) muta...	31	1.7
	emb AW694774 AW694774 NF080A05ST1F1036 Developing stem Medicago ...	34	1.8
	emb Y18012 TVE18012 Trametes versicolor mRNA for laccase.	33	2.3
	emb AQ500614 AQ500614 V35B5 mTn-3xHA/lacZ Insertion Library Sacc...	33	2.5
25	emb AW187498 AW187498 BNLGHi6414 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW187530 AW187530 BNLGHi6944 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW694072 AW694072 NF072B12ST1F1096 Developing stem Medicago ...	33	3.1
	emb AW186883 AW186883 BNLGHi6498 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW187537 AW187537 BNLGHi7006 Six-day Cotton fiber Gossypium ...	33	3.1
30	emb AW187474 AW187474 BNLGHi5936 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AA167859 AA167859 CpEST.053 uniZAPCpIOWAsporoLib1 Cryptospor...	33	3.5
	emb AV421993 AV421993 AV421993 Lotus japonicus young plants (two...	33	4.3
	emb AF129874 AF129874 Pichia angusta peroxin-6 (PEX6) gene, comp...	33	4.3
	emb AL112679 CNS01AA7 Botrytis cinerea strain T4 cDNA library un...	33	4.7
35	gb BE028433 BE028433 EtESTea78d07.y1 Eimeria M5-6 Merozoite stag...	32	5.9
	emb AI166784 AI166784 xylem.est.582 Poplar xylem Lambda ZAPII li...	32	5.9
	emb AQ941624 AQ941624 Sheared DNA-53E1.TF Sheared DNA Trypanosom...	32	5.9
	emb AW728623 AW728623 GA__Ea0017G06 Gossypium arboreum 7-10 dpa ...	32	5.9
	gb BE027723 BE027723 EtESTea86c08.y1 Eimeria M5-6 Merozoite stag...	32	5.9
40	emb AI757375 AI757375 EtESTea32d03.y1 Eimeria S5-2 Sporozoite st...	32	5.9
	gb BE027843 BE027843 EtESTea88c05.y1 Eimeria M5-6 Merozoite stag...	32	5.9
	emb AI973878 AI973878 sd13a09.y1 Gm-c1020 Glycine max cDNA clone...	32	5.9
	dbj D85261 D85261 Plasmodium vivax clone TD439B DNA for merozoit...	32	5.9
	dbj D85251 D85251 Plasmodium vivax clone TD207B DNA for merozoit...	32	5.9
45	emb Z69381 SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom...	32	6.5
	emb Z71509 SCYNL233W S.cerevisiae chromosome XIV reading frame O...	32	6.5
	emb AW707662 AW707662 832011E08.y1 C. reinhardtii CC-125 nutrien...	28	7.3
	emb AF083075 AF083075 Fusarium oxysporum f. sp. lycopersici exop...	32	8.1
	emb AV411934 AV411934 AV411934 Lotus japonicus young plants (two...	32	8.1
50	emb AW703740 AW703740 sk23g09.y1 Gm-c1028 Glycine max cDNA clone...	32	8.1
	emb AW703739 AW703739 sk23g08.y1 Gm-c1028 Glycine max cDNA clone...	32	8.1
	emb AV419698 AV419698 AV419698 Lotus japonicus young plants (two...	32	8.1
	emb AV419299 AV419299 AV419299 Lotus japonicus young plants (two...	32	8.1
	emb AV420652 AV420652 AV420652 Lotus japonicus young plants (two...	32	8.1
55	emb AV408860 AV408860 AV408860 Lotus japonicus young plants (two...	32	8.1
	emb AV420989 AV420989 AV420989 Lotus japonicus young plants (two...	32	8.1
	emb AV419314 AV419314 AV419314 Lotus japonicus young plants (two...	32	8.1
	emb AW720540 AW720540 LjNEST18h4r Lotus japonicus nodule library...	32	8.1
60	emb X77895 CPGPRNL28 G.pyrenaica chloroplast trnL gene intron.	32	8.1

Query= TSB2_s_at 14673_s_at /id_source genbank /description
gb|aaa32879.1| (m81620) tryptophan synthase beta-subunit [arabidopsis
thaliana] thaliana] /blast_score 0 /ec_number /family /chip nova
/gb_link /ncgi

5 (1526 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

10 Searching.....done

		Score	E	
	Sequences producing significant alignments:	(bits)	Value	
15	emb AF042320 AF042320 <i>Camptotheca acuminata</i> tryptophan synthase ...	858	0.0	
	emb AF047024 AF047024 <i>Chlamydomonas reinhardtii</i> tryptophan synth...	712	0.0	
	gb J04594 NEUTRP3A <i>N.crassa</i> tryptophan synthetase (trp3) alpha-2...	473	e-140	
	emb Z98974 SPAC19A8 <i>S.pombe</i> chromosome I cosmid c19A8.	462	e-135	
	emb AW031813 AW031813 EST275267 tomato callus, TAMU Lycopersicon...	429	e-119	
20	emb AF121272 AF121272 <i>Gracilaria gracilis</i> putative NAD-myo-inosi...	426	e-118	
	dbj D89113 D89113 <i>Schizosaccharomyces pombe</i> mRNA, partial cds, c...	310	e-114	
	emb AI055312 AI055312 coau0003K07 Cotton Boll Abscission Zone cD...	404	e-112	
	emb AF042321 AF042321 <i>Camptotheca acuminata</i> tryptophan synthase ...	346	e-109	
	gb BE126222 BE126222 DG1_68_D09.b1_A002 Dark Grown 1 (DG1) Sorgh...	379	e-104	
25	emb AW650635 AW650635 EST329089 tomato germinating seedlings, TA...	372	e-102	
	emb AI487343 AI487343 EST245665 tomato ovary, TAMU Lycopersicon ...	354	8e-97	
	emb AI488733 AI488733 EST247072 tomato ovary, TAMU Lycopersicon ...	353	2e-96	
	emb AA495663 AA495663 c313 Zhou and Ragan 1993 <i>Gracilaria gracil</i> ...	350	1e-95	
	emb AW160221 AW160221 EST290079 <i>L. pennellii</i> trichome, Cornell U...	327	1e-88	
30	emb V01342 SCTRP5A Yeast gene (trp5) for tryptophan synthetase.	270	6e-88	
	emb Z72548 SCYGL026C <i>S.cerevisiae</i> chromosome VII reading frame O...	270	6e-88	
	emb AI485149 AI485149 EST243453 tomato ovary, TAMU Lycopersicon ...	319	3e-86	
	emb AI966766 AI966766 sc57f10.y1 Gm-c1016 Glycine max cDNA clone...	306	3e-82	
	gb M91659 CCITRP08 <i>Coprinus cinereus</i> tryptophan synthetase (TRP1...	302	4e-81	
35	gb BE058277 BE058277 sn13h12.y1 Gm-c1016 Glycine max cDNA clone ...	259	6e-68	
	emb AI488512 AI488512 EST246851 tomato ovary, TAMU Lycopersicon ...	237	2e-63	
	emb AI487792 AI487792 EST246114 tomato ovary, TAMU Lycopersicon ...	232	8e-62	
	emb AW696637 AW696637 NF109C11ST1F1085 Developing stem Medicago ...	213	2e-59	
40	emb AI898827 AI898827 EST268270 tomato ovary, TAMU Lycopersicon ...	228	7e-59	
	emb AQ450225 AQ450225 500009D01.x1 CpIOWAM13mpl8gDNA1 <i>Cryptospor</i> ...	175	3e-58	
	emb AW160220 AW160220 EST290078 <i>L. pennellii</i> trichome, Cornell U...	223	3e-57	
	emb AF084902 AF084902 <i>Neurospora crassa</i> TD2(4A-4A)2A mutant trypt...	214	2e-54	
	emb AF084903 AF084903 <i>Neurospora crassa</i> TD71-19A mutant tryptoph...	213	3e-54	
45	emb AF084904 AF084904 <i>Neurospora crassa</i> TD54-6A mutant tryptopha...	210	3e-53	
	emb AI779245 AI779245 EST260124 tomato susceptible, Cornell Lyco...	208	8e-53	
	emb AI487088 AI487088 EST245410 tomato ovary, TAMU Lycopersicon ...	149	3e-51	
	emb AQ876415 AQ876415 V99F5 mTn-3xHA/lacZ Insertion Library, str...	183	4e-50	
	emb AL116518 CNS01D8U <i>Botrytis cinerea</i> strain T4 cDNA library un...	160	2e-47	
50	emb AW745773 AW745773 WS1_37_G06.b1_A002 Water-stressed 1 (WS1) ...	167	2e-40	
	emb AF084893 AF084893 <i>Neurospora crassa</i> TD24-2A-28A mutant trypt...	130	8e-38	
	emb AF084892 AF084892 <i>Neurospora crassa</i> 314-567-9A mutant trypto...	132	1e-37	
	emb AF084891 AF084891 <i>Neurospora crassa</i> 314-616-2A mutant trypto...	132	1e-37	
	emb AF084895 AF084895 <i>Neurospora crassa</i> TD10-8A mutant tryptopha...	130	1e-37	
55	emb AF084894 AF084894 <i>Neurospora crassa</i> TD7(13A-11A)13A mutant t...	130	1e-37	
	emb AF084901 AF084901 <i>Neurospora crassa</i> TD72-1-25A mutant trypto...	129	1e-37	
	emb AF084900 AF084900 <i>Neurospora crassa</i> TD85-1-24A mutant trypto...	129	1e-37	
	emb AF084899 AF084899 <i>Neurospora crassa</i> TD86-1-22A mutant trypto...	129	1e-37	
	emb AF084898 AF084898 <i>Neurospora crassa</i> TD6(1-8A)22A mutant trypt...	129	1e-37	
60	emb AF084896 AF084896 <i>Neurospora crassa</i> NG29-3A mutant tryptopha...	129	1e-37	
	emb AW745836 AW745836 WS1_37_G06.g1_A002 Water-stressed 1 (WS1) ...	157	2e-37	

- emb|AF084897|AF084897 *Neurospora crassa* TD3-32-16A mutant trypto... 128 3e-37
emb|AI399300|AI399300 NCW07F11T3 Westergaards *Neurospora crassa* ... 145 3e-37
emb|AF084906|AF084906 *Neurospora crassa* NG40-5A mutant tryptopha... 152 8e-36
emb|AF084905|AF084905 *Neurospora crassa* NG25-4A mutant tryptopha... 152 8e-36
5 gb|BE024522|BE024522 894003E01.y1 *C. reinhardtii* CC-1690, normal... 142 6e-33
emb|AJ229567|KLAJ9567 *Khuyveromyces lactis* DNA fragment for sequ... 137 3e-31
emb|AQ449630|AQ449630 500002F12.x2 CpIOWAM13mp18gDNA1 *Cryptospor...* 116 1e-27
emb|AW695848|AW695848 NF099D01ST1F1012 Developing stem *Medicago* ... 116 9e-27
10 emb|AW098758|AW098758 ga01a03.y1 Moss EST library CPU *Ceratodon* ... 118 1e-25
gb|M91658|CCITRP07 *Coprinus cinereus* tryptophan synthetase (TRP1... 115 8e-25
emb|AW086510|AW086510 ga01a03.x1 Moss EST library CPU *Ceratodon* ... 103 4e-21
emb|AW221168|AW221168 EST297637 tomato fruit mature green, TAMU ... 96 5e-19
emb|AW650217|AW650217 EST328671 tomato germinating seedlings, TA... 95 1e-18
15 emb|AV408265|AV408265 AV408265 *Lotus japonicus* young plants (two... 77 4e-13
emb|AW688230|AW688230 NF005A01ST1F1000 Developing stem *Medicago* ... 72 1e-11
emb|AI488384|AI488384 EST246706 tomato ovary, TAMU *Lycopersicon* ... 70 4e-11
emb|AW032971|AW032971 EST276530 tomato callus, TAMU *Lycopersicon*... 60 6e-08
emb|AW755317|AW755317 sl01e06.y1 Gm-c1036 Glycine max cDNA clone... 57 4e-07
20 emb|AW153250|AW153250 se37h08.y1 Gm-c1015 Glycine max cDNA clone... 56 1e-06
emb|AQ450041|AQ450041 500007C05.x1 CpIOWAM13mp18gDNA1 *Cryptospor...* 37 2e-04
emb|AW625162|AW625162 EST319069 tomato radicle, 5 d post-imbibit... 45 0.001
gb|M91656|CCITRP05 *Coprinus cinereus* tryptophan synthetase (TRP1... 45 0.002
emb|AW926725|AW926725 HVSMEg0007P16 *Hordeum vulgare* pre-anthesis... 42 0.013
25 emb|X99652|ANG3PDEHY *A.niger* gpd gene. 35 0.084
emb|AV418759|AV418759 AV418759 *Lotus japonicus* young plants (two... 38 0.17
emb|AV417838|AV417838 AV417838 *Lotus japonicus* young plants (two... 38 0.17
emb|AV414417|AV414417 AV414417 *Lotus japonicus* young plants (two... 38 0.17
emb|AV419253|AV419253 AV419253 *Lotus japonicus* young plants (two... 38 0.17
30 emb|AV424994|AV424994 AV424994 *Lotus japonicus* young plants (two... 38 0.17
emb|AA901537|AA901537 NCC2B7T7 *Conidial Neurospora crassa* cDNA c... 38 0.23
gb|BE060085|BE060085 HVSMEg0011G11f *Hordeum vulgare* pre-anthesis... 38 0.23
gb|U30626|SCU30626 *Saccharomyces cerevisiae* var. diastaticus glu... 37 0.32
emb|AJ010201|GMA010201 Glycine max mRNA for inosine monophosphat... 37 0.32
35 emb|AW185330|AW185330 se90b04.y1 Gm-c1027 Glycine max cDNA clone... 37 0.32
emb|Z38061|SC9168 *S.cerevisiae* chromosome IX cosmid 9168. 37 0.32
emb|AF160799|AF160799 *Sporidiobolus salmonicolor* aldehyde reduct... 37 0.44
emb|AC016161|AC016161 *Leishmania major* chromosome 35 clone L8149... 37 0.44
emb|AW185636|AW185636 se80e06.y1 Gm-c1023 Glycine max cDNA clone... 37 0.44
40 emb|AB030490|AB030490 Glycine max SG-05 gene for thiamin biosynt... 36 0.60
emb|AW278827|AW278827 sf99b01.y1 Gm-c1019 Glycine max cDNA clone... 36 0.60
emb|Z93048|SLZ93048 *S.latifolia* mRNA, clone CCLS 37.1. 30 0.72
emb|AV393412|AV393412 AV393412 *Chlamydomonas reinhardtii* C9 Chla... 36 0.83
emb|AL035581|SPBC1677 *S.pombe* chromosome II cosmid c1677. 36 0.83
45 emb|AV425767|AV425767 AV425767 *Lotus japonicus* young plants (two... 36 0.83
emb|AI727538|AI727538 BNLGHi8343 Six-day Cotton fiber *Gossypium* ... 35 1.1
gb|BE053957|BE053957 GA_Ea0033K12f *Gossypium arboreum* 7-10 dpa ... 35 1.1
emb|AI731384|AI731384 BNLGHi8894 Six-day Cotton fiber *Gossypium* ... 35 1.1
emb|AW596016|AW596016 si96g09.y1 Gm-c1032 Glycine max cDNA clone... 35 1.1
50 emb|AI730998|AI730998 BNLGHi8370 Six-day Cotton fiber *Gossypium* ... 35 1.1
emb|AJ276509|TAE276509 *Triticum aestivum* grp1 gene for glycine-r... 28 1.3
gb|B13527|B13527 jd421 Trypanosome Shotgun M13 genomic Trypanoso... 29 1.4
gb|U56698|CPU56698 *Ceratodon purpureus* phytochrome photoreceptor... 35 2.2
emb|AF079252|AF079252 *Dichanthium aristatum* granule-bound starch... 35 2.2
55 emb|AJ133604|TAE133604 *Triticum aestivum* mRNA for alpha-gliadin ... 34 4.1

Query= WT1012A_RC_i_at14682_i_at /id_source genbank /description no
hits found. /blast_score /ec_number /family /chip nova /gb_link
60. [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|wt1012a|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|wt1012a|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|wt1012a|/ncgi)

<http://www.ncgr.org/cgi-bin/ff?wt1012a>
(257 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	(bits)	Value
10 Sequences producing significant alignments:				
emb AL115243 CNS01C9F Botrytis cinerea strain T4 cDNA library un...	29	5.7		
gb S69616 S69616 Ant18=dihydroflavonol-4-reductase [Hordeum vulg...	29	7.8		

15

Query= WT1096_at 14691_at /id_source genbank /description no hits
found. /blast_score /ec_number /family /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|wt1096|/ncgi)
post/entrez/query?db=n&form=6&dopt=g&uid=gb|wt1096|/ncgi
20 <http://www.ncgr.org/cgi-bin/ff?wt1096>
(371 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

25

Searching.....done

	Score	E	(bits)	Value
30 Sequences producing significant alignments:				
emb AW203566 AW203566 sf35f11.y1 Gm-c1028 Glycine max cDNA clone...	36	0.099		
emb AW776554 AW776554 EST335619 DSIL Medicago truncatula cDNA cl...	36	0.099		
emb AW171733 AW171733 N100627e rootphos(-) Medicago truncatula c...	36	0.099		
emb AW185514 AW185514 se80g03.y1 Gm-c1023 Glycine max cDNA clone...	36	0.099		
35 emb AI777176 AI777176 EST258141 tomato resistant, Cornell Lycopen...	35	0.26		
gb C22084 C22084 C22084 Miyagawa-wase satsuma mandarin orange (M...	35	0.26		
emb AW755041 AW755041 PC10A02 Pine TriplEx pollen cone library P...	35	0.26		
emb AW218263 AW218263 EST303444 tomato radicle, 5 d post-imbibit...	35	0.26		
emb AI488300 AI488300 EST246622 tomato ovary, TAMU Lycopersicon ...	35	0.26		
40 emb AA557085 AA557085 927 Loblolly pine N Pinus taeda cDNA clone...	35	0.26		
emb AW981718 AW981718 PC15H05 Pine TriplEx pollen cone library P...	35	0.26		
emb AW982079 AW982079 PC23E11 Pine TriplEx pollen cone library P...	35	0.35		
emb AF101786 AF101786 Pinus taeda clone PtaADH1 adhesive/proline...	35	0.35		
emb AA785548 AA785548 g8e04a1.fl Aspergillus nidulans 24hr asexu...	35	0.35		
45 emb AI812646 AI812646 17D5 Pine Lambda Zap Xylem library Pinus t...	35	0.35		
emb AI776730 AI776730 EST257830 tomato resistant, Cornell Lycopen...	34	0.49		
emb AW040418 AW040418 EST283282 tomato mixed elicitor, BTI Lycop...	34	0.49		
emb AI490164 AI490164 EST246756 tomato resistant, Cornell Lycopen...	34	0.49		
emb AA739624 AA739624 389 PtIFG2 Pinus taeda cDNA clone 8646M 3'...	34	0.49		
50 emb AI490158 AI490158 EST246750 tomato resistant, Cornell Lycopen...	34	0.49		
emb AW625280 AW625280 EST319283 tomato radicle, 5 d post-imbibit...	34	0.49		
emb AA740016 AA740016 781 PtIFG2 Pinus taeda cDNA clone 9242M 3'...	34	0.49		
emb AW329045 AW329045 N200244e rootphos(-) Medicago truncatula c...	34	0.67		
emb AA556671 AA556671 526 Loblolly pine CA Pinus taeda cDNA clon...	34	0.67		
55 emb AI416531 AI416531 sal0c07.y1 Gm-c1003 Glycine max cDNA clone...	33	0.92		
emb AI416664 AI416664 sal0c07.x1 Gm-c1003 Glycine max cDNA clone...	33	0.92		
gb BE023931 BE023931 sm94c10.y1 Gm-c1015 Glycine max cDNA clone ...	33	0.92		
emb AW064558 AW064558 ST33A05 Pine TriplEx shoot tip library Pin...	33	1.3		
gb BE033882 BE033882 MG01E10 MG Mesembryanthemum crystallinum cD...	33	1.3		
60 emb AW011244 AW011244 ST18E01 Pine TriplEx shoot tip library Pin...	33	1.3		
gb BE034004 BE034004 MG03C08 MG Mesembryanthemum crystallinum cD...	33	1.3		

emb|AW043113|AW043113 ST29E06 Pine TriplEx shoot tip library Pin... 33 1.3
emb|AA749493|AA749493 L30-34T3 Ice plant Lambda Uni-Zap XR expre... 33 1.3
emb|AW042623|AW042623 ST24A10 Pine TriplEx shoot tip library Pin... 33 1.3
emb|AW216739|AW216739 EST295453 tomato callus, TAMU Lycopersicon... 33 1.3
5 emb|AA660660|AA660660 00548 MtRHE Medicago truncatula cDNA 5', m... 33 1.3
emb|AW011516|AW011516 ST21G04 Pine TriplEx shoot tip library Pin... 33 1.3
emb|AW310413|AW310413 sf35f11.x1 Gm-cl028 Glycine max cDNA clone... 32 1.7
emb|AW043248|AW043248 ST31B02 Pine TriplEx shoot tip library Pin... 32 1.7
emb|AW255053|AW255053 ML1348 peppermint glandular trichome Menth... 32 2.4
10 emb|AW255347|AW255347 ML358 peppermint glandular trichome Menta... 32 2.4
emb|AW349069|AW349069 GM210003B22D9R Gm-r1021 Glycine max cDNA 3... 31 3.3
emb|AW597162|AW597162 sj74c10.y1 Gm-cl034 Glycine max cDNA clone... 31 3.3
emb|AI482974|AI482974 EST242297 tomato shoot, Cornell Lycopersic... 31 3.3
emb|AI482971|AI482971 EST242294 tomato shoot, Cornell Lycopersic... 31 3.3
15 emb|AW568662|AW568662 si60e08.y1 Gm-r1030 Glycine max cDNA clone... 31 3.3
emb|AI442234|AI442234 sa49d06.y1 Gm-cl004 Glycine max cDNA clone... 31 3.3
emb|AI484234|AI484234 EST248461 tomato susceptible, Cornell Lyco... 31 3.3
emb|AW568685|AW568685 si60g08.y1 Gm-r1030 Glycine max cDNA clone... 31 3.3
emb|AW218238|AW218238 EST303419 tomato radicle, 5 d post-imbibit... 31 3.3
20 emb|AW102024|AW102024 sd82b01.y1 Gm-cl009 Glycine max cDNA clone... 31 3.3
emb|AI484230|AI484230 EST248457 tomato susceptible, Cornell Lyco... 31 3.3
gb|BE020040|BE020040 sm38c04.y1 Gm-cl028 Glycine max cDNA clone ... 31 3.3
emb|AW064689|AW064689 ST34E09 Pine TriplEx shoot tip library Pin... 31 4.5
emb|AI212169|AI212169 w9d03a1.fl Aspergillus nidulans 24hr asexu... 31 4.5
25 emb|AI938315|AI938315 sc42h10.y1 Gm-cl014 Glycine max cDNA clone... 31 4.5
emb|AW010715|AW010715 ST11D03 Pine TriplEx shoot tip library Pin... 31 4.5
emb|AW064688|AW064688 ST34E08 Pine TriplEx shoot tip library Pin... 31 4.5
emb|AW705091|AW705091 sk57e09.y1 Gm-cl019 Glycine max cDNA clone... 30 6.2
emb|AW218605|AW218605 EST303788 tomato radicle, 5 d post-imbibit... 30 6.2
30 emb|AF039708|AF039708 Maackia amurensis early nodulin (ENOD2) mR... 30 8.5
emb|AW747425|AW747425 WS1_68_B12.b1_A002 Water-stressed 1 (WS1) ... 30 8.5
emb|AW687627|AW687627 NF011F08RT1F1074 Developing root Medicago ... 30 8.5
emb|AW329000|AW329000 N200194e rootphos(-) Medicago truncatula c... 30 8.5
emb|AW745895|AW745895 WS1_38_C08.b1_A002 Water-stressed 1 (WS1) ... 30 8.5
35 emb|AW683985|AW683985 NF004G11NR1F1000 Nodulated root Medicago t... 30 8.5
emb|AQ639472|AQ639472 927P1-2C7.TV 927P1 Trypanosoma brucei geno... 30 8.5
emb|AW747471|AW747471 WS1_68_B12.g1_A002 Water-stressed 1 (WS1) ... 30 8.5
emb|AW208288|AW208288 M110945e GVSN Medicago truncatula cDNA clo... 30 8.5

40 Query= WT768_RC_s_at 14704_s_at /id_source genbank /description
gb|aad15461.1| (ac006067) unknown protein [arabidopsis thaliana]
/blast_score 1.00e-48 /ec_number /family /chip nova /gb_link /ncgi
(315 letters)

45 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

50 Score E
Sequences producing significant alignments: (bits) Value

emb|AI771551|AI771551 EST252651 tomato ovary, TAMU Lycopersicon ... 105 1e-22
emb|AI896756|AI896756 EST266199 tomato callus, TAMU Lycopersicon... 105 1e-22
55 emb|AI778651|AI778651 EST259530 tomato susceptible, Cornell Lyco... 105 1e-22
emb|AI898070|AI898070 EST267513 tomato ovary, TAMU Lycopersicon ... 105 1e-22
emb|AW030559|AW030559 EST273814 tomato callus, TAMU Lycopersicon... 105 1e-22
emb|AW930095|AW930095 EST340552 tomato fruit mature green, TAMU ... 105 1e-22
emb|AI894447|AI894447 EST263902 tomato callus, TAMU Lycopersicon... 105 1e-22
60 emb|AW219398|AW219398 EST301976 tomato root during/after fruit s... 105 1e-22
emb|AW399345|AW399345 EST309845 L. pennellii trichome, Cornell U... 104 2e-22

	emb AW399412 AW399412 EST309912 <i>L. pennellii</i> trichome, Cornell U...	104	2e-22
	emb AI773854 AI773854 EST254954 tomato resistant, Cornell Lycopersicon...	104	3e-22
	gb BE125244 BE125244 DG1_18_B07.b1_A002 Dark Grown 1 (DG1) Sorgh...	99	9e-21
	emb AI736542 AI736542 sb30b04.y1 Gm-c1009 Glycine max cDNA clone...	64	5e-17
5	emb AI938176 AI938176 sc40e07.y1 Gm-c1014 Glycine max cDNA clone...	84	2e-16
	emb AI938151 AI938151 sc40a07.y1 Gm-c1014 Glycine max cDNA clone...	84	3e-16
	emb AW133238 AW133238 se16b04.y1 Gm-c1013 Glycine max cDNA clone...	84	3e-16
	emb AW568464 AW568464 si59b03.y1 Gm-r1030 Glycine max cDNA clone...	84	3e-16
	emb AW832123 AW832123 sm30h02.y1 Gm-c1028 Glycine max cDNA clone...	84	5e-16
10	emb AI899328 AI899328 EST268771 tomato ovary, TAMU Lycopersicon ...	82	2e-15
	emb AW348772 AW348772 GM210003A22G1R Gm-r1021 Glycine max cDNA 3...	80	6e-15
	emb AI443600 AI443600 sa42b08.y1 Gm-c1004 Glycine max cDNA clone...	72	1e-12
	gb BE057559 BE057559 sn04a01.y1 Gm-c1015 Glycine max cDNA clone ...	70	5e-12
	emb AI896759 AI896759 EST266202 tomato callus, TAMU Lycopersicon...	61	3e-09
15	gb BE123900 BE123900 EST394025 <i>DSIL Medicago truncatula</i> cDNA clo...	58	2e-08
	emb AW030966 AW030966 EST274273 tomato callus, TAMU Lycopersicon...	34	8e-05
	emb AW185963 AW185963 se61h02.y1 Gm-c1019 Glycine max cDNA clone...	40	0.004
	gb T14912 T14912 crs394 lambdaZAPST <i>Ricinus communis</i> cDNA clone ...	40	0.004
	emb AW184959 AW184959 se84d10.y1 Gm-c1023 Glycine max cDNA clone...	40	0.004
20	emb AW217201 AW217201 EST295915 tomato callus, TAMU Lycopersicon...	29	0.010
	emb AI487153 AI487153 EST245475 tomato ovary, TAMU Lycopersicon ...	35	0.14
	emb AA556663 AA556663 518 Loblolly pine CA <i>Pinus taeda</i> cDNA clon...	35	0.26
	emb AW472418 AW472418 si24h07.y1 Gm-c1029 Glycine max cDNA clone...	29	0.37
	emb AW831124 AW831124 sm09c06.y1 Gm-c1027 Glycine max cDNA clone...	28	0.56
25	gb BE059192 BE059192 sn27d12.y1 Gm-c1016 Glycine max cDNA clone ...	32	1.3
	emb AW101722 AW101722 sd69d02.y1 Gm-c1008 Glycine max cDNA clone...	32	1.3
	emb AW395281 AW395281 sh46b07.y1 Gm-c1017 Glycine max cDNA clone...	32	1.8
	emb AW932541 AW932541 EST358384 tomato fruit mature green, TAMU ...	31	2.4
	emb AV428275 AV428275 AV428275 <i>Lotus japonicus</i> young plants (two...	31	2.4
30	emb AV415030 AV415030 AV415030 <i>Lotus japonicus</i> young plants (two...	31	2.4
	emb AW702436 AW702436 TgESTzz76b07.y1 TgRH*-Tachyzoite cDNA Toxo...	31	2.4
	emb AW621293 AW621293 EST312091 tomato root during/after fruit s...	31	2.4
	gb BE036447 BE036447 MO24G12 <i>MO Mesembryanthemum crystallinum</i> cD...	31	2.4
	emb AW509230 AW509230 sh92h07.y1 Gm-c1016 Glycine max cDNA clone...	31	2.4
35	emb AW034791 AW034791 EST278827 tomato callus, TAMU Lycopersicon...	31	2.4
	emb AI780125 AI780125 EST261004 tomato susceptible, Cornell Lyco...	31	2.4
	gb BE021558 BE021558 sm49e02.y1 Gm-c1028 Glycine max cDNA clone ...	31	2.4
	emb AW220250 AW220250 EST302733 tomato root during/after fruit s...	31	2.4
	emb AW442607 AW442607 EST307537 tomato mixed elicitor, BTI Lycop...	31	2.4
40	emb AW623982 AW623982 EST321927 tomato flower buds 3-8 mm, Corne...	29	2.5
	emb AW719534 AW719534 LjNEST5c5rW <i>Lotus japonicus</i> nodule library...	31	3.3
	emb AW926699 AW926699 HVSMEg0007O14 <i>Hordeum vulgare</i> pre-anthesis...	31	3.3
	emb AL035264 LMFL8032 <i>Leishmania major</i> Friedlin chromosome 4 cos...	30	4.5
	emb AF015462 AF015462 <i>Plasmodium falciparum</i> microsatellite 14D s...	30	4.5
45	emb AQ989347 AQ989347 Gm_ISb001_080_I14R ISU Soybean BAC Library...	30	4.5
	emb AL354553 LMFL232 <i>Leishmania major</i> Friedlin chromosome 14 cos...	30	6.2
	emb AL049498 SPCC645 <i>S.pombe</i> chromosome III cosmid c645.	30	6.2
	emb AI352775 AI352775 MB58-8A PZ204.BNlib <i>Brassica napus</i> cDNA cl...	30	6.2
	emb AZ216688 AZ216688 Sheared DNA-84G11.TF Sheared DNA Trypanoso...	30	6.2
50	emb AQ160113 AQ160113 mgxb0003K19r CUGI Rice Blast BAC Library P...	30	6.2
	emb AF105143 AF105143 <i>Brassica napus</i> chromosome N3 disease resis...	29	8.6
	emb AV394954 AV394954 AV394954 <i>Chlamydomonas reinhardtii</i> C9 Chla...	29	8.6
	emb AF162071 AF162071 <i>Mortierella verticillata</i> beta-tubulin 1 (b...	29	8.6
	emb AV395268 AV395268 AV395268 <i>Chlamydomonas reinhardtii</i> C9 Chla...	29	8.6
55	emb AI960376 AI960376 sc82g12.y1 Gm-c1018 Glycine max cDNA clone...	29	8.6
	emb AV393824 AV393824 AV393824 <i>Chlamydomonas reinhardtii</i> C9 Chla...	29	8.6
	emb AW711896 AW711896 f6el1ne.r1 <i>Neurospora crassa</i> evening cDNA ...	29	8.6
	emb AV396392 AV396392 AV396392 <i>Chlamydomonas reinhardtii</i> C9 Chla...	29	8.6
	emb AQ659750 AQ659750 Sheared DNA-16J7.TF Sheared DNA Trypanosom...	29	8.6
60	emb AL163505 LMFL3640 <i>Leishmania major</i> Friedlin chromosome 21 co...	29	8.6

Query= WT788_at 14709_at /id_source genbank /description no hits found
less than or equal to 1e-15. /blast_score /ec_number /family /chip
nova /gb_link

5 http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|wt788|/ncgi
http://www.ncgr.org/cgi-bin/ff?wt788
(528 letters)

10 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	
	Sequences producing significant alignments:			(bits) Value
	emb AW156276 AW156276 se21h09.y1 Gm-c1015 Glycine max cDNA clone...	39	0.025	
	emb AW688406 AW688406 NF007A07ST1F1000 Developing stem Medicago ...	35	0.59	
20	emb AW729009 AW729009 GA__Ea0019F23 Gossypium arboreum 7-10 dpa ...	35	0.59	
	emb AI210929 AI210929 m0d12a1.r1 Aspergillus nidulans 24hr asexu...	34	0.81	
	emb AI212271 AI212271 x1d11a1.r1 Aspergillus nidulans 24hr asexu...	34	0.81	
	emb AI210928 AI210928 m0d12a1.fl Aspergillus nidulans 24hr asexu...	34	0.81	
	emb AA783628 AA783628 c6e11a1.r1 Aspergillus nidulans 24hr asexu...	34	0.81	
25	emb AF093253 AF093253 Selaginella deflexa ribulose biphosphate ...	34	1.1	
	emb AW692476 AW692476 NF052A03ST1F1000 Developing stem Medicago ...	33	1.5	
	emb AW756661 AW756661 sl25e12.y1 Gm-c1027 Glycine max cDNA clone...	33	1.5	
	emb AW278522 AW278522 sf45e07.y1 Gm-c1009 Glycine max cDNA clone...	33	1.5	
	emb AW424313 AW424313 sh63h04.y1 Gm-c1015 Glycine max cDNA clone...	33	1.5	
30	emb AW696170 AW696170 NF103B07ST1F1060 Developing stem Medicago ...	33	1.5	
	emb AW569414 AW569414 si86g10.y1 Gm-c1031 Glycine max cDNA clone...	33	1.5	
	emb AW830833 AW830833 sm36c08.y1 Gm-c1028 Glycine max cDNA clone...	33	1.5	
	emb AW831982 AW831982 sm18e08.y1 Gm-c1027 Glycine max cDNA clone...	33	1.5	
	emb AW734341 AW734341 sk81h11.y1 Gm-c1016 Glycine max cDNA clone...	33	1.5	
35	emb Y07940 SSY07940 S.selaginoides chloroplast rbcL gene.	33	2.1	
	emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi...	32	4.0	
	emb AQ946352 AQ946352 Sheared DNA-45B22.TF Sheared DNA Trypanoso...	31	5.5	
	emb AW180477 AW180477 MgA0600fMgA Library Mycosphaerella gramin...	31	5.5	
	emb AQ651798 AQ651798 Sheared DNA-20J13.TR Sheared DNA Trypanoso...	31	5.5	

40 Query= af121356_f_at 15116_f_at /id_source genbank /description
gb|aad28243.1|af121356_1 (af121356) peroxiredoxin tpx2 [arabidopsis
thaliana] /blast_score 6.00e-81
(647 letters)

45 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	
	Sequences producing significant alignments:			(bits) Value
	emb AF133302 AF133302 Brassica rapa subsp. pekinensis type 2 per...	331	2e-90	
55	emb AW667697 AW667697 GA__Ea0010E14 Gossypium arboreum 7-10 dpa ...	287	6e-77	
	emb AI778230 AI778230 EST259109 tomato susceptible, Cornell Lyco...	287	6e-77	
	emb AW218621 AW218621 EST303804 tomato radicle, 5 d post-imbibit...	287	6e-77	
	emb AW668548 AW668548 GA__Ea0014I16 Gossypium arboreum 7-10 dpa ...	287	6e-77	
	emb AW668413 AW668413 GA__Ea0013N18 Gossypium arboreum 7-10 dpa ...	287	6e-77	
60	emb AI782495 AI782495 EST263374 tomato susceptible, Cornell Lyco...	285	3e-76	
	emb AI779421 AI779421 EST260300 tomato susceptible, Cornell Lyco...	285	3e-76	

- emb|AI775630|AI775630 EST256730 tomato resistant, Cornell Lycopersicon... 285 3e-76
gb|BE055389|BE055389 GA__Ea0026N20f Gossypium arboreum 7-10 dpa ... 284 5e-76
emb|AI779420|AI779420 EST260299 tomato susceptible, Cornell Lycopersicon... 282 2e-75
emb|AW349482|AW349482 GM210007A20G5R Gm-r1021 Glycine max cDNA 3... 282 2e-75
- 5
emb|AW041006|AW041006 EST283870 tomato mixed elicitor, BTI Lycopersicon... 279 2e-74
emb|AW597183|AW597183 sj74f03.y1 Gm-c1034 Glycine max cDNA clone... 278 3e-74
gb|BE055703|BE055703 GA__Ea0033C16f Gossypium arboreum 7-10 dpa ... 275 2e-73
emb|AW567736|AW567736 si54c02.y1 Gm-r1030 Glycine max cDNA clone... 275 2e-73
- 10
emb|AW569109|AW569109 si63e02.y1 Gm-r1030 Glycine max cDNA clone... 275 2e-73
emb|AW472050|AW472050 si19d05.y1 Gm-c1029 Glycine max cDNA clone... 273 8e-73
emb|AW568096|AW568096 si68d05.y1 Gm-r1030 Glycine max cDNA clone... 273 1e-72
emb|AW568074|AW568074 si68b05.y1 Gm-r1030 Glycine max cDNA clone... 272 1e-72
emb|AW733947|AW733947 sk85e02.y1 Gm-c1035 Glycine max cDNA clone... 271 4e-72
- 15
emb|AW508057|AW508057 si49e04.y1 Gm-r1030 Glycine max cDNA clone... 271 4e-72
emb|AW573705|AW573705 EST316296 GVN Medicago truncatula cDNA clone... 271 4e-72
emb|AW508326|AW508326 si52e11.y1 Gm-r1030 Glycine max cDNA clone... 270 7e-72
emb|AW980703|AW980703 EST391856 GVN Medicago truncatula cDNA clone... 269 1e-71
emb|AI930835|AI930835 sc47h06.y1 Gm-c1015 Glycine max cDNA clone... 269 1e-71
- 20
emb|AI930828|AI930828 sc47g06.y1 Gm-c1015 Glycine max cDNA clone... 269 1e-71
emb|AW035526|AW035526 EST281264 tomato callus, TAMU Lycopersicon... 266 1e-70
emb|AW568472|AW568472 si59c02.y1 Gm-r1030 Glycine max cDNA clone... 262 2e-69
emb|AW729878|AW729878 GA__Ea0026I18 Gossypium arboreum 7-10 dpa ... 261 4e-69
emb|AW101773|AW101773 sd70b02.y1 Gm-c1008 Glycine max cDNA clone... 261 4e-69
- 25
emb|AW559683|AW559683 EST314795 DSIR Medicago truncatula cDNA clone... 260 6e-69
emb|AW317108|AW317108 sg44d09.y1 Gm-c1025 Glycine max cDNA clone... 260 8e-69
emb|AW397034|AW397034 sg66b12.y1 Gm-c1007 Glycine max cDNA clone... 258 3e-68
emb|AW349372|AW349372 GM210004B12G2R Gm-r1021 Glycine max cDNA 3... 256 1e-67
- 30
emb|AW094638|AW094638 EST287806 tomato mixed elicitor, BTI Lycopersicon... 255 3e-67
emb|AW585325|AW585325 EST306020 KV2 Medicago truncatula cDNA clone... 251 3e-66
emb|AW351217|AW351217 GM210010B20H5R Gm-r1021 Glycine max cDNA 3... 250 8e-66
- 35
emb|AW666097|AW666097 sk32b07.y1 Gm-c1028 Glycine max cDNA clone... 248 4e-65
emb|AW756544|AW756544 sl23d11.y1 Gm-c1036 Glycine max cDNA clone... 247 6e-65
emb|AA556985|AA556985 827 Loblolly pine N Pinus taeda cDNA clone... 237 6e-62
emb|AW279163|AW279163 sf67b11.y1 Gm-c1013 Glycine max cDNA clone... 237 8e-62
emb|AW201089|AW201089 se97f12.y1 Gm-c1027 Glycine max cDNA clone... 236 1e-61
emb|AI162549|AI162549 A019P27U Hybrid aspen plasmid library Populus... 236 2e-61
- 40
emb|AW720300|AW720300 LjNEST20d9r Lotus japonicus nodule library... 236 2e-61
emb|AW065021|AW065021 ST38F08 Pine TriplEx shoot tip library Pinus... 236 2e-61
emb|AI440757|AI440757 sa53g03.y1 Gm-c1004 Glycine max cDNA clone... 234 6e-61
emb|AW043308|AW043308 ST31G09 Pine TriplEx shoot tip library Pinus... 230 1e-59
emb|AW508348|AW508348 si52g09.y1 Gm-r1030 Glycine max cDNA clone... 229 2e-59
- 45
emb|AI774108|AI774108 EST255208 tomato resistant, Cornell Lycopersicon... 227 7e-59
emb|AI163857|AI163857 A050p05u Hybrid aspen plasmid library Populus... 226 9e-59
emb|AW065077|AW065077 ST39D01 Pine TriplEx shoot tip library Pinus... 225 2e-58
emb|AW704118|AW704118 sk16b03.y1 Gm-c1028 Glycine max cDNA clone... 221 4e-57
emb|AI507795|AI507795 sb12g09.y1 Gm-c1004 Glycine max cDNA clone... 216 1e-55
- 50
emb|AW289649|AW289649 NXNV003G05F Nsf Xylem Normal wood Vertical... 215 2e-55
emb|AV422946|AV422946 AV422946 Lotus japonicus young plants (two... 122 3e-55
gb|T14824|T14824 crs266 lambdaZAPST Ricinus communis cDNA clone ... 212 2e-54
emb|AW443507|AW443507 EST308437 tomato mixed elicitor, BTI Lycopersicon... 207 6e-53
emb|AW226029|AW226029 ST76E07 Pine TriplEx shoot tip library Pinus... 207 8e-53
- 55
emb|AW747461|AW747461 WS1_68_B01.g1_A002 Water-stressed 1 (WS1) ... 181 1e-51
emb|AI162776|AI162776 A023P56U Hybrid aspen plasmid library Populus... 132 7e-51
gb|BE054071|BE054071 GA__Ea0035D19f Gossypium arboreum 7-10 dpa ... 93 4e-50
gb|C96251|C96251 C96251 Marchantia polymorpha immature sex organ... 98 5e-50
emb|AI442544|AI442544 sa32h03.y1 Gm-c1004 Glycine max cDNA clone... 196 2e-49
- 60
emb|AI164569|AI164569 A065P13U Hybrid aspen plasmid library Populus... 180 2e-48
emb|AW888188|AW888188 NXNV_105_F04_F Nsf Xylem Normal wood Vertical... 183 1e-45

emb|AI855650|AI855650 sc32c06.y1 Gm-c1014 Glycine max cDNA clone... 127 3e-45
 emb|AI777234|AI777234 EST258199 tomato resistant, Cornell Lycopen... 148 1e-44
 emb|AI165310|AI165310 A081P03U Hybrid aspen plasmid library Popu... 152 7e-44
 emb|AW870064|AW870064 NXNV_123_F09_F Nsf Xylem Normal wood Verti... 176 1e-43
 5 emb|AI484178|AI484178 EST249331 tomato resistant, Cornell Lycopen... 144 2e-43
 emb|AI162101|AI162101 A012P21U Hybrid aspen plasmid library Popu... 164 3e-42
 emb|AW255890|AW255890 ML976 peppermint glandular trichome Menta... 143 7e-42
 emb|AW733771|AW733771 sk84b01.y1 Gm-c1035 Glycine max cDNA clone... 149 7e-42
 emb|AW010084|AW010084 PC01E03 Pine TriplEx pollen cone library P... 160 7e-39
 10 emb|AI161700|AI161700 A005P46U Hybrid aspen plasmid library Popu... 150 3e-38
 emb|AW443795|AW443795 EST308725 tomato mixed elicitor, BTI Lycop... 157 6e-38
 emb|AI774615|AI774615 EST255715 tomato resistant, Cornell Lycopen... 157 6e-38
 emb|AW651357|AW651357 EST329811 tomato germinating seedlings, TA... 157 6e-38
 emb|AW623884|AW623884 EST321829 tomato flower buds 3-8 mm, Corne... 157 6e-38
 15 emb|AI484189|AI484189 EST249342 tomato resistant, Cornell Lycopen... 157 9e-38
 gb|L37653|L37653 BNAESTGU Mustard flower buds Brassica rapa cDNA... 156 1e-37
 emb|AW944894|AW944894 EST336944 tomato flower buds 3-8 mm, Corne... 154 8e-37
 emb|AW726742|AW726742 GA_Ea0022J15 Gossypium arboreum 7-10 dpa ... 152 2e-36
 emb|AW694116|AW694116 NF072H11ST1F1095 Developing stem Medicago ... 150 2e-36
 20 emb|AW649234|AW649234 EST327688 tomato germinating seedlings, TA... 151 5e-36
 emb|AW725828|AW725828 GA_Ea0019N04 Gossypium arboreum 7-10 dpa ... 95 8e-36
 emb|AI777997|AI777997 EST258876 tomato susceptible, Cornell Lyco... 149 3e-35
 emb|AW317704|AW317704 sg56c06.y1 Gm-c1007 Glycine max cDNA clone... 148 4e-35
 emb|AW432260|AW432260 sh71d04.y1 Gm-c1015 Glycine max cDNA clone... 143 2e-33
 25 emb|AI165031|AI165031 A073p61u Hybrid aspen plasmid library Popu... 131 6e-32
 emb|AI507718|AI507718 sb10g09.y1 Gm-c1004 Glycine max cDNA clone... 131 2e-31
 emb|AW756555|AW756555 sl23g03.y1 Gm-c1036 Glycine max cDNA clone... 133 2e-30
 emb|AI164114|AI164114 A055P05U Hybrid aspen plasmid library Popu... 89 2e-29
 emb|AV428084|AV428084 AV428084 Lotus japonicus young plants (two... 127 1e-28
 30 emb|AI899479|AI899479 EST268922 tomato susceptible, Cornell Lyco... 124 7e-28
 emb|AI460396|AI460396 sa81a06.y1 Gm-c1004 Glycine max cDNA clone... 119 2e-26
 emb|AT002745|AT002745 AT002745 POSLM01 Pleurotus ostreatus cDNA ... 116 9e-26
 emb|AW508566|AW508566 si33e04.y1 Gm-r1030 Glycine max cDNA clone... 115 4e-25
 emb|AI166161|AI166161 B00964U Hybrid aspen plasmid library Popul... 113 1e-24

35

Query= atu90522_s_at 15161_s_at /id_source genbank /description
 gb|aa53975.1| (u90522) lysine-ketoglutarate reductase/saccharopine
 dehydrogenase [arabidopsis thaliana] /blast_score 0
 (3267 letters)

40

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

45

Score E
 Sequences producing significant alignments: (bits) Value

emb|AI486200|AI486200 EST244521 tomato ovary, TAMU Lycopersicon ... 377 e-103
 50 emb|AI894899|AI894899 EST264342 tomato callus, TAMU Lycopersicon... 357 4e-97
 emb|AI488742|AI488742 EST247081 tomato ovary, TAMU Lycopersicon ... 347 2e-94
 emb|AF042184|AF042184 Brassica napus lysine-ketoglutarate reduct... 334 1e-93
 emb|AI054604|AI054604 coau0001I01 Cotton Boll Abscission Zone cD... 319 3e-92
 emb|AW034280|AW034280 EST277851 tomato callus, TAMU Lycopersicon... 316 7e-85
 55 emb|AI894874|AI894874 EST264317 tomato callus, TAMU Lycopersicon... 307 4e-82
 emb|AW932187|AW932187 EST358030 tomato fruit mature green, TAMU ... 294 2e-78
 emb|AW933092|AW933092 EST358935 tomato fruit mature green, TAMU ... 287 4e-76
 emb|AW442160|AW442160 EST311556 tomato fruit red ripe, TAMU Lyco... 220 8e-74
 emb|AW681014|AW681014 WS1_8_B05.b1_A002 Water-stressed 1 (WS1) S... 275 1e-72
 60 emb|AW933411|AW933411 EST359350 tomato fruit mature green, TAMU ... 272 1e-71
 emb|AW931846|AW931846 EST357689 tomato fruit mature green, TAMU ... 264 3e-69

- emb|AI485129|AI485129 EST243433 tomato ovary, TAMU Lycopersicon ... 253 8e-66
emb|AW035300|AW035300 EST280663 tomato callus, TAMU Lycopersicon... 241 3e-62
emb|AW934545|AW934545 EST353353 tomato flower buds 0-3 mm, Corne... 230 4e-59
emb|AI771941|AI771941 EST253041 tomato ovary, TAMU Lycopersicon ... 228 2e-58
5 emb|AL022244|SPBC3B8 *S.pombe* chromosome II cosmid c3B8. 181 2e-56
emb|AW037965|AW037965 EST279609 tomato mixed elicitor, BTI Lycop... 211 2e-53
emb|AW931630|AW931630 EST357473 tomato fruit mature green, TAMU ... 208 3e-52
emb|AW035261|AW035261 EST280523 tomato callus, TAMU Lycopersicon... 142 4e-52
emb|AI896768|AI896768 EST266211 tomato callus, TAMU Lycopersicon... 192 2e-47
10 emb|Z71665|SCYNR050C *S.cerevisiae* chromosome XIV reading frame O... 155 5e-47
emb|X77363|SCLYS9 *S.cerevisiae* LYS9 gene. 155 5e-47
emb|AW224200|AW224200 EST301107 tomato fruit red ripe, TAMU Lyco... 188 2e-46
emb|AW930672|AW930672 EST356515 tomato fruit mature green, TAMU ... 110 4e-45
emb|AI771935|AI771935 EST253035 tomato ovary, TAMU Lycopersicon ... 173 6e-42
15 emb|AI899372|AI899372 EST268815 tomato ovary, TAMU Lycopersicon ... 172 1e-41
emb|AI486726|AI486726 EST245048 tomato ovary, TAMU Lycopersicon ... 110 2e-40
emb|AI483615|AI483615 EST249479 tomato ovary, TAMU Lycopersicon ... 110 2e-40
emb|AW441656|AW441656 EST311052 tomato fruit red ripe, TAMU Lyco... 110 2e-38
emb|AI486762|AI486762 EST245084 tomato ovary, TAMU Lycopersicon ... 161 3e-38
20 emb|AI488387|AI488387 EST246709 tomato ovary, TAMU Lycopersicon ... 160 6e-38
emb|AW093830|AW093830 EST287010 tomato mixed elicitor, BTI Lycop... 98 4e-33
emb|AV427683|AV427683 AV427683 *Lotus japonicus* young plants (two... 142 2e-32
emb|AI782310|AI782310 EST263189 tomato susceptible, Cornell Lyco... 139 1e-31
emb|AW432287|AW432287 sh71g03.y1 Gm-c1015 Glycine max cDNA clone... 82 6e-31
25 emb|AL111972|CNS019QK *Botrytis cinerea* strain T4 cDNA library un... 136 1e-30
emb|AU012735|AU012735 AU012735 *Schizosaccharomyces pombe* late lo... 125 5e-30
emb|AI771382|AI771382 EST252482 tomato ovary, TAMU Lycopersicon ... 132 1e-29
emb|AW681093|AW681093 WS1_8_B05.g1_A002 Water-stressed 1 (WS1) S... 127 7e-28
emb|AU010645|AU010645 AU010645 *Schizosaccharomyces pombe* late lo... 118 2e-25
30 emb|AW038858|AW038858 EST280814 tomato mixed elicitor, BTI Lycop... 114 5e-24
emb|AW201969|AW201969 sf09e01.y1 Gm-c1027 Glycine max cDNA clone... 113 9e-24
emb|AI487518|AI487518 EST245840 tomato ovary, TAMU Lycopersicon ... 110 6e-23
emb|AI486763|AI486763 EST245085 tomato ovary, TAMU Lycopersicon ... 110 6e-23
emb|AI399018|AI399018 NCW10A5T3 *Westergaards Neurospora crassa* c... 63 1e-21
35 emb|AW031018|AW031018 EST274325 tomato callus, TAMU Lycopersicon... 101 4e-20
emb|AW932183|AW932183 EST358026 tomato fruit mature green, TAMU ... 72 9e-13
emb|AW096237|AW096237 EST289417 tomato mixed elicitor, BTI Lycop... 67 8e-10
emb|AA577639|AA577639 EST213 Sugarcane leaf roll *Saccharum* sp. c... 65 3e-09
emb|AW224318|AW224318 EST301045 tomato fruit red ripe, TAMU Lyco... 51 5e-05
40 emb|AI900022|AI900022 sb97g03.y1 Gm-c1012 Glycine max cDNA clone... 50 1e-04
gb|M34929|YSJSACDHY *Y.lipolytica* saccharopine dehydrogenase (LYS... 46 0.002
emb|Z38061|SC9168 *S.cerevisiae* chromosome IX cosmid 9168. 45 0.004
emb|X77362|SCLYS1 *S.cerevisiae* LYS1 gene. 45 0.004
emb|AQ448181|AQ448181 mgxb0018C10r CUGI Rice Blast BAC Library P... 41 0.041
45 gb|U13233|CAU13233 *Candida albicans* saccharopine dehydrogenase (... 40 0.078
emb|AL110979|CNS018Z0 *Botrytis cinerea* strain T4 cDNA library un... 35 0.079
emb|AL133156|SPAC227 *S.pombe* chromosome I cosmid c227. 40 0.15
emb|AF178855|AF178855 *Candida albicans* Crm1p (CRM1) gene, comple... 37 0.99
emb|AI667978|AI667978 TENG0800 *T. Cruzi* epimastigote normalised ... 36 1.4
50 emb|AW310192|AW310192 sf32e10.x1 Gm-c1028 Glycine max cDNA clone... 36 1.4
emb|AW705872|AW705872 sk52a01.y1 Gm-c1019 Glycine max cDNA clone... 35 2.6
emb|AL355930|NCB208 *Neurospora crassa* DNA linkage group II BAC c... 35 3.5
gb|N82089|N82089 TgESTzy41f01.r1 TgRH Tachyzoite cDNA *Toxoplasma*... 35 3.5
emb|AW713255|AW713255 g6f04ne.fl *Neurospora crassa* evening cDNA ... 33 4.1
55 emb|AW710105|AW710105 elc07ne.fl *Neurospora crassa* evening cDNA ... 33 4.1
emb|AW712320|AW712320 gla02ne.fl *Neurospora crassa* evening cDNA ... 33 4.2
emb|AA451583|AA451583 AJK252 Onion seedling leaf cDNA library Al... 35 4.8
emb|AQ660868|AQ660868 Sheared DNA-27G4.TF Sheared DNA *Trypanosom*... 35 4.8
emb|AI773473|AI773473 EST254573 tomato resistant, Cornell Lycop... 30 5.4
60 emb|X99000|CS39KBCIV *S.cerevisiae* 39kb DNA segment of chromosome... 34 6.7
gb|BE021261|BE021261 sm56g06.y1 Gm-c1028 Glycine max cDNA clone ... 34 6.7

emb|AA556567|AA556567 422 Loblolly pine C Pinus taeda cDNA clone... 34 6.7
 emb|Z74265|SCYDL217C S.cerevisiae chromosome IV reading frame OR... 34 6.7
 emb|Z73529|SCYPL173W S.cerevisiae chromosome XVI reading frame O... 34 6.7
 emb|AI486066|AI486066 EST244387 tomato ovary, TAMU Lycopersicon ... 34 6.7
 5 emb|AV420631|AV420631 AV420631 Lotus japonicus young plants (two... 34 6.7
 emb|AW759867|AW759867 sl55b07.y1 Gm-cl027 Glycine max cDNA clone... 34 6.7
 emb|AL049181|PFMAL13P4 Plasmodium falciparum chromosome 13 strai... 34 9.2
 emb|AW278000|AW278000 sf89e04.y1 Gm-cl019 Glycine max cDNA clone... 34 9.2
 emb|AL033391|CAC20C1 C.albicans cosmid Ca20C1. 34 9.2
 10 emb|AF202183|AF202183 Glycine max isoflavone reductase homolog 1... 34 9.2
 emb|AW648458|AW648458 EST326912 tomato germinating seedlings, TA... 34 9.2
 emb|AA051847|AA051847 Cn0025-5 Cryptococcus neoformans, Stratage... 34 9.2
 emb|AI960767|AI960767 sc90b07.y1 Gm-cl019 Glycine max cDNA clone... 34 9.2
 emb|Z49384|SCYJL109C S.cerevisiae chromosome X reading frame ORF... 34 9.2
 15 emb|AF106954|AF106954 Brassica napus galactinol synthase (GS) mR... 34 9.2
 emb|AW164589|AW164589 se73h03.y1 Gm-cl023 Glycine max cDNA clone... 34 9.2
 emb|AW731148|AW731148 GA__Ea0010C07 Gossypium arboreum 7-10 dpa ... 34 9.2
 emb|AW308914|AW308914 sf91g02.y1 Gm-cl019 Glycine max cDNA clone... 34 9.2
 emb|X85021|SCXLTORFS S.cerevisiae DNA from left arm of chromosom... 34 9.2
 20 emb|AV423166|AV423166 AV423166 Lotus japonicus young plants (two... 34 9.2
 emb|Z99164|SPAC29B12 S.pombe chromosome I cosmid c29B12. 29 9.4

Query= athpro25a_s_at 15616_s_at /id_source genbank /description
 25 emb|caa08794.1| (aj009696) wall-associated kinase 1 [arabidopsis
 thaliana] /blast_score 0
 (2138 letters)

Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	
				(bits) Value
35	Sequences producing significant alignments:			
	emb AW565461 AW565461 LG1_344_F11.gl_A002 Light Grown 1 (LG1) So...	269	7e-71	
	emb AW455238 AW455238 EST311898 tomato root during/after fruit s...	229	1e-63	
	emb AW568861 AW568861 si73b10.y1 Gm-cl031 Glycine max cDNA clone...	139	3e-61	
40	emb AI487264 AI487264 EST245586 tomato ovary, TAMU Lycopersicon ...	205	1e-55	
	emb AI485585 AI485585 EST243906 tomato ovary, TAMU Lycopersicon ...	205	1e-54	
	emb AW667985 AW667985 GA__Ea0012C15 Gossypium arboreum 7-10 dpa ...	128	4e-54	
	emb AI485223 AI485223 EST243527 tomato ovary, TAMU Lycopersicon ...	203	5e-54	
	emb AI897690 AI897690 EST267133 tomato ovary, TAMU Lycopersicon ...	205	7e-54	
45	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	162	1e-53	
	emb AI486547 AI486547 EST244868 tomato ovary, TAMU Lycopersicon ...	150	1e-53	
	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	165	1e-53	
	emb AI489882 AI489882 EST248221 tomato ovary, TAMU Lycopersicon ...	205	3e-53	
	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k...	168	5e-53	
50	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	163	9e-53	
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	170	8e-52	
	emb AI485022 AI485022 EST243302 tomato ovary, TAMU Lycopersicon ...	205	1e-51	
	emb AI484547 AI484547 EST242777 tomato ovary, TAMU Lycopersicon ...	205	1e-51	
	emb AI484020 AI484020 EST249891 tomato ovary, TAMU Lycopersicon ...	205	1e-51	
55	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti...	160	2e-51	
	emb AF142596 AF142596 Nicotiana tabacum LRR receptor-like protei...	144	2e-51	
	emb AW616916 AW616916 EST323327 L. hirsutum trichome, Cornell Un...	145	3e-51	
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	165	1e-50	
	emb AI487456 AI487456 EST245778 tomato ovary, TAMU Lycopersicon ...	139	3e-50	
60	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR...	154	7e-50	
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	164	7e-50	

- emb|AF220602|AF220602 *Lycopersicon pimpinellifolium* Rio Grande 7... 96 2e-49
emb|Y14285|BOY14285 *Brassica oleracea* mRNA for SFR1 protein. 156 1e-48
emb|AB024416|AB024416 *Brassica oleracea* SRK2-b mRNA, complete cds. 153 3e-48
emb|AW266297|AW266297 L30-3030T3 Ice plant Lambda Uni-Zap XR exp... 169 3e-48
5 emb|AB008191|AB008191 *Brassica rapa* mRNA for SRK29, complete cds. 154 4e-48
emb|AI898374|AI898374 EST267817 tomato ovary, TAMU *Lycopersicon* ... 192 1e-47
emb|AI484550|AI484550 EST242780 tomato ovary, TAMU *Lycopersicon* ... 191 2e-47
emb|AI967314|AI967314 Ljimp00-017 Ljimp Lambda HybriZap two... 89 3e-47
dbj|D38564|BOLRPKB *Brassica campestris* mRNA for receptor protein... 127 5e-47
10 emb|X98520|BOSFR2 *B.oleracea* mRNA for receptor-like kinase, SFR2. 153 7e-47
emb|Y18259|BOY18259 *Brassica oleracea* mRNA for SRK5 protein, par... 152 7e-47
emb|AI483733|AI483733 EST249604 tomato ovary, TAMU *Lycopersicon* ... 188 1e-46
emb|AB032474|AB032474 *Brassica oleracea* SRK60 mRNA for S60 S-loc... 127 1e-46
emb|Y18260|BOY18260 *Brassica oleracea* mRNA for SRK15 protein, pa... 150 1e-46
15 gb|U20948|ITU20948 *Ipomoea trifida* receptor protein kinase (IRK1... 126 2e-46
gb|BE060160|BE060160 HVSMEg0011B12f *Hordeum vulgare* pre-anthesis... 151 3e-46
emb|AW597214|AW597214 si71g06.y1 Gm-c1031 *Glycine max* cDNA clone... 187 4e-46
emb|AF088885|AF088885 *Nicotiana tabacum* receptor-like kinase CHR... 156 6e-46
emb|AW694732|AW694732 NF079D07ST1F1061 Developing stem *Medicago* ... 185 9e-46
20 emb|Y14286|BOY14286 *Brassica oleracea* SFR3 gene, partial. 91 1e-45
emb|AW774582|AW774582 EST333733 KV3 *Medicago truncatula* cDNA clo... 81 1e-45
emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber *Gossypium*... 81 1e-45
dbj|D38563|BOLRPKA *Brassica campestris* mRNA for receptor protein... 127 2e-45
dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 134 2e-45
25 emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 145 2e-45
emb|AI898918|AI898918 EST268361 tomato ovary, TAMU *Lycopersicon* ... 183 5e-45
emb|AF131222|AF131222 *Lophopyrum elongatum* protein serine/threon... 138 2e-44
emb|AW756743|AW756743 sl26f10.y1 Gm-c1027 *Glycine max* cDNA clone... 181 2e-44
emb|AF220603|AF220603 *Lycopersicon esculentum* VFNT Cherry Pto lo... 96 2e-44
30 emb|AI731504|AI731504 BNLGHi9991 Six-day Cotton fiber *Gossypium* ... 132 3e-44
emb|AW929662|AW929662 EST338450 tomato flower buds 8 mm to pre-a... 151 4e-44
emb|AI489009|AI489009 EST247348 tomato ovary, TAMU *Lycopersicon* ... 117 7e-44
emb|AI483732|AI483732 EST249603 tomato ovary, TAMU *Lycopersicon* ... 177 4e-43
emb|AA738545|AA738545 SbRLK3 *Sorghum bicolor* cv. TX430 leaf Sorg... 153 6e-43
35 gb|U59315|LPU59315 *Lycopersicon pimpinellifolium* serine/threonin... 88 1e-42
gb|U02271|LEU02271 *Lycopersicon pimpinellifolium* Rio Grande-PtoR... 88 1e-42
emb|AJ245479|BNA245479 *Brassica napus* Sl13, slk, srk, CePP, Fmt,... 80 2e-42
emb|AI490032|AI490032 EST248371 tomato ovary, TAMU *Lycopersicon* ... 149 2e-42
emb|AW220490|AW220490 EST297043 tomato fruit mature green, TAMU ... 116 2e-42
40 gb|U28007|LEU28007 *Lycopersicon esculentum* Pto kinase interactor... 83 3e-42
emb|AW621706|AW621706 EST312504 tomato root during/after fruit s... 143 4e-42
emb|AW031255|AW031255 EST274630 tomato callus, TAMU *Lycopersicon*... 149 6e-42
emb|AW684940|AW684940 NF023C12NR1F1000 Nodulated root *Medicago* t... 113 6e-42
emb|AB000971|AB000971 *Brassica campestris* pseudogene for recepto... 78 8e-42
45 gb|U59316|LEU59316 *Lycopersicon esculentum* serine/threonine prot... 87 1e-41
emb|AW687233|AW687233 NF007D09RT1F1077 Developing root *Medicago* ... 93 1e-41
emb|AW220491|AW220491 EST297044 tomato fruit mature green, TAMU ... 116 2e-41
dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 81 2e-41
dbj|E05046|E05046 DNA encoding ZmPK1 homologue protein in tobacco. 81 2e-41
50 emb|AB041503|AB041503 *Populus nigra* PnPK1 mRNA for protein kinas... 77 3e-41
emb|AW220489|AW220489 EST297042 tomato fruit mature green, TAMU ... 112 3e-41
emb|AI937984|AI937984 sc06e07.y1 Gm-c1012 *Glycine max* cDNA clone... 170 5e-41
emb|AB041504|AB041504 *Populus nigra* PnPK2 mRNA for protein kinas... 75 1e-40
emb|AI484701|AI484701 EST242962 tomato ovary, TAMU *Lycopersicon* ... 127 1e-40
55 emb|AA738544|AA738544 SbRLK2 *Sorghum bicolor* cv. TX430 leaf Sorg... 122 1e-40
emb|AW672145|AW672145 LG1_357_A10.b1_A002 Light Grown 1 (LG1) So... 167 2e-40
gb|U59317|LPU59317 *Lycopersicon pimpinellifolium* serine/threonin... 93 3e-40
gb|U13923|LEU13923 *Lycopersicon pimpinellifolium* serine/threonin... 93 3e-40
emb|Z73295|CRPK1 *C.roseus* mRNA for receptor-like protein kinase. 74 5e-40
60 gb|U59318|LEU59318 *Lycopersicon esculentum* serine/threonine prot... 92 6e-40
emb|AW729859|AW729859 GA_Ea0026H04 *Gossypium arboreum* 7-10 dpa ... 81 1e-39

- emb|AW982539|AW982539 HVSMEg0003I16f Hordeum vulgare pre-anthesi... 129 1e-39.
 emb|A67797|A67797 Sequence 2 from Patent WO9743427. 125 1e-39
 gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor-... 125 1e-39
 emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 72 2e-39
 5 emb|AW284352|AW284352 LG1_275_D12.g1_A002 Light Grown 1 (LG1) So... 165 2e-39
 emb|Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 123 2e-39
 emb|AW222552|AW222552 EST299363 tomato fruit red ripe, TAMU Lyco... 82 2e-39
 emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 70 4e-39
 emb|AI901283|AI901283 sc31d08.y1 Gm-cl014 Glycine max cDNA clone... 163 5e-39
 10 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 71 5e-39
 emb|AW223870|AW223870 EST300681 tomato fruit red ripe, TAMU Lyco... 99 6e-39
 gb|BE053916|BE053916 GA__Ea0031D03f Gossypium arboreum 7-10 dpa ... 77 1e-38
 emb|AW760240|AW760240 sl59g07.y1 Gm-cl027 Glycine max cDNA clone... 130 2e-38
 emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 73 3e-38

15

Query= ab003280_s_at 15629_s_at /id_source genbank /description
 dbj|baa24440.1| (ab010407) phosphoglycerate dehydrogenase [arabidopsis
 thaliana] /blast_score 0
 20 (2127 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

25 Searching.....done

- | | | Score | E |
|----|---|--------|-------|
| | Sequences producing significant alignments: | (bits) | Value |
| 30 | emb AW930291 AW930291 EST340748 tomato fruit mature green, TAMU ... | 403 | e-111 |
| | emb AW625643 AW625643 EST319550 tomato radicle, 5 d post-imbibit... | 377 | e-103 |
| | emb AW688234 AW688234 NF005A05ST1F1000 Developing stem Medicago ... | 367 | e-100 |
| | emb AW666282 AW666282 sk34f11.y1 Gm-cl028 Glycine max cDNA clone... | 360 | 2e-98 |
| | emb AW691093 AW691093 NF041B09ST1F1000 Developing stem Medicago ... | 332 | 5e-96 |
| 35 | gb BE055044 BE055044 GA__Ea0031H08f Gossypium arboreum 7-10 dpa ... | 332 | 9e-95 |
| | emb AW696933 AW696933 NF112E03ST1F1021 Developing stem Medicago ... | 347 | 3e-94 |
| | emb AW926942 AW926942 HVSMEg0009B01 Hordeum vulgare pre-anthesis... | 295 | 6e-89 |
| | emb AW737130 AW737130 EST338557 tomato flower buds, anthesis, Co... | 325 | 1e-87 |
| | emb AW689358 AW689358 NF018C09ST1F1000 Developing stem Medicago ... | 281 | 3e-85 |
| 40 | emb AW650696 AW650696 EST329150 tomato germinating seedlings, TA... | 179 | 2e-84 |
| | emb AW625020 AW625020 EST313849 tomato radicle, 5 d post-imbibit... | 301 | 1e-80 |
| | emb AI813214 AI813214 3C4 Pine Lambda Zap Xylem library Pinus ta... | 297 | 2e-80 |
| | emb AW692700 AW692700 NF054C07ST1F1000 Developing stem Medicago ... | 279 | 6e-80 |
| | gb BE036418 BE036418 MO24D12 MO Mesembryanthemum crystallinum cD... | 258 | 2e-79 |
| 45 | gb BE020170 BE020170 sm39e05.y1 Gm-cl028 Glycine max cDNA clone ... | 293 | 3e-78 |
| | emb AW423801 AW423801 sh52b02.y1 Gm-cl017 Glycine max cDNA clone... | 293 | 4e-78 |
| | emb AW731385 AW731385 GA__Ea0030K22 Gossypium arboreum 7-10 dpa ... | 289 | 6e-77 |
| | gb BE052354 BE052354 GA__Ea0034P16f Gossypium arboreum 7-10 dpa ... | 282 | 5e-75 |
| | emb AW687344 AW687344 NF008F03RT1F1029 Developing root Medicago ... | 269 | 5e-71 |
| 50 | emb AW926887 AW926887 HVSMEg0008N09 Hordeum vulgare pre-anthesis... | 264 | 1e-69 |
| | emb AW944677 AW944677 00152 leafy spurge Lambda HybriZAP 2.1 two... | 248 | 1e-64 |
| | emb AW727978 AW727978 GA__Ea0029C18 Gossypium arboreum 7-10 dpa ... | 231 | 2e-61 |
| | emb AW755716 AW755716 sl08b12.y1 Gm-cl036 Glycine max cDNA clone... | 234 | 2e-60 |
| | emb AW923236 AW923236 DG1_50_A11.g1_A002 Dark Grown 1 (DG1) Sorg... | 233 | 3e-60 |
| 55 | gb BE060782 BE060782 HVSMEg0013F14f Hordeum vulgare pre-anthesis... | 226 | 7e-58 |
| | emb AW203801 AW203801 sf38d05.y1 Gm-cl028 Glycine max cDNA clone... | 215 | 1e-54 |
| | emb AW317181 AW317181 sf38d05.x1 Gm-cl028 Glycine max cDNA clone... | 200 | 4e-50 |
| | emb AW398821 AW398821 EST309321 L. pennellii trichome, Cornell U... | 177 | 2e-43 |
| | emb AW650818 AW650818 EST329272 tomato germinating seedlings, TA... | 148 | 2e-42 |
| 60 | emb AW697347 AW697347 NF115F08ST1F1074 Developing stem Medicago ... | 168 | 2e-40 |
| | emb AW428657 AW428657 Ljirnp22-731-a5 Ljirnp Lambda HybriZap ... | 168 | 2e-40 |

- emb|AW695961|AW695961 NF101A09ST1F1068 Developing stem Medicago ... 168 2e-40
emb|AV395160|AV395160 AV395160 Chlamydomonas reinhardtii C9 Chla... 164 2e-39
emb|AW907004|AW907004 EST343231 potato stolon, Cornell Universit... 163 5e-39
5 emb|AW736943|AW736943 NXNV_081_H10_F Nsf Xylem Normal wood Verti... 161 1e-38
gb|BE123645|BE123645 NXNV_150_D07_F Nsf Xylem Normal wood Vertic... 158 1e-37
gb|L47851|L47851 BNAF1389 Mustard flower buds Brassica rapa cDNA... 155 1e-36
gb|BE058285|BE058285 sn14b01.y1 Gm-c1016 Glycine max cDNA clone ... 152 8e-36
gb|BE055879|BE055879 GA__Ea0026P04f Gossypium arboreum 7-10 dpa ... 149 5e-35
emb|AA660997|AA660997 00894 MtRHE Medicago truncatula cDNA 5' si... 72 2e-34
10 emb|AW693956|AW693956 NF071B03ST1F1027 Developing stem Medicago ... 92 8e-33
emb|AI165568|AI165568 A086P59U Hybrid aspen plasmid library Popu... 137 1e-31
emb|AV428639|AV428639 AV428639 Lotus japonicus young plants (two... 133 7e-30
emb|AV408249|AV408249 AV408249 Lotus japonicus young plants (two... 133 7e-30
emb|Z97052|SPCC4G3 S.pombe chromosome III cosmid c4G3. 82 7e-30
15 gb|BE060772|BE060772 HVSMEEg0013F04f Hordeum vulgare pre-anthesis... 99 2e-29
dbj|E12500|E12500 Nucleotide sequence of eta gene of cephalospor... 78 2e-29
emb|AJ273311|AJ273311 AJ273311 Metarhizium anisopliae ARSEF 2575... 77 4e-28
emb|AA840711|AA840711 CAN22 Anther cDNA library of Hot pepper Ca... 93 5e-28
emb|AW688606|AW688606 NF009E07ST1F1000 Developing stem Medicago ... 124 2e-27
20 emb|AC005761|AC005761 Leishmania major chromosome 3 clone L952 s... 78 5e-27
emb|AL157811|SPAC186 S.pombe chromosome I cosmid c186. 90 2e-26
gb|U18839|SCE9747 Saccharomyces cerevisiae chromosome V cosmids ... 80 2e-23
emb|AL033389|SPBC1773 S.pombe chromosome II cosmid c1773. 106 1e-22
emb|Z37997|SC9877 S.cerevisiae chromosome IX cosmid 9877. 80 2e-22
25 emb|AW689996|AW689996 NF026G01ST1F1000 Developing stem Medicago ... 91 7e-20
emb|AL031180|SPUNK4 S.pombe chromosome I cosmid c2E11. 99 2e-19
dbj|D89185|D89185 Schizosaccharomyces pombe mRNA, partial cds, c... 99 2e-19
emb|AF079881|AF079881 Entodinium caudatum D-3-phosphoglycerate d... 53 2e-19
emb|AW736063|AW736063 EST332049 KV3 Medicago truncatula cDNA clo... 93 9e-18
30 gb|BE054038|BE054038 GA__Ea0008F24f Gossypium arboreum 7-10 dpa ... 88 2e-16
emb|AW599036|AW599036 gb01c10.y1 Moss EST library PPN Physcomitr... 87 6e-16
gb|U43503|SCU43503 Saccharomyces cerevisiae chromosome XVI cosmi... 84 3e-15
emb|AW283359|AW283359 LG1_223_C04.g1_A002 Light Grown 1 (LG1) So... 84 5e-15
emb|AW625680|AW625680 EST319587 tomato radicle, 5 d post-imbibit... 83 1e-14
35 emb|AI486949|AI486949 EST245271 tomato ovary, TAMU Lycopersicon ... 83 1e-14
emb|Z71550|SCYNL274C S.cerevisiae chromosome XIV reading frame O... 83 1e-14
emb|AW442114|AW442114 EST311510 tomato fruit red ripe, TAMU Lyco... 83 1e-14
emb|AW030822|AW030822 EST274077 tomato callus, TAMU Lycopersicon... 83 1e-14
emb|AI484846|AI484846 EST243107 tomato ovary, TAMU Lycopersicon ... 83 1e-14
40 emb|AW442123|AW442123 EST311519 tomato fruit red ripe, TAMU Lyco... 83 1e-14
emb|AW651324|AW651324 EST329778 tomato germinating seedlings, TA... 83 1e-14
emb|AW647711|AW647711 EST307192 tomato germinating seedlings, TA... 83 1e-14
emb|Z21493|MISTFDHD S.tuberosum mRNA for formate dehydrogenase. 83 1e-14
emb|AI822999|AI822999 L30-850T3 Ice plant Lambda Uni-Zap XR expr... 82 1e-14
45 emb|AW693443|AW693443 NF065D03ST1F1000 Developing stem Medicago ... 71 2e-14
emb|AI488120|AI488120 EST246442 tomato ovary, TAMU Lycopersicon ... 80 5e-14
emb|AT000538|AT000538 AT000538 Brassica rapa guard cell Brassica... 80 7e-14
emb|AI490350|AI490350 EST248676 tomato ovary, TAMU Lycopersicon ... 79 9e-14
emb|AQ874261|AQ874261 VI05E9 mTn-3xHA/lacZ Insertion Library, st... 79 1e-13
50 emb|AI490396|AI490396 EST248734 tomato ovary, TAMU Lycopersicon ... 78 2e-13
dbj|D88272|D88272 Hordeum vulgare mRNA for formate dehydrogenase... 78 3e-13
emb|AW037837|AW037837 EST279466 tomato mixed elicitor, BTI Lycop... 75 2e-12
emb|AW266848|AW266848 L48-192T3 Ice plant Lambda Uni-Zap XR expr... 74 3e-12
emb|AI897727|AI897727 EST267170 tomato ovary, TAMU Lycopersicon ... 74 4e-12
55 emb|AI898003|AI898003 EST267446 tomato ovary, TAMU Lycopersicon ... 74 4e-12
emb|AI898454|AI898454 EST267897 tomato ovary, TAMU Lycopersicon ... 74 4e-12
emb|AI898267|AI898267 EST267710 tomato ovary, TAMU Lycopersicon ... 74 4e-12
emb|AW278707|AW278707 sf96b06.y1 Gm-c1019 Glycine max cDNA clone... 73 6e-12
emb|AI483926|AI483926 EST249797 tomato ovary, TAMU Lycopersicon ... 73 8e-12
60 emb|AW930862|AW930862 EST356705 tomato fruit mature green, TAMU ... 73 1e-11
emb|AI899038|AI899038 EST268481 tomato ovary, TAMU Lycopersicon ... 73 1e-11

- gb|BE055276|BE055276 GA_Ea0034L16f Gossypium arboreum 7-10 dpa ... 57 2e-11
 emb|AI488243|AI488243 EST246565 tomato ovary, TAMU Lycopersicon ... 72 2e-11
 emb|AW153099|AW153099 se34h11.y1 Gm-cl015 Glycine max cDNA clone... 71 4e-11
 emb|AI940852|AI940852 sb80b11.y1 Gm-cl010 Glycine max cDNA clone... 71 4e-11
 5 emb|AW100275|AW100275 sd22a06.y2 Gm-cl012 Glycine max cDNA clone... 71 4e-11
 emb|AW164250|AW164250 se23h05.y1 Gm-cl015 Glycine max cDNA clone... 70 5e-11
 emb|AW981354|AW981354 EST392507 DSIL Medicago truncatula cDNA cl... 69 1e-10
- 10 Query= afl17063_s_at 15641_s_at /id_source genbank /description
 gb|aad10829.1| (afl17063) putative inositol polyphosphate
 5-phosphatase at5p2 [arabidopsis thaliana] /blast_score 0
 (2458 letters)
- 15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
- Searching.....done
- 20 Score E
 Sequences producing significant alignments: (bits) Value
- emb|AI898446|AI898446 EST267889 tomato ovary, TAMU Lycopersicon ... 209 e-108
 emb|AW217248|AW217248 EST295962 tomato callus, TAMU Lycopersicon... 245 3e-89
 25 emb|AI485780|AI485780 EST244101 tomato ovary, TAMU Lycopersicon ... 242 2e-86
 emb|AI485695|AI485695 EST244016 tomato ovary, TAMU Lycopersicon ... 261 5e-86
 emb|AI899197|AI899197 EST268640 tomato ovary, TAMU Lycopersicon ... 161 2e-78
 emb|AI485239|AI485239 EST243543 tomato ovary, TAMU Lycopersicon ... 291 1e-77
 emb|AW034573|AW034573 EST278257 tomato callus, TAMU Lycopersicon... 272 9e-72
 30 emb|AI488812|AI488812 EST247151 tomato ovary, TAMU Lycopersicon ... 251 1e-65
 emb|AW687082|AW687082 NF005G09RT1F1071 Developing root Medicago ... 182 7e-65
 emb|AI898248|AI898248 EST267691 tomato ovary, TAMU Lycopersicon ... 206 2e-64
 emb|AI483614|AI483614 EST249464 tomato ovary, TAMU Lycopersicon ... 238 1e-61
 emb|AI897089|AI897089 EST266532 tomato ovary, TAMU Lycopersicon ... 226 8e-58
 35 emb|AW774994|AW774994 EST334145 KV3 Medicago truncatula cDNA clo... 182 3e-56
 emb|AW559604|AW559604 EST314652 DSIR Medicago truncatula cDNA cl... 177 4e-53
 emb|AI485284|AI485284 EST243588 tomato ovary, TAMU Lycopersicon ... 206 5e-52
 emb|AI485664|AI485664 EST243985 tomato ovary, TAMU Lycopersicon ... 198 2e-49
 emb|AW774741|AW774741 EST333892 KV3 Medicago truncatula cDNA clo... 90 2e-48
 40 emb|AI487608|AI487608 EST245930 tomato ovary, TAMU Lycopersicon ... 187 3e-46
 emb|AI483438|AI483438 EST249259 tomato ovary, TAMU Lycopersicon ... 169 7e-41
 emb|AI485008|AI485008 EST243271 tomato ovary, TAMU Lycopersicon ... 157 3e-37
 emb|AI938737|AI938737 sb58c06.y1 Gm-cl018 Glycine max cDNA clone... 151 2e-35
 emb|AI967736|AI967736 Ljimpest11-837-a7 Ljimp Lambda HybriZap ... 147 4e-34
 45 emb|AW775688|AW775688 EST334753 DSIL Medicago truncatula cDNA cl... 108 8e-34
 emb|Z50161|SCC14ORFS S.cerevisiae orfs and LEU4, MET4, POL1, RAS... 60 1e-33
 emb|Z71382|SCYNL106C S.cerevisiae chromosome XIV reading frame O... 60 1e-33
 emb|AI973618|AI973618 sd07d04.y1 Gm-cl020 Glycine max cDNA clone... 141 3e-32
 emb|AI485392|AI485392 EST243713 tomato ovary, TAMU Lycopersicon ... 138 2e-31
 50 emb|X94335|SC130KBXV S.cerevisiae 130kb DNA fragment from chromo... 51 1e-29
 emb|Z75017|SCYOR109W S.cerevisiae chromosome XV reading frame OR... 51 1e-29
 emb|AL022103|SPBC2G2 S.pombe chromosome II cosmid c2G2. 78 3e-27
 emb|X79743|SCBPPS S.cerevisiae BET1, PAN1 PRI1 and STS1 genes. 72 3e-27
 emb|Z38062|SC9687 S.cerevisiae chromosome IX cosmid 9687. 72 3e-27
 55 emb|AI488810|AI488810 EST247149 tomato ovary, TAMU Lycopersicon ... 121 3e-26
 gb|BE020060|BE020060 sm38e06.y1 Gm-cl028 Glycine max cDNA clone ... 118 2e-25
 emb|AW685248|AW685248 NF028A10NR1F1000 Nodulated root Medicago t... 116 2e-24
 emb|AW257207|AW257207 EST305344 KV2 Medicago truncatula cDNA clo... 75 2e-24
 emb|AV406995|AV406995 AV406995 Lotus japonicus young plants (two... 67 2e-23
 60 emb|AW034093|AW034093 EST277588 tomato callus, TAMU Lycopersicon... 111 3e-23
 emb|Z98763|SPAC9G1 S.pombe chromosome I cosmid c9G1. 59 9e-23

	emb AQ502761 AQ502761 V84A11 mTn-3xHA/lacZ Insertion Library Sac...	52	2e-22
	emb AI897134 AI897134 EST266577 tomato ovary, TAMU Lycopersicon ...	107	4e-22
	emb AI771644 AI771644 EST252744 tomato ovary, TAMU Lycopersicon ...	104	4e-21
	emb AW731056 AW731056 GA__Ea0008D13 Gossypium arboreum 7-10 dpa ...	100	5e-20
5	emb AV413397 AV413397 AV413397 Lotus japonicus young plants (two...	100	9e-20
	emb AW616540 AW616540 EST322951 L. hirsutum trichome, Cornell Un...	98	2e-19
	emb AL110506 SPBC577 S.pombe chromosome II cosmid c577.	74	2e-18
	emb AW126841 AW126841 gal16f04.y1 Moss EST library PPU Physcomitr...	94	4e-18
	emb AI780067 AI780067 EST260946 tomato susceptible, Cornell Lyco...	94	6e-18
10	emb AW687035 AW687035 NF005C05RT1F1037 Developing root Medicago ...	73	2e-17
	emb AW685930 AW685930 NF036F03NR1F1000 Nodulated root Medicago t...	73	2e-17
	emb AV415287 AV415287 AV415287 Lotus japonicus young plants (two...	90	5e-17
	gb BE124605 BE124605 EST393640 GVN Medicago truncatula cDNA clon...	65	6e-15
	emb AW220291 AW220291 EST302774 tomato root during/after fruit s...	68	1e-14
15	emb AQ644913 AQ644913 RPCI93-EcoRI-2C7.TV RPCI93-EcoRI Trypanoso...	53	2e-13
	emb AA495505 AA495505 c430 Zhou and Ragan 1993 Gracilaria gracil...	49	5e-13
	emb AW830613 AW830613 sm04c07.y1 Gm-c1027 Glycine max cDNA clone...	77	5e-13
	emb AW666237 AW666237 sk34b04.y1 Gm-c1028 Glycine max cDNA clone...	77	5e-13
	emb AW285758 AW285758 LG1_223_C03.b1_A002 Light Grown 1 (LG1) So...	74	5e-12
20	emb AQ658256 AQ658256 Sheared DNA-13C5.TR Sheared DNA Trypanosom...	73	1e-11
	emb AW704333 AW704333 sk18a03.y1 Gm-c1028 Glycine max cDNA clone...	71	5e-11
	emb AV390446 AV390446 AV390446 Chlamydomonas reinhardtii C9 Chla...	70	6e-11
	emb AL160371 LMFLCHR15 Leishmania major Friedlin assembled chrom...	64	8e-11
	emb AW695904 AW695904 NF099H04ST1F1043 Developing stem Medicago ...	49	2e-10
25	emb AZ048449 AZ048449 PSB67 Barley PstI genomic clones Hordeum v...	67	8e-10
	emb AW760518 AW760518 sl51d02.y1 Gm-c1027 Glycine max cDNA clone...	66	1e-09
	emb AW332143 AW332143 S4G7 AGS-1 Pneumocystis carinii f. sp. car...	36	1e-09
	emb AW687790 AW687790 NF013E04RT1F1034 Developing root Medicago ...	65	3e-09
	emb AI486692 AI486692 EST245014 tomato ovary, TAMU Lycopersicon ...	54	3e-09
30	emb AW333870 AW333870 S27C11 AGS-1 Pneumocystis carinii f. sp. c...	36	5e-09
	emb AQ850639 AQ850639 LMAJFV1_lm41a04.x1 Leishmania major FV1 ra...	44	6e-09
	emb AW127178 AW127178 M110117 GVN Medicago truncatula cDNA clone...	63	1e-08
	emb AW616547 AW616547 EST322958 L. hirsutum trichome, Cornell Un...	62	2e-08
	emb AW399291 AW399291 EST309791 L. pennellii trichome, Cornell U...	62	2e-08
35	emb AW693686 AW693686 NF068A05ST1F1036 Developing stem Medicago ...	62	3e-08
	emb AW208046 AW208046 M111077e DSIR Medicago truncatula cDNA clo...	61	5e-08
	emb AQ642482 AQ642482 RPCI93-EcoRI-1A17.TV RPCI93-EcoRI Trypanos...	53	7e-08
	emb AW686583 AW686583 NF039G02NR1F1000 Nodulated root Medicago t...	45	5e-07
	emb AQ849089 AQ849089 LMAJFV1_lm41a04.y1 Leishmania major FV1 ra...	44	6e-06
40	emb AI781410 AI781410 EST262277 tomato susceptible, Cornell Lyco...	52	2e-05
	emb AW617564 AW617564 EST323975 L. hirsutum trichome, Cornell Un...	49	2e-04
	emb AQ946427 AQ946427 Sheared DNA-49M8.TF Sheared DNA Trypanosom...	47	5e-04
	emb AW099113 AW099113 sd34f04.y1 Gm-c1012 Glycine max cDNA clone...	46	0.002
	emb Z74807 SCYOL065C S.cerevisiae chromosome XV reading frame OR...	29	0.003
45	emb AQ655271 AQ655271 Sheared DNA-27A17.TR Sheared DNA Trypanoso...	38	0.004
	emb AW685854 AW685854 NF031A06NR1F1000 Nodulated root Medicago t...	43	0.009
	emb AW437996 AW437996 ST83C09 Pine TriplEx shoot tip library Pin...	42	0.016
	emb AI440709 AI440709 sa62e11.y1 Gm-c1004 Glycine max cDNA clone...	31	0.045
	emb AW979881 AW979881 EST341528 tomato root deficiency, Cornell ...	37	0.54
50	emb AF263282 AF263282 Filobasidiella neoformans var. neoformans ...	34	0.64
	emb AW702543 AW702543 TgESTzz85a12.y1 TgRH*-Tachyzoite cDNA Toxo...	32	0.69
	emb AZ214873 AZ214873 Sheared DNA-109E2.TR Sheared DNA Trypanoso...	37	0.74
	emb AQ939979 AQ939979 Sheared DNA-42A15.TF Sheared DNA Trypanoso...	37	0.74
	emb AQ651205 AQ651205 Sheared DNA-30N15.TF Sheared DNA Trypanoso...	37	0.74
55	emb AQ945454 AQ945454 Sheared DNA-54H22.TF Sheared DNA Trypanoso...	37	0.74
	emb AW774740 AW774740 EST333891 KV3 Medicago truncatula cDNA clo...	36	1.4
	emb Z38060 SC5610 S.cerevisiae chromosome IX sequence derived fr...	36	1.4
	emb AL049183 PFMAL13P6 Plasmodium falciparum chromosome 13 strai...	35	2.6
	gb M28064 PFAHRKP Plasmodium brasilianum DNA homologous to the h...	35	2.6
60	emb AI482770 AI482770 EST242093 tomato shoot, Cornell Lycopersic...	35	2.6
	emb AQ653909 AQ653909 Sheared DNA-1G20.TR Sheared DNA Trypanosom...	35	2.6

Query= af022658_s_at 15665_s_at /id_source genbank /description
 gb|aab80922.1| (af022658) putative c2h2 zinc finger transcription
 5 factor [arabidopsis thaliana] /blast_score 3.00e-94
 (938 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

10

Searching.....done

	Score	E	(bits)	Value
15	Sequences producing significant alignments:			
	gb U68763 GMU68763	Glycine max putative transcription factor SCO...	71	1e-35
	emb Y18788 MSY18788	Medicago sativa mRNA for putative TFIIIA (or...	71	3e-35
	emb AF053077 AF053077	Nicotiana tabacum osmotic stress-induced z...	70	3e-33
	emb AW729218 AW729218	GA__Ea0024G18 Gossypium arboreum 7-10 dpa ...	71	5e-33
20	emb AW781249 AW781249	sk67b08.y1 Gm-c1016 Glycine max cDNA clone...	70	7e-31
	dbj D26086 PETZFP4	Petunia zinc-finger protein gene.	68	3e-30
	emb AW560934 AW560934	EST315982 DSIR Medicago truncatula cDNA cl...	68	8e-30
	emb AW775559 AW775559	EST334624 DSIL Medicago truncatula cDNA cl...	70	1e-29
	gb BE123920 BE123920	EST394045 DSIL Medicago truncatula cDNA cl...	70	1e-29
25	emb AI988657 AI988657	sd06b03.y1 Gm-c1020 Glycine max cDNA clone...	70	9e-29
	emb AW102472 AW102472	sd88f02.y1 Gm-c1009 Glycine max cDNA clone...	64	1e-28
	dbj D26084 PETZFDB2	Petunia mRNA for zinc-finger DNA binding pro...	69	1e-28
	dbj D26083 PETZFDB1	Petunia hybrida gene for zinc-finger DNA bin...	68	4e-28
	emb AI988290 AI988290	sc98f10.y1 Gm-c1020 Glycine max cDNA clone...	64	3e-27
30	emb AW706944 AW706944	sk08e10.y1 Gm-c1023 Glycine max cDNA clone...	69	2e-26
	emb AW153229 AW153229	se37f05.y1 Gm-c1015 Glycine max cDNA clone...	69	3e-26
	emb AW616587 AW616587	EST322998 L. hirsutum trichome, Cornell Un...	68	5e-26
	gb BE095284 BE095284	00345 leafy spurge Lambda HybriZAP 2.1 two-...	69	5e-26
	emb AW278572 AW278572	sf46c03.y1 Gm-c1009 Glycine max cDNA clone...	65	8e-26
35	emb AI487287 AI487287	EST245609 tomato ovary, TAMU Lycopersicon ...	68	9e-26
	dbj D26085 PETZFDB3	Petunia zinc-finger DNA binding protein gene.	60	1e-25
	emb AI778714 AI778714	EST259593 tomato susceptible, Cornell Lyco...	68	1e-25
	emb AW279005 AW279005	sg04d04.y1 Gm-c1019 Glycine max cDNA clone...	67	2e-25
	emb AW164639 AW164639	se74f02.y1 Gm-c1023 Glycine max cDNA clone...	67	2e-25
40	emb AF119050 AF119050	Datisca glomerata zinc-finger protein 1 (z...	71	2e-25
	gb BE059872 BE059872	sn38c04.y1 Gm-c1016 Glycine max cDNA clone ...	71	4e-25
	gb U76554 BRU76554	Brassica rapa zinc-finger protein-1 (BR42) mR...	63	9e-25
	gb U76555 BRU76555	Brassica rapa zinc-finger protein BcZFP1 (BcA...	62	3e-24
	emb AI966679 AI966679	sc55a11.y1 Gm-c1015 Glycine max cDNA clone...	64	4e-24
45	emb AW034622 AW034622	EST278306 tomato callus, TAMU Lycopersicon...	62	6e-24
	emb AI488218 AI488218	EST246540 tomato ovary, TAMU Lycopersicon ...	62	9e-24
	emb AW037956 AW037956	EST279600 tomato mixed elicitor, BTI Lycop...	59	4e-23
	emb Y16131 Y16131	Y16131 young root nodules Medicago sativa subs...	67	8e-23
	emb AW030858 AW030858	EST274148 tomato callus, TAMU Lycopersicon...	66	9e-23
50	emb AW032112 AW032112	EST275566 tomato callus, TAMU Lycopersicon...	68	5e-22
	emb AW625323 AW625323	EST319146 tomato radicle, 5 d post-imbibit...	59	8e-21
	emb AW033257 AW033257	EST276828 tomato callus, TAMU Lycopersicon...	66	2e-20
	emb AI485651 AI485651	EST243972 tomato ovary, TAMU Lycopersicon ...	62	2e-20
	emb AW033574 AW033574	EST277145 tomato callus, TAMU Lycopersicon...	66	2e-20
55	emb AI896031 AI896031	EST265474 tomato callus, TAMU Lycopersicon...	66	3e-20
	emb AI771191 AI771191	EST252387 tomato ovary, TAMU Lycopersicon ...	66	3e-20
	emb AW032357 AW032357	EST275811 tomato callus, TAMU Lycopersicon...	66	3e-20
	emb AW219736 AW219736	EST302218 tomato root during/after fruit s...	59	1e-19
	emb AW219517 AW219517	EST301915 tomato root during/after fruit s...	59	2e-19
60	emb AW706014 AW706014	sk64g01.y1 Gm-c1016 Glycine max cDNA clone...	69	1e-18
	emb AV426673 AV426673	AV426673 Lotus japonicus young plants (two...	60	5e-18

	emb AV423639 AV423639 AV423639 Lotus japonicus young plants (two...	66 7e-18
	gb BE021759 BE021759 sm62a09.y1 Gm-c1028 Glycine max cDNA clone ...	71 3e-17
	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon...	55 4e-17
	emb AW720367 AW720367 LjNEST21g11r Lotus japonicus nodule librar...	64 6e-17
5	emb AW648971 AW648971 EST327425 tomato germinating seedlings, TA...	59 9e-17
	emb AB000455 AB000455 Petunia hybrida mRNA for PETHy;ZPT4-1, com...	60 1e-16
	gb BE058334 BE058334 sn14g01.y1 Gm-c1016 Glycine max cDNA clone ...	62 1e-16
	emb AW035987 AW035987 EST282846 tomato callus, TAMU Lycopersicon...	55 2e-16
	emb AV422432 AV422432 AV422432 Lotus japonicus young plants (two...	66 3e-16
10	emb AW277333 AW277333 sf80a11.y1 Gm-c1019 Glycine max cDNA clone...	64 4e-16
	emb AI900061 AI900061 sb98d02.y1 Gm-c1012 Glycine max cDNA clone...	64 5e-16
	emb AW684558 AW684558 NF018C10NR1F1000 Nodulated root Medicago t...	63 6e-16
	emb AI960244 AI960244 sc80g07.y1 Gm-c1018 Glycine max cDNA clone...	64 7e-16
	emb AI055219 AI055219 coau0003G03 Cotton Boll Abscission Zone cD...	62 1e-15
15	emb AI736394 AI736394 sb28a06.y1 Gm-c1009 Glycine max cDNA clone...	67 5e-15
	emb AI894999 AI894999 EST264442 tomato callus, TAMU Lycopersicon...	68 9e-15
	emb AW622660 AW622660 EST313460 tomato root during/after fruit s...	68 9e-15
	emb AW755973 AW755973 sl11h06.y1 Gm-c1036 Glycine max cDNA clone...	64 4e-14
	emb AI938565 AI938565 sb55e03.y1 Gm-c1018 Glycine max cDNA clone...	64 4e-14
20	emb AB035133 AB035133 Petunia x hybrida gene for C2H2 zinc-finge...	52 1e-13
	emb AB006605 AB006605 Petunia x hybrida mRNA for ZPT3-3, complet...	52 1e-13
	emb AB035132 AB035132 Petunia x hybrida gene for C2H2 zinc-finge...	50 4e-13
	emb AB006597 AB006597 Petunia x hybrida mRNA for ZPT2-10, comple...	50 4e-13
	emb AB006606 AB006606 Petunia x hybrida mRNA for ZPT4-4, complet...	51 8e-13
25	emb AW684455 AW684455 NF017B06NR1F1000 Nodulated root Medicago t...	54 8e-13
	emb AW776204 AW776204 EST335269 DSIL Medicago truncatula cDNA cl...	65 1e-12
	emb AB000451 AB000451 Petunia hybrida mRNA for PETHy;ZPT2-5, com...	50 2e-12
	emb AI485306 AI485306 EST243610 tomato ovary, TAMU Lycopersicon ...	66 2e-12
	emb AW216968 AW216968 EST295682 tomato callus, TAMU Lycopersicon...	55 2e-12
30	emb AV422972 AV422972 AV422972 Lotus japonicus young plants (two...	60 3e-12
	emb AV423707 AV423707 AV423707 Lotus japonicus young plants (two...	60 3e-12
	emb AV424707 AV424707 AV424707 Lotus japonicus young plants (two...	60 3e-12
	emb AV411009 AV411009 AV411009 Lotus japonicus young plants (two...	60 3e-12
	emb AV413230 AV413230 AV413230 Lotus japonicus young plants (two...	60 3e-12
35	emb AV418453 AV418453 AV418453 Lotus japonicus young plants (two...	60 3e-12
	emb AV412443 AV412443 AV412443 Lotus japonicus young plants (two...	60 3e-12
	emb AV411580 AV411580 AV411580 Lotus japonicus young plants (two...	60 3e-12
	emb AV412455 AV412455 AV412455 Lotus japonicus young plants (two...	60 3e-12
	emb AB006600 AB006600 Petunia x hybrida mRNA for ZPT2-13, comple...	48 4e-12
40	emb AW687462 AW687462 NF009H03RT1F1031 Developing root Medicago ...	50 4e-12
	emb AB006603 AB006603 Petunia x hybrida mRNA for ZPT2-8, complet...	49 5e-12
	emb AB006601 AB006601 Petunia x hybrida mRNA for ZPT2-14, comple...	50 7e-12
	emb AI442517 AI442517 sa32e09.y1 Gm-c1004 Glycine max cDNA clone...	58 7e-12
	gb BE023156 BE023156 sm79a08.y1 Gm-c1015 Glycine max cDNA clone ...	69 1e-11
45	dbj D16415 WHTWZF1A Wheat gene for WZF1, complete cds.	56 1e-11
	dbj D16416 WHTWZF1B Wheat mRNA for WZF1, complete cds.	56 1e-11
	emb AB006599 AB006599 Petunia x hybrida mRNA for ZPT2-12, comple...	48 1e-11
	emb AW685937 AW685937 NF031H10NR1F1000 Nodulated root Medicago t...	48 1e-11
	emb AV424248 AV424248 AV424248 Lotus japonicus young plants (two...	58 1e-11
50	emb AI775063 AI775063 EST256163 tomato resistant, Cornell Lycope...	59 2e-11
	emb AI484099 AI484099 EST249970 tomato ovary, TAMU Lycopersicon ...	59 2e-11
	emb AW738399 AW738399 EST339826 tomato flower buds, anthesis, Co...	59 2e-11
	emb AB006602 AB006602 Petunia x hybrida mRNA for ZPT2-7, complet...	49 2e-11
	emb AI959966 AI959966 sc35g05.x1 Gm-c1014 Glycine max cDNA clone...	50 2e-11
55		

Query= ab004796_s_at 16061_s_at /id_source genbank /description
gb|aab97145.1| (af000977) mek1 [arabidopsis thaliana] thaliana]
/blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
(1352 letters)

60

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments: (bits) Value

	emb AJ000728 LEAJ728 <i>Lycopersicon esculentum</i> mRNA for MAP kinase...	555	e-157
10	emb AF165186 AF165186 <i>Nicotiana tabacum</i> MAP kinase kinase mRNA, ...	540	e-153
	emb AW945105 AW945105 EST337156 tomato flower buds 3-8 mm, Corne...	318	6e-86
	emb AW756736 AW756736 sl26f02.y1 Gm-cl027 Glycine max cDNA clone...	174	9e-75
	dbj D31964 TOBNPK2 Tobacco mRNA for protein kinase (NPK2), compl...	183	8e-65
	gb BE054500 BE054500 GA_Ea0031F11f <i>Gossypium arboreum</i> 7-10 dpa ...	165	1e-59
15	emb AW220008 AW220008 EST302491 tomato root during/after fruit s...	228	6e-59
	emb AW624623 AW624623 EST322568 tomato flower buds 3-8 mm, Corne...	215	9e-55
	emb AI438023 AI438023 sa34h10.y1 Gm-cl004 Glycine max cDNA clone...	208	7e-53
	emb AW617901 AW617901 EST296829 <i>L. hirsutum</i> trichome, Cornell Un...	203	2e-51
	emb AJ007393 YLI7393 <i>Yarrowia lipolytica</i> ste7 gene.	92	4e-49
20	emb AW931392 AW931392 EST357235 tomato fruit mature green, TAMU ...	189	3e-47
	emb AW039087 AW039087 EST281060 tomato mixed elicitor, BTI Lycop...	183	2e-45
	emb Z99259 SPAC2C4 <i>S.pombe</i> chromosome I cosmid c2C4.	85	6e-43
	emb AW032808 AW032808 EST276367 tomato callus, TAMU <i>Lycopersicon</i> ...	175	9e-43
	gb U07801 UMU07801 <i>Ustilago maydis</i> serine/threonine/tyrosine kin...	121	2e-42
25	emb AJ009609 BNA9609 <i>Brassica napus</i> mRNA for MAP4K alpha2 protein.	87	1e-41
	dbj D13001 YSCSSP32 Yeast Mkk1/SSP32 gene for Mkk1 protein kinas...	72	3e-41
	emb Z75139 SCYOR231W <i>S.cerevisiae</i> chromosome XV reading frame OR...	72	3e-41
	emb AF169644 AF169644 <i>Glomerella cingulata</i> MAP kinase kinase (EM...	82	7e-41
	emb AJ009608 BNA9608 <i>Brassica napus</i> mRNA for MAP4K alpha 1 protein.	82	8e-41
30	emb AW127406 AW127406 M110589 DSIL <i>Medicago truncatula</i> cDNA clon...	94	2e-39
	emb AJ225532 AJ225532 AJ225532 Absciscic acid-treated protonemata...	162	5e-39
	emb AZ215495 AZ215495 Sheared DNA-56D6.TR Sheared DNA Trypanosom...	113	3e-38
	dbj D13785 YSCMKK2 <i>S.cerevisiae</i> gene for Mkk2 protein kinase, co...	68	1e-37
	gb U72980 CAU72980 <i>Candida albicans</i> Map kinase kinase (STE7) gen...	128	2e-37
35	gb L19195 YSASTKIN <i>Candida albicans</i> (clone pKB66) serine/threoni...	128	2e-37
	emb AL109822 SPBC409 <i>S.pombe</i> chromosome II cosmid c409.	68	2e-37
	gb U43703 SCU43703 <i>Saccharomyces cerevisiae</i> chromosome XVI cosmi...	68	2e-37
	emb X62631 SPWIS1 <i>S.pombe</i> wis1 gene for protein kinase.	68	3e-37
	emb AW625928 AW625928 EST319823 tomato radicle, 5 d post-imbibit...	90	8e-37
40	emb AW348493 AW348493 GM210002B12A8R Gm-r1021 Glycine max cDNA 3...	154	1e-36
	emb AZ213240 AZ213240 Sheared DNA-102E10.TF Sheared DNA Trypanos...	140	3e-36
	emb AW497308 AW497308 ga57h06.y1 Moss EST library PPU Physcomitr...	150	2e-35
	emb Z49403 SCYJL128C <i>S.cerevisiae</i> chromosome X reading frame ORF...	78	5e-35
45	gb U12237 SCU12237 <i>Saccharomyces cerevisiae</i> suppressor of fluori...	78	5e-35
	gb J02946 YSCPBS2 <i>Saccharomyces cerevisiae</i> putative protein kina...	78	5e-35
	emb AJ243184 LN243184 <i>Leishmania infantum</i> mkk gene for putative...	78	2e-34
	emb AW032663 AW032663 EST276222 tomato callus, TAMU <i>Lycopersicon</i> ...	82	2e-34
	emb AJ243118 LME243118 <i>Leishmania mexicana</i> mkk gene for putative...	78	3e-34
50	emb AJ243187 LTR243187 <i>Leishmania tropica</i> mkk gene for putative ...	78	3e-34
	emb AJ243188 LMA243188 <i>Leishmania major</i> mkk gene for putative mi...	78	3e-34
	emb AJ243183 LAM243183 <i>Leishmania amazonensis</i> mkk gene for putat...	78	3e-34
	emb AJ243186 LAE243186 <i>Leishmania aethiopica</i> mkk gene for putati...	78	3e-34
	emb AW185502 AW185502 se80e12.y1 Gm-cl023 Glycine max cDNA clone...	85	6e-34
55	gb U16029 U16029 <i>Leishmania donovani</i> protein kinase (lpk) mRNA, ...	78	1e-33
	emb AJ243185 LDO243185 <i>Leishmania donovani</i> mkk gene for putative...	78	1e-33
	emb AI781759 AI781759 EST262638 tomato susceptible, Cornell Lyco...	97	3e-33
	gb BE059041 BE059041 sn24d08.y1 Gm-cl016 Glycine max cDNA clone ...	143	3e-33
	emb AW929787 AW929787 EST354057 tomato flower buds 8 mm to pre-a...	102	9e-32
60	emb AW981083 AW981083 EST392236 GVN <i>Medicago truncatula</i> cDNA clo...	88	3e-31
	gb BE036317 BE036317 MO23C02 MO <i>Mesembryanthemum crystallinum</i> cD...	82	1e-30

emb|AF069777|AF069777 *Cryphonectria parasitica* mitogen-activated... 66 2e-30
emb|AW099876|AW099876 sd17g06.y2 *Gm-c1012* Glycine max cDNA clone... 80 3e-30
emb|AF249887|AF249887 *Pneumocystis carinii* map kinase kinase (mk... 72 6e-30
emb|AW622016|AW622016 EST312814 tomato root during/after fruit s... 97 7e-29
5 emb|Z69239|SPAC1D4 *S.pombe* chromosome I cosmid c1D4. 116 2e-28
emb|X07445|SPBYR1 Fission yeast *byr1* gene. 116 2e-28
emb|Z67750|SC41KCIV *S.cerevisiae* DNA (cosmid 31A2; chromosome IV... 77 7e-28
emb|X97751|SCIV23 *S.cerevisiae* chrIV genes STE7, CLB3, MSH5, RPC... 77 7e-28
emb|Z74207|SCYDL159W *S.cerevisiae* chromosome IV reading frame OR... 77 8e-28
10 gb|M14097|YSCSTE7 Yeast (*S.cerevisiae*) regulatory gene STE7, com... 77 8e-28
dbj|D26601|TOBPK Tobacco mRNA for protein kinase, complete cds. 54 1e-27
dbj|E05289|E05289 DNA encoding a protein kinase that is homologo... 54 1e-27
emb|AL358652|LMFP1408 *Leishmania major* Friedlin chromosome 14 PA... 100 3e-27
emb|AW349565|AW349565 GM210005A21F10R *Gm-r1021* Glycine max cDNA ... 85 4e-27
15 emb|AF169643|AF169643 *Glomerella cingulata* MAP kinase kinase (EM... 74 5e-27
emb|AQ849880|AQ849880 LMAJFV1_lm51a11.x1 *Leishmania major* FV1 ra... 104 1e-26
emb|AW564378|AW564378 LG1_292_H08.b1_A002 Light Grown 1 (LG1) So... 121 1e-26
emb|AC005140|AC005140 *Plasmodium falciparum* chromosome 12 clone ... 88 2e-26
emb|AW030150|AW030150 EST273405 tomato callus, TAMU Lycopersicon... 120 3e-26
20 emb|Z28126|SCYKL126W *S.cerevisiae* chromosome XI reading frame OR... 84 5e-26
gb|M21307|YSCPKN Yeast (*S.cerevisiae*) protein kinase (YPK1) gene... 84 7e-26
emb|AW676925|AW676925 DG1_2_B05.b1_A002 Dark Grown 1 (DG1) Sorgh... 89 9e-26
emb|Z49702|SC9718 *S.cerevisiae* chromosome XIII cosmid 9718. 85 9e-26
gb|M24929|YSCYKR2A *Saccharomyces cerevisiae* protein kinase (YKR2... 85 9e-26
25 emb|AI779511|AI779511 EST260390 tomato susceptible, Cornell Lyco... 118 1e-25
emb|AZ048376|AZ048376 LMAJFV1_lm77f10.x1 *Leishmania major* FV1 ra... 100 1e-25
gb|U11581|YSCHL5018 *Saccharomyces cerevisiae* chromosome VIII cos... 86 2e-25
gb|M94719|YSCSTE20P *Saccharomyces cerevisiae* protein kinase (Ste... 86 2e-25
gb|L04655|YSCSERKIN *Saccharomyces cerevisiae* serine/threonine ki... 86 2e-25
30 emb|AW922296|AW922296 DG1_17_G11.g1_A002 Dark Grown 1 (DG1) Sorg... 116 4e-25
emb|Z98763|SPAC9G1 *S.pombe* chromosome I cosmid c9G1. 92 4e-25
emb|AE001376|AE001376 *Plasmodium falciparum* chromosome 2, sectio... 49 6e-25
emb|Z97211|SPBC2F12 *S.pombe* chromosome II cosmid c2F12. 56 2e-24
emb|Z98270|SPBC1D7 *S.pombe* chromosome II cosmid c1D7. 56 2e-24
35 emb|AW351150|AW351150 GM210011A20C11R *Gm-r1021* Glycine max cDNA ... 78 2e-24
gb|M74293|YSPBYR2 *Schizosaccharomyces pombe* *byr2* gene, complete ... 56 2e-24
emb|X68851|SPSTE8A *S.pombe* *ste8* gene encoding protein kinase. 56 2e-24
emb|AJ238845|BNA238845 *Brassica napus* mRNA for MAP3K epsilon 1 p... 78 3e-24
gb|L47210|YSASTPK *Candida albicans* serine/threonine protein kina... 86 8e-24
40 gb|U73457|CAU73457 *Candida albicans* Cst20p (CST20) gene, complet... 86 8e-24
emb|AJ005079|AJKL5079 *Kluyveromyces lactis* BCK1 gene, complete CDS. 51 8e-24
emb|AF157632|AF157632 *Schizosaccharomyces pombe* MAPK kinase Skh1... 73 2e-23
dbj|D82023|D82023 *Schizosaccharomyces pombe* *mkk1+* gene for MAP k... 73 2e-23
emb|AF034090|AF034090 *Neurospora crassa* MAPKK kinase (*nrc-1*) gen... 58 2e-23
45 emb|AQ501953|AQ501953 V11H7 mTn-3xHA/lacZ Insertion Library Sacc... 72 2e-23
emb|AL034433|SPBC1604 *S.pombe* chromosome II cosmid c1604. 87 4e-23
gb|U22371|SPU22371 *Schizosaccharomyces pombe* Pak1p (PAK1) mRNA, ... 87 5e-23
gb|L41552|YSPSHK1A *Schizosaccharomyces pombe* Ste20 homologous pr... 87 5e-23

50

Query= af153283_s_at 16083_s_at /id_source genbank /description
gb|aad34615.1|af153283_1 (af153283) putative progesterone-binding
protein homolog [*arabidopsis thaliana*] /blast_score 1.00e-116
(930 letters)

55

Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

60

Score E

	Sequences producing significant alignments:	(bits)	Value
	gb BE052137 BE052137 GA__Ea0031L11f Gossypium arboreum 7-10 dpa ...	257	8e-77
	emb AW727234 AW727234 GA__Ea0011E21 Gossypium arboreum 7-10 dpa ...	257	1e-76
5	emb AW728196 AW728196 GA__Ea0014P01 Gossypium arboreum 7-10 dpa ...	257	1e-76
	emb AW737982 AW737982 EST339409 tomato flower buds, anthesis, Co...	287	2e-76
	emb AW626347 AW626347 EST320254 tomato radicle, 5 d post-imbibit...	287	2e-76
	emb AW622517 AW622517 EST313317 tomato root during/after fruit s...	287	2e-76
	emb AW623663 AW623663 EST321608 tomato flower buds 3-8 mm, Corne...	287	2e-76
10	emb AW622008 AW622008 EST312806 tomato root during/after fruit s...	287	2e-76
	emb AI777165 AI777165 EST258130 tomato resistant, Cornell Lycope...	287	2e-76
	emb AW730733 AW730733 GA__Ea0027I13 Gossypium arboreum 7-10 dpa ...	254	7e-76
	emb AW705652 AW705652 sk50g08.y1 Gm-c1019 Glycine max cDNA clone...	248	1e-74
	emb AW755296 AW755296 sl01c07.y1 Gm-c1036 Glycine max cDNA clone...	245	6e-74
15	emb AW775898 AW775898 EST334963 DSIL Medicago truncatula cDNA cl...	243	2e-71
	emb AW774377 AW774377 EST333528 KV3 Medicago truncatula cDNA clo...	242	4e-71
	emb AW620616 AW620616 sj07e05.y1 Gm-c1032 Glycine max cDNA clone...	230	3e-69
	emb AW398755 AW398755 EST309255 L. pennellii trichome, Cornell U...	251	3e-68
	emb AW559353 AW559353 EST314401 DSIR Medicago truncatula cDNA cl...	231	6e-68
20	emb AI727590 AI727590 BNLGHi8481 Six-day Cotton fiber Gossypium ...	226	2e-67
	emb AW696709 AW696709 NF109H10ST1F1091 Developing stem Medicago ...	211	7e-67
	gb T24185 T24185 crs173 lambdaZAPST Ricinus communis cDNA clone ...	254	2e-66
	emb AW255061 AW255061 ML1356 peppermint glandular trichome Menth...	219	4e-64
	emb AW678629 AW678629 WS1_1_D02.b1_A002 Water-stressed 1 (WS1) S...	245	1e-63
25	emb AW672535 AW672535 LG1_360_B02.b1_A002 Light Grown 1 (LG1) So...	245	1e-63
	emb AW678699 AW678699 WS1_1_D02.b2_A002 Water-stressed 1 (WS1) S...	245	1e-63
	emb AI776227 AI776227 EST257327 tomato resistant, Cornell Lycope...	244	3e-63
	emb AI899451 AI899451 EST268894 tomato susceptible, Cornell Lyco...	242	9e-63
	gb BE125791 BE125791 DG1_57_D06.b1_A002 Dark Grown 1 (DG1) Sorgh...	241	2e-62
30	emb AI482787 AI482787 EST242110 tomato shoot, Cornell Lycopersic...	241	2e-62
	gb BE123902 BE123902 EST394027 DSIL Medicago truncatula cDNA clo...	231	2e-62
	emb AW704889 AW704889 sk40g12.y1 Gm-c1019 Glycine max cDNA clone...	241	2e-62
	emb AW185657 AW185657 se81h10.y1 Gm-c1023 Glycine max cDNA clone...	238	1e-61
	emb AW254869 AW254869 ML1292 peppermint glandular trichome Menth...	211	1e-61
35	emb AW255550 AW255550 ML584 peppermint glandular trichome Mentha...	237	4e-61
	emb AW704813 AW704813 sk55h01.y1 Gm-c1019 Glycine max cDNA clone...	236	5e-61
	emb AI895103 AI895103 EST264546 tomato callus, TAMU Lycopersicon...	232	7e-60
	gb BE059713 BE059713 sn35h07.y1 Gm-c1016 Glycine max cDNA clone ...	232	7e-60
	emb AW705371 AW705371 sk48b10.y1 Gm-c1019 Glycine max cDNA clone...	228	2e-58
40	emb AW755523 AW755523 sl05a05.y1 Gm-c1036 Glycine max cDNA clone...	223	4e-57
	emb AW727353 AW727353 GA__Ea0011L19 Gossypium arboreum 7-10 dpa ...	220	3e-56
	emb AW201709 AW201709 sf06d02.y1 Gm-c1027 Glycine max cDNA clone...	216	6e-55
	emb AW203472 AW203472 sf30f04.y1 Gm-c1028 Glycine max cDNA clone...	216	6e-55
	emb AI161953 AI161953 A010P20U Hybrid aspen plasmid library Popu...	149	2e-54
45	emb AI162696 AI162696 A022P09U Hybrid aspen plasmid library Popu...	152	2e-54
	emb AV410373 AV410373 AV410373 Lotus japonicus young plants (two...	186	4e-54
	emb AW217074 AW217074 EST295788 tomato callus, TAMU Lycopersicon...	213	5e-54
	emb AI441526 AI441526 sa67a03.y1 Gm-c1004 Glycine max cDNA clone...	177	2e-53
	emb AW678831 AW678831 WS1_1_D02.g1_A002 Water-stressed 1 (WS1) S...	208	2e-52
50	emb AW100277 AW100277 sd22a12.y2 Gm-c1012 Glycine max cDNA clone...	192	2e-52
	emb AW745340 AW745340 WS1_33_H02.b1_A002 Water-stressed 1 (WS1) ...	154	4e-48
	emb AW185605 AW185605 se79h09.y1 Gm-c1023 Glycine max cDNA clone...	193	6e-48
	emb AW278821 AW278821 sf99a06.y1 Gm-c1019 Glycine max cDNA clone...	192	8e-48
	gb BE035142 BE035142 MM03H05 MM Mesembryanthemum crystallinum cD...	178	1e-47
55	emb AW255911 AW255911 ML998 peppermint glandular trichome Mentha...	124	2e-47
	emb AW683421 AW683421 NF011G07LF1F1055 Developing leaf Medicago ...	190	4e-47
	emb AI778919 AI778919 EST259798 tomato susceptible, Cornell Lyco...	188	1e-46
	emb AI938231 AI938231 sc41d07.y1 Gm-c1014 Glycine max cDNA clone...	184	2e-45
	emb AW677289 AW677289 DG1_7_D03.b1_A002 Dark Grown 1 (DG1) Sorgh...	182	1e-44
60	emb AW287668 AW287668 LG1_244_H12.b1_A002 Light Grown 1 (LG1) So...	180	4e-44
	emb AW625474 AW625474 EST319381 tomato radicle, 5 d post-imbibit...	156	1e-41

emb|AI729205|AI729205 BNLGHi12887 Six-day Cotton fiber Gossypium... 171 1e-41
 emb|AI941012|AI941012 sb83c05.y1 Gm-c1010 Glycine max cDNA clone... 168 1e-40
 emb|AI855517|AI855517 sc20b06.y1 Gm-c1013 Glycine max cDNA clone... 168 1e-40
 emb|AV429287|AV429287 AV429287 Lotus japonicus young plants (two... 163 3e-39
 5 emb|AW255564|AW255564 ML599 peppermint glandular trichome Mentha... 137 7e-39
 emb|AW677432|AW677432 DG1_7_F03.b1_A002 Dark Grown 1 (DG1) Sorgh... 157 3e-37
 emb|AV426850|AV426850 AV426850 Lotus japonicus young plants (two... 126 3e-37
 gb|BE125876|BE125876 DG1_59_A12.b1_A002 Dark Grown 1 (DG1) Sorgh... 155 1e-36
 gb|BE125862|BE125862 DG1_58_G08.b1_A002 Dark Grown 1 (DG1) Sorgh... 155 1e-36
 10 emb|AV417826|AV417826 AV417826 Lotus japonicus young plants (two... 121 7e-36
 emb|AV426599|AV426599 AV426599 Lotus japonicus young plants (two... 121 7e-36
 emb|AI812547|AI812547 12F5 Pine Lambda Zap Xylem library Pinus t... 150 2e-35
 emb|AW145544|AW145544 ga26e09.y1 Moss EST library PPN Physcomitr... 149 6e-35
 emb|AW156347|AW156347 se22h07.y1 Gm-c1015 Glycine max cDNA clone... 147 3e-34
 15 emb|AI482794|AI482794 EST242117 tomato shoot, Cornell Lycopersic... 146 5e-34
 gb|BE125045|BE125045 DG1_14_A09.b1_A002 Dark Grown 1 (DG1) Sorgh... 144 1e-33
 emb|AW092409|AW092409 EST285589 tomato mixed elicitor, BTI Lycop... 141 2e-32
 emb|AI774296|AI774296 EST255312 tomato resistant, Cornell Lycop... 141 2e-32
 emb|AW037498|AW037498 EST276719 tomato mixed elicitor, BTI Lycop... 141 2e-32
 20 emb|AW037272|AW037272 EST274122 tomato mixed elicitor, BTI Lycop... 141 2e-32
 emb|AW094681|AW094681 EST287849 tomato mixed elicitor, BTI Lycop... 141 2e-32
 emb|AW649965|AW649965 EST328419 tomato germinating seedlings, TA... 141 2e-32
 emb|AW041262|AW041262 EST284126 tomato mixed elicitor, BTI Lycop... 139 4e-32
 gb|BE022031|BE022031 sm65f07.y1 Gm-c1028 Glycine max cDNA clone ... 139 6e-32
 25 emb|AW093288|AW093288 EST286468 tomato mixed elicitor, BTI Lycop... 136 4e-31
 emb|AW596364|AW596364 sj02e02.y1 Gm-c1032 Glycine max cDNA clone... 80 6e-31
 emb|AW981553|AW981553 PC14A01 Pine TriplEx pollen cone library P... 135 8e-31
 emb|AW832150|AW832150 sm20d11.y1 Gm-c1027 Glycine max cDNA clone... 135 1e-30
 emb|AI440919|AI440919 sa56f12.y1 Gm-c1004 Glycine max cDNA clone... 135 1e-30
 30 emb|AW349246|AW349246 GM210004B21F9R Gm-r1021 Glycine max cDNA 3... 134 1e-30
 emb|AW759979|AW759979 sl56e07.y1 Gm-c1027 Glycine max cDNA clone... 134 2e-30
 emb|AW782208|AW782208 sm02h06.y1 Gm-c1027 Glycine max cDNA clone... 134 2e-30
 emb|AW832627|AW832627 sm14h06.y1 Gm-c1027 Glycine max cDNA clone... 134 2e-30
 emb|AW666184|AW666184 sk33d03.y1 Gm-c1028 Glycine max cDNA clone... 121 3e-30
 35 emb|AW925882|AW925882 HVSMEg0005M05 Hordeum vulgare pre-anthesis... 133 3e-30
 emb|AW559445|AW559445 EST314493 DSIR Medicago truncatula cDNA cl... 132 7e-30
 emb|AW761414|AW761414 sl67b12.y1 Gm-c1027 Glycine max cDNA clone... 130 2e-29
 emb|AW754652|AW754652 PC04G03 Pine TriplEx pollen cone library P... 130 3e-29
 emb|AW679942|AW679942 WS1_33_H02.g1_A002 Water-stressed 1 (WS1) ... 129 5e-29
 40 emb|AW754728|AW754728 PC07B03 Pine TriplEx pollen cone library P... 127 3e-28
 emb|AW756987|AW756987 sk82g11.y1 Gm-c1016 Glycine max cDNA clone... 126 4e-28.

Query= athhsp83_s_at 16091_s_at /id_source
 45 /description gb|aaa32822.1| (m62984) heat shock protein 83
 [arabidopsis thaliana] /blast_score 0
 (2390 letters)

Database: plantfungal
 50 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 55 Sequences producing significant alignments: (bits) Value

gb|M99431|PHNHSP83A Pharbitis nil heat shock protein 83 (Hsp83) ... 597 0.0
 gb|M96549|TOMHSC80P Tomato heat shock cognate protein 80 gene, 3... 577 0.0
 gb|U55859|TAU55859 Triticum aestivum heat shock protein 80 mRNA,... 575 0.0
 60 emb|X98582|TAX98582 T.aestivum mRNA for HSP80-2 protein. 572 0.0
 emb|X63195|NTHSP82 N.tabacum mRNA for heat shock protein 82. 601 0.0

	emb AF123259 AF123259	Lycopersicon esculentum heat shock protein...	483	0.0
	emb AF165818 AF165818	Guillardia theta nucleomorph 5S ribosomal ...	505	0.0
	emb AF042329 AF042329	Eimeria tenella heat shock protein 90 (hsp...	514	0.0
	gb M57386 THEHSP90	T.parva heat shock protein 90 (hsp90) mRNA, c...	500	0.0
5	emb Z29667 PFHESHPR	P.falciparum (7) mRNA for heat-shock protein.	507	0.0
	gb U45449 EBU45449	Eimeria bovis heat shock protein 90 (hsp90) m...	495	0.0
	emb AF151114 AF151114	Tetrahymena thermophila strain B2086 hsp82...	486	0.0
	emb AF136649 AF136649	Babesia bovis heat shock protein 90 (HSP90...	487	0.0
	gb M15346 TRBHSC	T.cruzi tandemly repeated gene encoding an 85 k...	457	0.0
10	emb X14176 TBHSP83	Trypanosoma brucei HSP83 gene.	452	0.0
	gb M73492 LEIHSP90	Leishmania donovani heat shock protein 90 mRN...	456	0.0
	emb X87770 LIHSP83GN	L.infantum hsp83 gene.	454	0.0
	gb M92926 LEIHSP01	Leishmania amazonensis heat shock protein 83 ...	449	0.0
	gb U92465 AFU92465	Aspergillus fumigatus heat shock protein (Hsp...	458	e-165
15	emb AF212996 AF212996	Neurospora crassa heat shock protein 80 ge...	473	e-165
	emb AL110469 SPAC926	S.pombe chromosome I cosmid c926.	460	e-165
	gb L35550 YSPHSP90X	Schizosaccharomyces pombe heat shock protein...	460	e-162
	gb U81165 PAU81165	Podospira anserina suppressor of vegetative i...	292	e-161
	emb Z67751 SC38KCXVI	S.cerevisiae DNA (chromosome XVI; 38 kb).	448	e-159
20	emb Z73596 SCYPL240C	S.cerevisiae chromosome XVI reading frame O...	448	e-159
	gb K01387 YSCHSP82A	Yeast (S.cerevisiae) HSP82 (heat shock-induc...	448	e-159
	emb X81025 CAHSP90	C.albicans hsp90 gene.	451	e-159
	emb AF251005 AF251005	Candida tropicalis heat shock protein 90 g...	444	e-158
	emb Z49808 SC8010	S.cerevisiae chromosome XIII cosmid 8010.	447	e-158
25	emb AF221856 AF221856	Euphorbia esula heat-shock protein 80 mRNA...	292	e-158
	gb M26044 YSCHSC82	S. cerevisiae HSC82 gene encoding hsc82, the ...	447	e-157
	emb AW729825 AW729825	GA__Ea0026E04 Gossypium arboreum 7-10 dpa ...	473	e-134
	emb AW727612 AW727612	GA__Ea0015C16 Gossypium arboreum 7-10 dpa ...	454	e-132
	emb AI489832 AI489832	EST248171 tomato ovary, TAMU Lycopersicon ...	471	e-132
30	emb AW982575 AW982575	HVSMEg0003K07f Hordeum vulgare pre-anthesi...	471	e-131
	emb AW774793 AW774793	EST333944 KV3 Medicago truncatula cDNA clo...	459	e-128
	emb AW221746 AW221746	EST298557 tomato fruit red ripe, TAMU Lyco...	350	e-128
	emb AW728021 AW728021	GA__Ea0029G22 Gossypium arboreum 7-10 dpa ...	315	e-127
	gb BE035845 BE035845	MO11A12 MO Mesembryanthemum crystallinum cD...	455	e-127
35	emb AW650299 AW650299	EST328753 tomato germinating seedlings, TA...	455	e-127
	emb AW982497 AW982497	HVSMEg0003G20f Hordeum vulgare pre-anthesi...	439	e-126
	emb AF078070 AF078070	Griffithsia japonica heat-shock protein 90...	245	e-126
	emb AW218188 AW218188	EST303369 tomato radicle, 5 d post-imbibit...	452	e-126
	emb AW731352 AW731352	GA__Ea0030E22 Gossypium arboreum 7-10 dpa ...	449	e-125
40	emb AW621485 AW621485	EST312283 tomato root during/after fruit s...	445	e-124
	emb AW905909 AW905909	EST342082 potato stolon, Cornell Universit...	331	e-124
	emb AW618647 AW618647	EST320633 L. pennellii trichome, Cornell U...	439	e-122
	emb AI730385 AI730385	BNLGH16770 Six-day Cotton fiber Gossypium ...	439	e-122
	emb AW931002 AW931002	EST356845 tomato fruit mature green, TAMU ...	436	e-121
45	emb AW186517 AW186517	se68g12.y1 Gm-c1019 Glycine max cDNA clone...	432	e-120
	gb BE055051 BE055051	GA__Ea0031H10f Gossypium arboreum 7-10 dpa ...	381	e-118
	emb AW217359 AW217359	EST296010 tomato flower buds 0-3 mm, Corne...	427	e-118
	emb AW216642 AW216642	EST295356 tomato callus, TAMU Lycopersicon...	423	e-117
	emb AW217696 AW217696	EST296410 tomato flower buds 8 mm to pre-a...	422	e-117
50	emb AW011081 AW011081	ST16E03 Pine TriplEx shoot tip library Pin...	421	e-116
	emb AI730419 AI730419	BNLGH17100 Six-day Cotton fiber Gossypium ...	417	e-115
	emb AW907064 AW907064	EST343096 potato stolon, Cornell Universit...	413	e-114
	emb AW696590 AW696590	NF108G11ST1F1087 Developing stem Medicago ...	413	e-114
	emb AW738699 AW738699	EST340126 tomato flower buds, anthesis, Co...	412	e-114
55	emb AI442468 AI442468	sa27d08.y1 Gm-c1004 Glycine max cDNA clone...	412	e-114
	emb AW684853 AW684853	NF022C08NR1F1000 Nodulated root Medicago t...	403	e-114
	emb AW693965 AW693965	NF071A06ST1F1040 Developing stem Medicago ...	408	e-113
	emb AW690869 AW690869	NF036A07ST1F1000 Developing stem Medicago ...	390	e-113
	emb AW030608 AW030608	EST273863 tomato callus, TAMU Lycopersicon...	407	e-112
60	emb AW983321 AW983321	HVSMEg0010D10f Hordeum vulgare pre-anthesi...	354	e-112
	emb AI726426 AI726426	BNLGH15602 Six-day Cotton fiber Gossypium ...	407	e-112

- emb|AW930252|AW930252 EST340709 tomato fruit mature green, TAMU ... 406 e-112
 emb|AW979717|AW979717 EST341337 tomato root deficiency, Cornell ... 404 e-111
 emb|AW695561|AW695561 NF096B09ST1F1076 Developing stem Medicago ... 404 e-111
 emb|AW691505|AW691505 NF045G02ST1F1000 Developing stem Medicago ... 361 e-111
 5 emb|AW735801|AW735801 EST336569 tomato flower buds 0-3 mm, Corne... 402 e-111
 emb|AW737406|AW737406 EST338749 tomato flower buds, anthesis, Co... 402 e-111
 emb|AL112936|CNS01AHC Botrytis cinerea strain T4 cDNA library un... 400 e-110
 emb|AW217697|AW217697 EST296411 tomato flower buds 8 mm to pre-a... 400 e-110
 emb|AW218948|AW218948 EST301430 tomato root during/after fruit s... 396 e-110
 10 emb|AW220869|AW220869 EST297338 tomato fruit mature green, TAMU ... 398 e-109
 emb|AW616417|AW616417 EST322828 *L. hirsutum* trichome, Cornell Un... 397 e-109
 emb|AW688548|AW688548 NF008H04ST1F1000 Developing stem Medicago ... 396 e-109
 emb|AW738535|AW738535 EST339962 tomato flower buds, anthesis, Co... 242 e-109
 emb|AW649397|AW649397 EST327851 tomato germinating seedlings, TA... 394 e-108
 15 emb|AW693115|AW693115 NF060C10ST1F1081 Developing stem Medicago ... 226 e-107
 emb|AI488065|AI488065 EST246387 tomato ovary, TAMU Lycopersicon ... 390 e-107
 emb|AI726157|AI726157 BNLGHi5098 Six-day Cotton fiber *Gossypium* ... 226 e-107
 gb|BE060856|BE060856 HVSMEg0013J20f *Hordeum vulgare* pre-anthesis... 388 e-107
 emb|AI781620|AI781620 EST262499 tomato susceptible, Cornell Lyco... 389 e-107
 20 emb|AL111751|CNS019KF Botrytis cinerea strain T4 cDNA library un... 389 e-107
 emb|AW092845|AW092845 EST286025 tomato mixed elicitor, BTI Lycop... 386 e-106
 emb|AW983154|AW983154 HVSMEg0008G17f *Hordeum vulgare* pre-anthesi... 224 e-106
 emb|AI780272|AI780272 EST261151 tomato susceptible, Cornell Lyco... 215 e-106
 emb|AW651194|AW651194 EST329648 tomato germinating seedlings, TA... 266 e-106
 25 emb|AW690804|AW690804 NF035B11ST1F1000 Developing stem Medicago ... 375 e-106
 emb|AW154860|AW154860 EST290253 tomato root deficiency, Cornell ... 385 e-105
 emb|AI780075|AI780075 EST260954 tomato susceptible, Cornell Lyco... 383 e-105
 emb|AW928471|AW928471 EST337259 tomato flower buds 8 mm to pre-a... 382 e-105
 gb|L34028|PFAHSP86B *Plasmodium falciparum* (clone HB3) heat shock... 382 e-105
 30 emb|AF030694|AF030694 *Plasmodium falciparum* strain Dd2 heat shoc... 382 e-105
 gb|L34027|PFAHSP86A *Plasmodium falciparum* (clone Dd2) heat shock... 382 e-105
 emb|AW737397|AW737397 EST338740 tomato flower buds, anthesis, Co... 381 e-104
 emb|AW334905|AW334905 S40F8 AGS-1 *Pneumocystis carinii* f. sp. ca... 381 e-104
 emb|AW035244|AW035244 EST280506 tomato callus, TAMU Lycopersicon... 380 e-104
 35

Query= atu68017_s_at 16105_s_at /id_source
 /description gb|aac31756.1| (u68017) heat shock transcription
 factor 4 [arabidopsis thaliana] /blast_score 1.00e-113
 40 (1422 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

45 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

- 50 emb|AB014483|AB014483 *Nicotiana tabacum* NtHSF1 mRNA for heat sho... 213 2e-62
 emb|X55347|LPHSF24 Tomato mRNA for heat stress transcription fac... 210 2e-53
 emb|AI900223|AI900223 sc02f05.y1 Gm-cl012 Glycine max cDNA clone... 205 3e-53
 emb|Z46953|GMHSF34 G.max mRNA for heat shock transcription facto... 203 6e-53
 emb|AV408054|AV408054 AV408054 *Lotus japonicus* young plants (two... 203 3e-51
 55 emb|AV415115|AV415115 AV415115 *Lotus japonicus* young plants (two... 197 2e-49
 emb|AW774951|AW774951 EST334102 KV3 *Medicago truncatula* cDNA clo... 194 1e-48
 emb|AW689532|AW689532 NF021G10ST1F1000 Developing stem Medicago ... 194 1e-48
 emb|AI728175|AI728175 BNLGHi10028 Six-day Cotton fiber *Gossypium*... 192 5e-48
 emb|AI055366|AI055366 coau0003M17 Cotton Boll Abscission Zone cD... 191 1e-47
 60 emb|AW703969|AW703969 sk14g08.y1 Gm-cl023 Glycine max cDNA clone... 191 1e-47
 emb|AW428882|AW428882 Ljirnp25-001-b9 Ljirnp Lambda HybriZap ... 190 2e-47

- emb|AW931781|AW931781 EST357624 tomato fruit mature green, TAMU ... 189 3e-47
emb|AW686121|AW686121 NF033H01NR1F1000 Nodulated root Medicago t... 188 1e-46
emb|Z46956|GMHSF5 G.max mRNA for heat shock transcription factor 5. 185 6e-46
5 emb|AW109013|AW109013 gate0002O16f Gossypium arboreum 7-10 dpa f... 179 4e-44
gb|BE054274|BE054274 GA__Ea0002O16f Gossypium arboreum 7-10 dpa ... 179 4e-44
gb|BE020791|BE020791 sm52h09.y1 Gm-c1028 Glycine max cDNA clone ... 178 1e-43
emb|AW696868|AW696868 NF111F05ST1F1046 Developing stem Medicago ... 166 3e-43
emb|AW686271|AW686271 NF039H06NR1F1000 Nodulated root Medicago t... 171 5e-42
10 emb|AW931176|AW931176 EST357019 tomato fruit mature green, TAMU ... 168 8e-41
gb|C95479|C95479 C95479 Citrus unshiu Miyagawa-wase maturation s... 166 5e-40
emb|AW033421|AW033421 EST276992 tomato callus, TAMU Lycopersicon... 165 1e-39
emb|AW030725|AW030725 EST273980 tomato callus, TAMU Lycopersicon... 165 1e-39
emb|AW041695|AW041695 EST284559 tomato mixed elicitor, BTI Lycop... 165 1e-39
emb|AW217982|AW217982 EST296697 tomato flower buds, anthesis, Co... 165 1e-39
15 emb|X67600|LPHSF8 L.peruvianum Lp-hsf8 mRNA for heat stress tran... 161 1e-38
emb|AW774397|AW774397 EST333548 KV3 Medicago truncatula cDNA clo... 160 2e-38
emb|AW686582|AW686582 NF042H04NR1F1000 Nodulated root Medicago t... 155 6e-37
emb|AW776460|AW776460 EST335525 DSIL Medicago truncatula cDNA cl... 152 7e-36
emb|AW738023|AW738023 EST339450 tomato flower buds, anthesis, Co... 150 3e-35
20 emb|AW036683|AW036683 EST278726 tomato fruit mature green, TAMU ... 149 5e-35
emb|AI729182|AI729182 BNLGHi12855 Six-day Cotton fiber Gossypium... 149 5e-35
emb|AI489721|AI489721 EST248060 tomato ovary, TAMU Lycopersicon ... 149 5e-35
emb|AW034402|AW034402 EST277973 tomato callus, TAMU Lycopersicon... 148 7e-35
emb|X67601|LPHSF30 L.peruvianum Lp-hsf30 mRNA for heat stress tr... 148 9e-35
25 emb|AW906822|AW906822 EST342945 potato stolon, Cornell Universit... 147 2e-34
emb|AW164509|AW164509 se74f12.y1 Gm-c1023 Glycine max cDNA clone... 147 2e-34
emb|AW034874|AW034874 EST279103 tomato callus, TAMU Lycopersicon... 147 2e-34
emb|Z46952|GMHSF21 G.max mRNA for heat shock transcription facto... 145 8e-34
emb|AF235958|AF235958 Medicago sativa heat shock transcription f... 145 8e-34
30 emb|AW559623|AW559623 EST314671 DSIR Medicago truncatula cDNA cl... 144 2e-33
emb|AW222011|AW222011 EST298822 tomato fruit red ripe, TAMU Lyco... 144 2e-33
emb|AW930998|AW930998 EST356841 tomato fruit mature green, TAMU ... 143 4e-33
emb|AW906840|AW906840 EST342963 potato stolon, Cornell Universit... 140 2e-32
emb|AB014484|AB014484 Nicotiana tabacum NtHSF2 mRNA for heat sho... 140 3e-32
35 emb|AF208544|AF208544 Lycopersicon peruvianum heat stress transc... 139 4e-32
emb|AW738534|AW738534 EST339961 tomato flower buds, anthesis, Co... 139 5e-32
emb|AI725043|AI725043 942 PtIFG2 Pinus taeda cDNA clone 8824r, m... 139 5e-32
emb|AW596493|AW596493 sj13a09.y1 Gm-c1032 Glycine max cDNA clone... 138 1e-31
emb|AW874988|AW874988 00109 leafy spurge Lambda HybriZAP 2.1 two... 138 1e-31
40 emb|AV415736|AV415736 AV415736 Lotus japonicus young plants (two... 138 1e-31
emb|AW979619|AW979619 EST341218 tomato root deficiency, Cornell ... 137 2e-31
emb|AW932142|AW932142 EST357985 tomato fruit mature green, TAMU ... 136 3e-31
emb|Z46954|GMHSF33 G.max mRNA for heat shock transcription facto... 135 9e-31
emb|AW569138|AW569138 si63g09.y1 Gm-r1030 Glycine max cDNA clone... 134 1e-30
45 emb|AW569256|AW569256 si64g09.y1 Gm-r1030 Glycine max cDNA clone... 134 1e-30
emb|AW203851|AW203851 sf38h11.y1 Gm-c1028 Glycine max cDNA clone... 133 3e-30
emb|AW220758|AW220758 EST297227 tomato fruit mature green, TAMU ... 132 6e-30
emb|AI728806|AI728806 BNLGHi11701 Six-day Cotton fiber Gossypium... 108 2e-28
emb|AW736596|AW736596 EST333088 KV3 Medicago truncatula cDNA clo... 103 3e-28
50 emb|AI895934|AI895934 EST265377 tomato callus, TAMU Lycopersicon... 123 3e-27
emb|Z46951|GMHSF29 G.max mRNA for heat shock transcription facto... 120 2e-26
gb|BE019974|BE019974 sm38b12.y1 Gm-c1028 Glycine max cDNA clone ... 119 6e-26
emb|Z46955|GMHSF31 G.max mRNA for heat shock transcription facto... 115 8e-25
emb|X67599|LEHSF8 L.esculentum Le-hsf8 gene for heat stress tran... 114 2e-24
55 emb|AQ579554|AQ579554 T135016b shotgun sub-library of BAC clone ... 113 4e-24
emb|AW775388|AW775388 EST334453 DSIL Medicago truncatula cDNA cl... 66 1e-23
emb|AW931892|AW931892 EST357735 tomato fruit mature green, TAMU ... 104 2e-21
emb|AQ579623|AQ579623 T135087b shotgun sub-library of BAC clone ... 103 4e-21
emb|AW736595|AW736595 EST333087 KV3 Medicago truncatula cDNA clo... 103 4e-21
60 emb|AW697097|AW697097 NF112C08ST1F1065 Developing stem Medicago ... 103 4e-21
emb|AV420766|AV420766 AV420766 Lotus japonicus young plants (two... 102 8e-21

- emb|AV413314|AV413314 AV413314 Lotus japonicus young plants (two... 102 8e-21
 emb|AW693546|AW693546 NF067D12ST1F1101 Developing stem Medicago ... 101 1e-20
 emb|AI895294|AI895294 EST264737 tomato callus, TAMU Lycopersicon... 101 1e-20
 emb|AJ010644|PSA010643 Pisum sativum hsfA gene, exons 1 to 2, pa... 99 7e-20
 5 emb|AW924303|AW924303 WS1_52_H11.b1_A002 Water-stressed 1 (WS1) ... 99 7e-20
 emb|AI895834|AI895834 EST265277 tomato callus, TAMU Lycopersicon... 95 9e-19
 emb|AW756148|AW756148 sl16e07.y1 Gm-c1036 Glycine max cDNA clone... 93 4e-18
 gb|M94683|YSPHSF Schizosaccharomyces pombe heat shock transcript... 93 6e-18
 emb|AW132703|AW132703 se09a08.y1 Gm-c1013 Glycine max cDNA clone... 93 6e-18
 10 emb|X55149|KLHSFG K. lactis HSF gene for heat shock transcriptio... 76 2e-17
 emb|AW933448|AW933448 EST359387 tomato fruit mature green, TAMU ... 89 8e-17
 emb|AI896906|AI896906 EST266349 tomato callus, TAMU Lycopersicon... 89 1e-16
 emb|AZ045432|AZ045432 T234030b shotgun sub-library of BAC clone ... 84 3e-15
 gb|U00485|YSCSKN7 Saccharomyces cerevisiae putative transcriptio... 83 5e-15
 15 emb|X83031|SCPOS9 S.cerevisiae POS9 gene. 83 5e-15
 gb|U00029|YSCH9177 Saccharomyces cerevisiae chromosome VIII cosm... 83 5e-15
 emb|Z69726|SPAC2E12 S.pombe chromosome I cosmid c2E12. 83 7e-15
 gb|M22040|YSCHSF1A S.cerevisiae heat shock transcription factor ... 81 2e-14
 gb|J03139|YSCHSF S.cerevisiae heat shock factor gene (HSF), comp... 81 2e-14
 20 emb|Z72596|SCYGL074C S.cerevisiae chromosome VII reading frame O... 81 2e-14
 emb|AI212342|AI212342 x3c12a1.r1 Aspergillus nidulans 24hr asexu... 73 8e-14
 emb|AW686674|AW686674 NF040F05NR1F1000 Nodulated root Medicago t... 79 8e-14
 emb|AZ048458|AZ048458 PSB119 Barley PstI genomic clones Hordeum ... 78 2e-13
 emb|AW034135|AW034135 EST277706 tomato callus, TAMU Lycopersicon... 57 9e-13
 25 emb|AW933529|AW933529 EST359288 tomato fruit mature green, TAMU ... 72 1e-11
 emb|AW307441|AW307441 sf57a06.y1 Gm-c1009 Glycine max cDNA clone... 70 5e-11
 emb|AW620962|AW620962 sj98b03.y1 Gm-c1023 Glycine max cDNA clone... 70 5e-11

30 Query= athpear_s_at 16150_s_at /id_source genbank /description
 emb|cab41718.1| (al049730) pearli 1 [arabidopsis thaliana]
 /blast_score 5.00e-43
 (810 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

- 40 Score E
 Sequences producing significant alignments: (bits) Value
- emb|AI352845|AI352845 MB69-3F PZ204.BNlib Brassica napus cDNA cl... 161 2e-55
 emb|AI352927|AI352927 MB74-12D PZ204.BNlib Brassica napus cDNA c... 169 8e-43
 45 gb|S68113|S68113 proline-rich SAC51 [Brassica napus=oilseed rape... 163 1e-42
 emb|X71618|BNPRPPDA B.napus proline-rich mRNA accumulating durin... 163 1e-42
 emb|AF109654|AF109654 AF109654 Capsicum annuum root susceptible ... 169 3e-41
 emb|AI352937|AI352937 MB74-5H PZ204.BNlib Brassica napus cDNA cl... 115 5e-40
 emb|AW621250|AW621250 EST312048 tomato root during/after fruit s... 162 6e-40
 50 emb|AW626221|AW626221 EST320128 tomato radicle, 5 d post-imbibit... 162 6e-40
 emb|AI779211|AI779211 EST260090 tomato susceptible, Cornell Lyco... 162 6e-40
 emb|AW443140|AW443140 EST308070 tomato mixed elicitor, BTI Lycop... 162 6e-40
 emb|AI776056|AI776056 EST257156 tomato resistant, Cornell Lycope... 162 6e-40
 emb|AW032764|AW032764 EST276323 tomato callus, TAMU Lycopersicon... 162 6e-40
 55 emb|AW217082|AW217082 EST295796 tomato callus, TAMU Lycopersicon... 162 6e-40
 emb|AW035571|AW035571 EST281309 tomato callus, TAMU Lycopersicon... 162 6e-40
 emb|AV413531|AV413531 AV413531 Lotus japonicus young plants (two... 163 1e-39
 gb|BE124752|BE124752 EST393787 GVN Medicago truncatula cDNA clon... 163 2e-39
 emb|AW980687|AW980687 EST391840 GVN Medicago truncatula cDNA clo... 163 2e-39
 60 gb|BE124520|BE124520 EST393555 GVN Medicago truncatula cDNA clon... 163 2e-39
 emb|AW980826|AW980826 EST391979 GVN Medicago truncatula cDNA clo... 163 2e-39

- emb|AW980547|AW980547 EST391700 GVN Medicago truncatula cDNA clo... 163 2e-39
 gb|BE124445|BE124445 EST393480 GVN Medicago truncatula cDNA clon... 163 2e-39
 gb|BE124789|BE124789 EST393824 GVN Medicago truncatula cDNA clon... 163 2e-39
 emb|AW725519|AW725519 GA__Ea0018G20 Gossypium arboreum 7-10 dpa ... 163 2e-39
 5 emb|AW685869|AW685869 NF031B09NR1F1000 Nodulated root Medicago t... 163 2e-39
 emb|AW287846|AW287846 N100689e rootphos(-) Medicago truncatula c... 163 2e-39
 gb|BE124744|BE124744 EST393779 GVN Medicago truncatula cDNA clon... 163 2e-39
 emb|AW560894|AW560894 EST315942 DSIR Medicago truncatula cDNA cl... 163 2e-39
 emb|AW684629|AW684629 NF019B05NR1F1000 Nodulated root Medicago t... 163 2e-39
 10 emb|AW329233|AW329233 N200445e rootphos(-) Medicago truncatula c... 163 2e-39
 emb|AW034083|AW034083 EST277578 tomato callus, TAMU Lycopersicon... 162 2e-39
 emb|AW094444|AW094444 EST287624 tomato mixed elicitor, BTI Lycop... 162 2e-39
 emb|AW907202|AW907202 EST343325 potato stolon, Cornell Universit... 160 1e-38
 emb|AW125962|AW125962 N100157e rootphos(-) Medicago truncatula c... 160 2e-38
 15 emb|AW217088|AW217088 EST295802 tomato callus, TAMU Lycopersicon... 159 3e-38
 emb|AW685279|AW685279 NF025G02NR1F1000 Nodulated root Medicago t... 158 4e-38
 emb|AF026382|AF026382 Fragaria x ananassa HyPRP mRNA, complete cds. 158 6e-38
 emb|AI779212|AI779212 EST260091 tomato susceptible, Cornell Lyco... 158 6e-38
 emb|AW257148|AW257148 EST305285 KV2 Medicago truncatula cDNA clo... 158 6e-38
 20 emb|AW349572|AW349572 GM210005A21F12R Gm-r1021 Glycine max cDNA ... 157 8e-38
 dbj|D83227|POPELPG Populus nigra gene for extensin like protein,... 157 1e-37
 dbj|D83226|POPELP Populus nigra mRNA for extensin like protein, ... 157 1e-37
 emb|AW624937|AW624937 EST313766 tomato radicle, 5 d post-imbibit... 156 2e-37
 emb|AW622601|AW622601 EST313401 tomato root during/after fruit s... 156 2e-37
 25 emb|AW287985|AW287985 N100829e rootphos(-) Medicago truncatula c... 153 2e-36
 emb|AW625740|AW625740 EST319647 tomato radicle, 5 d post-imbibit... 152 4e-36
 emb|X85206|CRRNAHPRP C.roseus mRNA for hybrid proline-rich protein. 152 4e-36
 emb|AW622645|AW622645 EST313445 tomato root during/after fruit s... 151 7e-36
 gb|BE021488|BE021488 sm59b04.y1 Gm-c1028 Glycine max cDNA clone ... 150 1e-35
 30 emb|Z26880|CR14KDPP C.roseus mRNA for 14 kDa polypeptide. 150 1e-35
 emb|AW309747|AW309747 sf24c01.x1 Gm-c1028 Glycine max cDNA clone... 131 3e-34
 emb|AW309357|AW309357 sf16d03.x1 Gm-c1028 Glycine max cDNA clone... 131 3e-34
 gb|BE022318|BE022318 sm73d03.y1 Gm-c1028 Glycine max cDNA clone ... 131 3e-34
 emb|AW234182|AW234182 sf22b12.y1 Gm-c1028 Glycine max cDNA clone... 131 3e-34
 35 emb|AW704401|AW704401 sk30f03.y1 Gm-c1028 Glycine max cDNA clone... 131 3e-34
 emb|AI736342|AI736342 sb27c03.y1 Gm-c1009 Glycine max cDNA clone... 129 4e-34
 gb|BE022083|BE022083 sm68c08.y1 Gm-c1028 Glycine max cDNA clone ... 130 4e-34
 dbj|D86629|D86629 Nicotiana tabacum mRNA for NT16 polypeptide, c... 144 1e-33
 emb|AI442014|AI442014 sa66e07.y1 Gm-c1004 Glycine max cDNA clone... 128 2e-33
 40 emb|AW306872|AW306872 sf49g05.y1 Gm-c1009 Glycine max cDNA clone... 128 2e-33
 emb|AW597518|AW597518 sj48b01.y1 Gm-c1033 Glycine max cDNA clone... 128 2e-33
 emb|AW597680|AW597680 sj49e04.y1 Gm-c1033 Glycine max cDNA clone... 128 2e-33
 emb|AW307412|AW307412 sf56f11.y1 Gm-c1009 Glycine max cDNA clone... 128 2e-33
 emb|AI441411|AI441411 sa59e12.y1 Gm-c1004 Glycine max cDNA clone... 128 2e-33
 45 emb|AI776903|AI776903 EST258003 tomato resistant, Cornell Lycop... 127 3e-33
 emb|AW092951|AW092951 EST286131 tomato mixed elicitor, BTI Lycop... 127 3e-33
 emb|AW650542|AW650542 EST328996 tomato germinating seedlings, TA... 127 3e-33
 emb|AI772831|AI772831 EST253931 tomato resistant, Cornell Lycop... 127 3e-33
 dbj|D86721|D86721 Nicotiana tabacum DNA for glycine-rich polypep... 142 3e-33
 50 emb|AW163963|AW163963 Ljirnpst17-382-g10 Ljirnp Lambda HybriZap... 142 3e-33
 gb|BE022257|BE022257 sm72g11.y1 Gm-c1028 Glycine max cDNA clone ... 127 4e-33
 emb|AW666281|AW666281 sk34f10.y1 Gm-c1028 Glycine max cDNA clone... 127 4e-33
 emb|AW706178|AW706178 sj52g11.y1 Gm-c1033 Glycine max cDNA clone... 127 4e-33
 emb|AB035125|AB035125 Nicotiana tabacum mRNA for glycine-rich pr... 140 1e-32
 55 dbj|D26454|TOBTID23 Nicotiana glauca X Nicotiana langsdorffii mR... 140 1e-32
 emb|AW443491|AW443491 EST308421 tomato mixed elicitor, BTI Lycop... 125 1e-32
 emb|X15436|DC215G Carrot DC 2.15 mRNA for 14 kD protein. 139 2e-32
 emb|AW622484|AW622484 EST313272 tomato root during/after fruit s... 124 3e-32
 emb|AW906384|AW906384 EST342506 potato stolon, Cornell Universit... 126 3e-32
 60 emb|AW093202|AW093202 EST286382 tomato mixed elicitor, BTI Lycop... 123 3e-32
 emb|AW649092|AW649092 EST327546 tomato germinating seedlings, TA... 123 3e-32

emb|AV411071|AV411071 AV411071 Lotus japonicus young plants (two... 135 3e-31
 emb|AW719418|AW719418 LjNEST4c12r Lotus japonicus nodule library... 126 4e-31
 emb|AV423170|AV423170 AV423170 Lotus japonicus young plants (two... 126 4e-31
 emb|AV422321|AV422321 AV422321 Lotus japonicus young plants (two... 125 6e-31
 5 emb|AV416097|AV416097 AV416097 Lotus japonicus young plants (two... 125 6e-31
 emb|AV413898|AV413898 AV413898 Lotus japonicus young plants (two... 125 6e-31
 emb|AV415427|AV415427 AV415427 Lotus japonicus young plants (two... 125 6e-31
 emb|AW309629|AW309629 sf22b12.x1 Gm-c1028 Glycine max cDNA clone... 123 1e-30
 emb|AW570545|AW570545 sj63d10.y1 Gm-c1033 Glycine max cDNA clone... 125 2e-30
 10 emb|AW152920|AW152920 se32g01.y1 Gm-c1015 Glycine max cDNA clone... 125 2e-30
 emb|AW830131|AW830131 sm23c07.y1 Gm-c1028 Glycine max cDNA clone... 125 2e-30
 emb|AI736269|AI736269 sb26b02.y1 Gm-c1008 Glycine max cDNA clone... 125 2e-30
 emb|AI442516|AI442516 sa32e08.y1 Gm-c1004 Glycine max cDNA clone... 125 2e-30
 emb|AW203388|AW203388 sf29f06.y1 Gm-c1028 Glycine max cDNA clone... 125 4e-30
 15 emb|AW309693|AW309693 sf23c12.x1 Gm-c1028 Glycine max cDNA clone... 123 4e-30
 emb|AW597294|AW597294 si71c07.y1 Gm-c1031 Glycine max cDNA clone... 125 4e-30
 emb|AW707234|AW707234 sk22d10.y1 Gm-c1028 Glycine max cDNA clone... 125 4e-30
 emb|AW568746|AW568746 si72e11.y1 Gm-c1031 Glycine max cDNA clone... 125 4e-30
 emb|AW568382|AW568382 si70b03.y1 Gm-c1031 Glycine max cDNA clone... 125 4e-30
 20 emb|AW830420|AW830420 sm26e07.y1 Gm-c1028 Glycine max cDNA clone... 125 4e-30

Query= ab008107_s_at 16536_s_at /id_source genbank /description
 dbj|baa32422.1| (ab008107) ethylene responsive element binding factor
 25 5 [arabidopsis thaliana] /blast_score 1.00e-117 /ec_number /family
 /chip nova /gb_link /ncgi
 (1059 letters)

Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	
35	Sequences producing significant alignments:	(bits)	Value
	emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone...	141	4e-37
	emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone...	149	5e-35
	emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl...	94	5e-33
40	emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl...	111	2e-32
	emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon ...	132	2e-30
	emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA ...	130	2e-29
	emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl...	125	2e-29
45	emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon ...	128	3e-29
	emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone...	108	8e-29
	dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds.	127	1e-28
	emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon ...	127	2e-28
	gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone ...	103	5e-28
50	emb AI897797 AI897797 EST267240 tomato ovary, TAMU Lycopersicon ...	124	1e-27
	emb AI794657 AI794657 sb67b03.y1 Gm-c1019 Glycine max cDNA clone...	124	1e-27
	emb AW507860 AW507860 si45h05.y1 Gm-r1030 Glycine max cDNA clone...	123	2e-27
	emb AW775819 AW775819 EST334884 DSIL Medicago truncatula cDNA cl...	95	5e-27
	emb AW685077 AW685077 NF024H04NR1F1000 Nodulated root Medicago t...	93	8e-27
55	emb AW573782 AW573782 EST316373 GVN Medicago truncatula cDNA clo...	93	9e-27
	emb AW620490 AW620490 sj05h02.y1 Gm-c1032 Glycine max cDNA clone...	121	1e-26
	emb AW759181 AW759181 sl38a09.y1 Gm-c1027 Glycine max cDNA clone...	121	1e-26
	emb AI778693 AI778693 EST259572 tomato susceptible, Cornell Lyco...	120	2e-26
	emb AW774176 AW774176 EST333259 KV3 Medicago truncatula cDNA clo...	118	6e-26
60	emb AW776668 AW776668 EST335733 DSIL Medicago truncatula cDNA cl...	118	6e-26
	emb AW574222 AW574222 EST316813 GVN Medicago truncatula cDNA clo...	118	6e-26

- emb|AI899889|AI899889 sb94g05.y1 Gm-c1017 Glycine max cDNA clone... 117 1e-25
emb|AW185128|AW185128 se87b10.y1 Gm-c1023 Glycine max cDNA clone... 116 2e-25
emb|AW688546|AW688546 NF008H02ST1F1000 Developing stem Medicago ... 89 2e-25
emb|AV425560|AV425560 AV425560 Lotus japonicus young plants (two... 115 5e-25
5 emb|AV423260|AV423260 AV423260 Lotus japonicus young plants (two... 115 5e-25
emb|AI782381|AI782381 EST263260 tomato susceptible, Cornell Lyco... 115 8e-25
emb|AF245119|AF245119 Mesembryanthemum crystallinum AP2-related ... 114 1e-24
emb|AW781602|AW781602 sl82d06.y1 Gm-c1037 Glycine max cDNA clone... 114 1e-24
emb|AW267820|AW267820 EST305948 DSIR Medicago truncatula cDNA cl... 113 2e-24
10 emb|AI965917|AI965917 sc79f12.y1 Gm-c1018 Glycine max cDNA clone... 113 3e-24
emb|AI484961|AI484961 EST243224 tomato ovary, TAMU Lycopersicon ... 112 5e-24
emb|AB035270|AB035270 Matricaria chamomilla McERE BP1 mRNA for et... 111 1e-23
emb|AW220395|AW220395 EST302878 tomato root during/after fruit s... 110 2e-23
emb|AV421566|AV421566 AV421566 Lotus japonicus young plants (two... 109 3e-23
15 dbj|D38126|TOBBY4D Tobacco mRNA for EREBP-2, complete cds. 109 3e-23
emb|AW101306|AW101306 sd77c11.y1 Gm-c1009 Glycine max cDNA clone... 89 5e-23
emb|AW349638|AW349638 GM210005B21A4R Gm-r1021 Glycine max cDNA 3... 107 2e-22
emb|AI771213|AI771213 EST252409 tomato ovary, TAMU Lycopersicon ... 107 2e-22
20 gb|U89255|LEU89255 Lycopersicon esculentum DNA-binding protein P... 107 2e-22
emb|AW596384|AW596384 sj02f12.y1 Gm-c1032 Glycine max cDNA clone... 107 2e-22
dbj|D38123|TOBBY4A Nicotiana tabacum mRNA for ERF1, complete cds. 105 8e-22
emb|AV417552|AV417552 AV417552 Lotus japonicus young plants (two... 103 2e-21
emb|AW034216|AW034216 EST277787 tomato callus, TAMU Lycopersicon... 103 2e-21
25 emb|AW278190|AW278190 sf40g11.y1 Gm-c1009 Glycine max cDNA clone... 103 2e-21
emb|AJ238740|CRO238740 Catharanthus roseus mRNA for AP2-domain D... 102 4e-21
emb|AI973653|AI973653 sd07h05.y1 Gm-c1020 Glycine max cDNA clone... 102 4e-21
emb|AW690929|AW690929 NF034G08ST1F1000 Developing stem Medicago ... 73 9e-21
emb|AW233956|AW233956 sf32e02.y1 Gm-c1028 Glycine max cDNA clone... 101 1e-20
30 emb|AW736415|AW736415 EST332429 KV3 Medicago truncatula cDNA clo... 73 2e-20
emb|AI440657|AI440657 sa63d09.y1 Gm-c1004 Glycine max cDNA clone... 100 2e-20
emb|AV422393|AV422393 AV422393 Lotus japonicus young plants (two... 100 2e-20
emb|AI967551|AI967551 Ljimpest05-400-d11 Ljirnp Lambda HybriZap... 100 2e-20
emb|AI731242|AI731242 BN LGHi9002 Six-day Cotton fiber Gossypium ... 100 3e-20
35 gb|U89256|LEU89256 Lycopersicon esculentum DNA-binding protein P... 99 5e-20
emb|AW030009|AW030009 EST273264 tomato callus, TAMU Lycopersicon... 99 5e-20
emb|AI894873|AI894873 EST264316 tomato callus, TAMU Lycopersicon... 99 5e-20
emb|AW030386|AW030386 EST273641 tomato callus, TAMU Lycopersicon... 99 5e-20
emb|AW729466|AW729466 GA__Ea0025B11 Gossypium arboreum 7-10 dpa ... 98 1e-19
40 emb|AW507898|AW507898 si46f03.y1 Gm-r1030 Glycine max cDNA clone... 98 1e-19
emb|AW618245|AW618245 EST314295 L. pennellii trichome, Cornell U... 98 1e-19
emb|AW840611|AW840611 00057 leafy spurge Lambda HybriZAP 2.1 two... 97 2e-19
emb|AI736796|AI736796 sb33f06.y1 Gm-c1012 Glycine max cDNA clone... 97 2e-19
emb|AI966559|AI966559 sc52a04.y1 Gm-c1015 Glycine max cDNA clone... 97 2e-19
45 emb|AF057373|AF057373 Nicotiana tabacum ethylene response elemen... 96 3e-19
emb|AI896308|AI896308 EST265751 tomato callus, TAMU Lycopersicon... 96 5e-19
emb|AI898992|AI898992 EST268435 tomato ovary, TAMU Lycopersicon ... 95 6e-19
emb|AW980654|AW980654 EST391807 GVN Medicago truncatula cDNA clo... 95 6e-19
emb|AI495036|AI495036 sa90a09.y1 Gm-c1004 Glycine max cDNA clone... 94 2e-18
50 gb|U81157|NTU81157 Nicotiana tabacum S25-XP1 DNA binding protein... 94 2e-18
emb|AW706628|AW706628 sj62g05.y1 Gm-c1033 Glycine max cDNA clone... 70 3e-18
emb|AI442716|AI442716 sa85d10.y1 Gm-c1004 Glycine max cDNA clone... 93 4e-18
emb|AW559315|AW559315 EST306358 DSIR Medicago truncatula cDNA cl... 93 4e-18
emb|AW035119|AW035119 EST280381 tomato callus, TAMU Lycopersicon... 91 1e-17
55 emb|AI490591|AI490591 EST249145 tomato ovary, TAMU Lycopersicon ... 91 1e-17
emb|AI489147|AI489147 EST247486 tomato ovary, TAMU Lycopersicon ... 91 1e-17
emb|AW782252|AW782252 sm03d11.y1 Gm-c1027 Glycine max cDNA clone... 63 1e-17
emb|AW348322|AW348322 GM210001B23F6R Gm-r1021 Glycine max cDNA 3... 90 2e-17
emb|AW759236|AW759236 sl38f08.y1 Gm-c1027 Glycine max cDNA clone... 90 2e-17
60 emb|AW686013|AW686013 NF033D04NR1F1000 Nodulated root Medicago t... 90 2e-17
emb|AI776626|AI776626 EST257726 tomato resistant, Cornell Lycope... 89 4e-17

emb|AW443265|AW443265 EST308195 tomato mixed elicitor, BTI Lycop... 89 5e-17
 emb|AW308784|AW308784 sf71h01.y1 Gm-c1013 Glycine max cDNA clone... 89 5e-17
 emb|AF211541|AF211541 AF211541 34.1B Nicotiana tabacum cDNA clon... 87 2e-16
 emb|AW621700|AW621700 EST312498 tomato root during/after fruit s... 87 2e-16
 5 emb|AI489709|AI489709 EST248048 tomato ovary, TAMU Lycopersicon ... 62 2e-16
 emb|AW560968|AW560968 EST316016 DSIR Medicago truncatula cDNA cl... 60 4e-16
 emb|AW560196|AW560196 EST315244 DSIR Medicago truncatula cDNA cl... 60 4e-16
 emb|AW185802|AW185802 se59h01.y1 Gm-c1019 Glycine max cDNA clone... 71 5e-16
 emb|AW734757|AW734757 sk88d02.y1 Gm-c1035 Glycine max cDNA clone... 85 1e-15
 10 emb|AV417624|AV417624 AV417624 Lotus japonicus young plants (two... 58 1e-15
 emb|AV407462|AV407462 AV407462 Lotus japonicus young plants (two... 58 1e-15
 emb|AW256448|AW256448 EST304585 KV2 Medicago truncatula cDNA clo... 59 1e-15
 emb|AW560135|AW560135 EST315183 DSIR Medicago truncatula cDNA cl... 59 2e-15
 emb|AW267756|AW267756 EST305884 DSIR Medicago truncatula cDNA cl... 59 2e-15
 15 emb|AW560134|AW560134 EST315182 DSIR Medicago truncatula cDNA cl... 59 2e-15
 emb|AW574073|AW574073 EST316664 GVN Medicago truncatula cDNA clo... 61 2e-15

Query= athrprp1b_s_at 16578_s_at /id_source
 20 /description "emb|cab68132.1|(al137080) beta-1, 3-glucanase
 2 (bg2) [arabidopsis thaliana]" /blast_score 0
 (1181 letters)

Database: plantfungal
 25 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	(bits)	Value
30	Sequences producing significant alignments:			
	emb X07280 NPGLUCB	Nicotiana plumbaginifolia mRNA for beta-gluca...	265	e-106
	gb U49454 PPU49454	Prunus persica beta-1,3-glucanase (Gns1) gene...	292	e-106
	gb M23120 TOBGLUCB2	Tobacco (N.plumbaginifolia) beta-glucanase m...	265	e-105
35	emb AJ277900 VVI277900	Vitis vinifera mRNA for beta 1-3 glucanas...	284	e-104
	dbj E03985 E03985	DNA encoding beta-1,3-endoglucanase.	226	e-100
	dbj E02108 E02108	cDNA sequence coding for beta-1,3-endoglucanase.	226	e-100
	gb M37753 SOYB13ENDG	Soybean beta-1,3-endoglucanase mRNA, comple...	226	e-100
	gb U41323 GMU41323	Glycine max beta-1,3-glucanase (SGN1) gene, c...	171	e-100
40	emb X77990 BCBGL	B.campestris (Just Right) bgl mRNA.	133	1e-99
	gb U01901 U01901	Solanum tuberosum Datura endo-1,3-beta-D-glucan...	209	8e-99
	gb M80608 TOMB13GLUB	Lycopersicon esculentum beta-1,3-glucanase ...	210	1e-98
	emb AF230109 AF230109	Populus alba x Populus tremula beta-1,3 gl...	289	1e-98
	emb AJ000081 CSAJ81	Citrus sinensis mRNA for beta-1,3-glucanase.	99	2e-98
45	gb U22147 HBU22147	Hevea brasiliensis beta-1,3-glucanase (HGN1) ...	265	1e-95
	emb X54456 NTEC32139	N. tabacum mRNA for acidic beta-1,3 glucana...	106	3e-95
	emb AF067863 AF067863	Solanum tuberosum 1,3-beta-glucan glucanoh...	210	6e-95
	gb U01900 U01900	Solanum tuberosum Datura endo-1,3-beta-D-glucan...	210	8e-95
	emb AJ133470 HBR133470	Hevea brasiliensis mRNA for beta-1,3-gluc...	262	1e-94
50	gb M60402 TOBGLA13B	Nicotiana tabacum glucan beta-1,3-glucanase ...	208	9e-94
	emb X53600 NTGLN2G	Tobacco gln2 gene for beta -1,3-glucanase.	208	9e-94
	emb A26453 A26453	Recombinant soya beta-1,3-glucanase plasmid.	244	3e-93
	emb A26449 A26449	Soya mutant beta-1,3-glucanase cDNA.	244	3e-93
	emb A26447 A26447	Soya beta-1,3-glucanase cDNA HindIII-HindIII f...	244	3e-93
55	emb Z68154 GHBGLUCS	G.hirsutum mRNA for 1,3-beta-glucanase.	174	3e-93
	gb M60403 TOBGLB13B	Nicotiana tabacum glucan beta-1,3-glucosidas...	207	3e-93
	emb X54742 NPB13GG	Nicotiana plumbaginifolia beta-(1,3)-glucanas...	205	4e-93
	gb M59442 TOBGLUCA	N.tabacum basic-1,3-glucanase gene, complete cds.	204	1e-92
	emb A16121 A16121	Intracellular Beta-1, 3 glucanase gene (SEQ ID...	204	1e-92
60	emb A26451 A26451	Soya beta-1,3-glucanase plasmid pBR59 NdeI-Hin...	244	3e-92
	emb X53129 PV13BDGL	P. vulgaris mRNA for 1,3-beta-D-glucanase.	240	6e-91

- emb|X74905|LEQA *L.esculentum* TomQ'a mRNA for beta(1,3)glucanase. 105 2e-90
emb|X89717|PVB13GLUC *P.vulgaris* beta-1,3-glucanase gene. 243 3e-89
gb|U01902|U01902 *Solanum tuberosum* Datura endo-1,3-beta-D-glucan... 210 2e-88
emb|AJ131047|CAR131047 *Cicer arietinum* mRNA for glucan-endo-1,3-... 188 5e-88
5 emb|X74906|LEQB *L.esculentum* TomQ'b mRNA for beta(1,3)glucanase. 110 1e-86
emb|AF227953|AF227953 *Capsicum annuum* basic beta-1,3-glucanase (... 252 3e-86
emb|AF001523|AF001523 *Musa acuminata* beta-1, 3-glucanase mRNA, ... 148 5e-86
emb|AF004838|AF004838 *Musa acuminata* beta-1,3-glucanase mRNA, pa... 148 7e-86
gb|L02212|PEABETAGLU *Pea* beta-1,3-glucanase gene, complete cds. 180 1e-85
10 gb|S51479|S51479 beta-1,3-glucanase [*Pisum sativum*=peas, cultiva... 180 2e-85
emb|AF186083|AF186083 AF186083 *Populus alba* x *Populus tremula* ba... 218 5e-85
gb|M20620|TOBGLUBC *N.tabacum* beta-1,3-glucanase mRNA, clone pGL43. 207 4e-84
gb|U27179|MSU27179 *Medicago sativa* acidic glucanase mRNA, comple... 138 7e-79
gb|M60463|TOBGL153A Tobacco GL153 protein mRNA, complete cds. 99 3e-77
15 emb|AF141654|AF141654 *Nicotiana tabacum* beta-1,3-glucanase (GGL4... 99 5e-77
gb|M60460|TOBPR2A Tobacco PR2 protein mRNA, complete cds. 100 3e-76
gb|M59443|TOBGLUCB *N.tabacum* acidic beta-1,3-glucanase gene, com... 100 1e-75
emb|A16120|A16120 Extracellular Beta-1, 3 glucanase gene (SEQ ID... 100 1e-75
gb|M63634|TOBGCBREG *Nicotiana plumbaginifolia* beta(1,3)-glucanas... 268 2e-75
20 emb|X54431|NTSP41B Tobacco sp41b mRNA for (1-3)-beta-glucanase. 100 1e-74
emb|X81560|NTSP41AGN *N.tabacum* Sp41a gene. 100 2e-74
emb|X54430|NTSP41A Tobacco sp41a mRNA for (1-3)-beta-glucanase. 100 2e-74
gb|M96941|BLYGCNHVI *Hordeum vulgare* glucan endo-1,3-beta-glucosi... 93 8e-74
emb|AJ012751|CAR012751 *Cicer arietinum* mRNA for glucan endo-beta... 140 4e-73
25 gb|M20618|TOBGLUBA *N.tabacum* beta-1,3-glucanase mRNA, clones pGL... 207 9e-73
emb|Z15131|ASBGLUCAN *A.sativa* mRNA for beta glucanase. 158 1e-70
gb|M62740|BLYGLB2 *Hordeum vulgare* 1,3-1,4-beta-D glucan 4-glucan... 158 2e-70
emb|Z22874|TABETGLUB *T.aestivum* (1,3;1,4) beta glucanase mRNA, c... 158 2e-70
emb|Z22873|TABETGLUA *T.aestivum* beta glucanase mRNA, complete CDS. 158 3e-70
30 emb|X52572|HVBDG Barley DNA for (1-3,1-4)-beta-D-glucanase (EC 3... 158 1e-69
emb|X56775|HVGLB1 *H.vulgare* Glb 1 gene for 1-3,1-4-beta-D-glucan... 158 1e-69
emb|X56260|HVGLUEND Barley DNA for (1,3;1,4)-beta-glucanase.(EC ... 158 1e-69
gb|M80604|TOMB13GLUA *Lycopersicon esculentum* beta-1,3-glucanase ... 94 2e-69
emb|AJ009932|STAJ9932 *Solanum tuberosum* mRNA for beta-1,3-glucan... 95 6e-69
35 emb|AF034107|AF034107 *Glycine max* beta-1,3-glucanase 2 (SGlu2) g... 122 2e-67
emb|AF112965|AF112965 *Triticum aestivum* beta-1,3-glucanase precu... 166 2e-66
gb|M60462|TOBPRNA Tobacco PRN protein mRNA, 3' end. 100 5e-65
emb|AW030776|AW030776 EST274031 tomato callus, TAMU *Lycopersicon*... 210 2e-64
emb|AF112967|AF112967 *Triticum aestivum* beta-1,3-glucanase precu... 175 2e-64
40 emb|AW216754|AW216754 EST295468 tomato callus, TAMU *Lycopersicon*... 202 7e-64
emb|AI895131|AI895131 EST264574 tomato callus, TAMU *Lycopersicon*... 202 7e-64
gb|U96096|HVU96096 *Hordeum vulgare* endo-1,3-beta-glucanase (Hv34... 72 3e-62
gb|M13237|BLYGLUCB Barley beta glucanase mRNA. 158 4e-62
emb|AW625790|AW625790 EST319697 tomato radicle, 5 d post-imbibit... 193 2e-61
45 gb|M96939|BLYGLCNHV *Hordeum vulgare* glucan endo-1,3-beta-glucosi... 121 3e-61
emb|AJ271367|HVU271367 *Hordeum vulgare* mRNA for beta-1,3-glucanase. 92 7e-61
gb|M23548|BLYGEH Barley (1->3)-beta-glucan endohydrolase mRNA, c... 92 7e-61
emb|Y18212|TAY18212 *Triticum aestivum* mRNA for beta-1,3-endogluc... 93 9e-61
emb|AF030771|AF030771 *Hordeum vulgare* beta-1,3-glucanase 2 (BGL3... 92 2e-60
50 gb|M62907|BLYCBGL32 *H.vulgare* L. (1-3)-beta-glucanase mRNA, comp... 92 2e-60
emb|A37992|A37992 Sequence 11 from Patent EP0616035. 92 2e-60
gb|M91814|BLYGLU2X Barley beta-1,3-glucanase (GLU2) gene, exons' ... 116 3e-60
emb|AW649248|AW649248 EST327702 tomato germinating seedlings, TA... 200 2e-59
emb|AF034109|AF034109 *Glycine max* beta-1,3-glucanase 4 (SGlu4) g... 139 2e-59
55 emb|AW033770|AW033770 EST277341 tomato callus, TAMU *Lycopersicon*... 122 3e-59
emb|AW830464|AW830464 sm27f06.y1 Gm-c1028 *Glycine max* cDNA clone... 221 4e-59
emb|AW034001|AW034001 EST277663 tomato callus, TAMU *Lycopersicon*... 202 8e-58
emb|X67099|HV13GEIII *H.vulgare* gene for 1,3-glucan endohydrolase... 153 2e-57
emb|AW034584|AW034584 EST278268 tomato callus, TAMU *Lycopersicon*... 164 2e-57
60 emb|AI894452|AI894452 EST263907 tomato callus, TAMU *Lycopersicon*... 210 4e-57
emb|AW034632|AW034632 EST278316 tomato callus, TAMU *Lycopersicon*... 124 4e-57

emb|AW034478|AW034478 EST278049 tomato callus, TAMU Lycopersicon... 162 9e-57
emb|AW216963|AW216963 EST295677 tomato callus, TAMU Lycopersicon... 202 1e-56
gb|BE020030|BE020030 sm41c02.y1 Gm-cl028 Glycine max cDNA clone ... 220 2e-56
emb|AW032447|AW032447 EST276006 tomato callus, TAMU Lycopersicon... 166 6e-56
5 emb|AW031387|AW031387 EST274841 tomato callus, TAMU Lycopersicon... 191 6e-56
emb|AW036009|AW036009 EST282868 tomato callus, TAMU Lycopersicon... 207 1e-55
emb|AW031078|AW031078 EST274385 tomato callus, TAMU Lycopersicon... 109 2e-55
emb|AW035366|AW035366 EST280928 tomato callus, TAMU Lycopersicon... 191 6e-55
emb|AI780513|AI780513 EST261392 tomato susceptible, Cornell Lyco... 110 6e-55
10

Query= ab008104_s_at 16609_s_at /id_source genbank /description
dbj|baa32419.1| (ab008104) ethylene responsive element binding factor
2 [arabidopsis thaliana] /blast_score 1.00e-112
15 (921 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

20 Searching.....done

Score E
Sequences producing significant alignments: (bits) Value

25 dbj|D38126|TOBBY4D Tobaccó mRNA for EREBP-2, complete cds. 144 7e-44
emb|AW220395|AW220395 EST302878 tomato root during/after fruit s... 132 9e-43
dbj|D38123|TOBBY4A Nicotiana tabacum mRNA for ERF1, complete cds. 134 6e-41
emb|AF245119|AF245119 Mesembryanthemum crystallinum AP2-related ... 161 5e-39
emb|AW267820|AW267820 EST305948 DSIR Medicago truncatula cDNA cl... 160 1e-38
30 emb|AB035270|AB035270 Matricaria chamomilla McEREBP1 mRNA for et... 155 5e-37
gb|U89255|LEU89255 Lycopersicon esculentum DNA-binding protein P... 138 3e-32
emb|AI771213|AI771213 EST252409 tomato ovary, TAMU Lycopersicon ... 135 1e-31
emb|AW034216|AW034216 EST277787 tomato callus, TAMU Lycopersicon... 134 1e-30
emb|AW729466|AW729466 GA__Ea0025B11 Gossypium arboreum 7-10 dpa ... 132 4e-30
35 emb|AF057373|AF057373 Nicotiana tabacum ethylene response elemen... 125 4e-28
emb|AW981151|AW981151 EST392345 DSIL Medicago truncatula cDNA cl... 124 8e-28
emb|AW396250|AW396250 sh26c01.y1 Gm-cl016 Glycine max cDNA clone... 116 2e-25
emb|AW233956|AW233956 sf32e02.y1 Gm-cl028 Glycine max cDNA clone... 115 5e-25
emb|AW185128|AW185128 se87b10.y1 Gm-cl023 Glycine max cDNA clone... 114 1e-24
40 emb|AI897834|AI897834 EST267277 tomato ovary, TAMU Lycopersicon... 113 2e-24
emb|AW349516|AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA ... 113 2e-24
emb|AV423260|AV423260 AV423260 Lotus japonicus young plants (two... 111 6e-24
emb|AV425560|AV425560 AV425560 Lotus japonicus young plants (two... 111 6e-24
45 emb|AW981228|AW981228 EST392318 DSIL Medicago truncatula cDNA cl... 89 6e-24
emb|AI899000|AI899000 EST268443 tomato ovary, TAMU Lycopersicon ... 110 2e-23
emb|AI965917|AI965917 sc79f12.y1 Gm-cl018 Glycine max cDNA clone... 110 2e-23
emb|AI794657|AI794657 sb67b03.y1 Gm-cl019 Glycine max cDNA clone... 110 2e-23
emb|AW200919|AW200919 se95c12.y1 Gm-cl027 Glycine max cDNA clone... 109 3e-23
50 emb|AW507860|AW507860 si45h05.y1 Gm-r1030 Glycine max cDNA clone... 109 3e-23
emb|AW507898|AW507898 si46f03.y1 Gm-r1030 Glycine max cDNA clone... 97 3e-23
dbj|D38125|TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 109 4e-23
emb|AW349638|AW349638 GM210005B21A4R Gm-r1021 Glycine max cDNA 3... 109 4e-23
55 emb|AW278190|AW278190 sf40g11.y1 Gm-cl009 Glycine max cDNA clone... 109 4e-23
emb|AI486689|AI486689 EST245011 tomato ovary, TAMU Lycopersicon ... 108 5e-23
emb|AW618245|AW618245 EST314295 L. pennellii trichome, Cornell U... 108 8e-23
emb|AW776671|AW776671 EST335736 DSIL Medicago truncatula cDNA cl... 108 8e-23
emb|AW759181|AW759181 sl38a09.y1 Gm-cl027 Glycine max cDNA clone... 107 1e-22
60 emb|AW596384|AW596384 sj02f12.y1 Gm-cl032 Glycine max cDNA clone... 107 1e-22
emb|AI897797|AI897797 EST267240 tomato ovary, TAMU Lycopersicon ... 107 1e-22

- emb|AI973653|AI973653 sd07h05.y1 Gm-cl020 Glycine max cDNA clone... 107 1e-22
emb|AW620490|AW620490 sj05h02.y1 Gm-cl032 Glycine max cDNA clone... 106 2e-22
emb|AI899889|AI899889 sb94g05.y1 Gm-cl017 Glycine max cDNA clone... 105 4e-22
emb|AW574222|AW574222 EST316813 GVN Medicago truncatula cDNA clo... 105 4e-22
5 emb|AI778693|AI778693 EST259572 tomato susceptible, Cornell Lyco... 105 4e-22
emb|AW776668|AW776668 EST335733 DSIL Medicago truncatula cDNA cl... 105 4e-22
emb|AW774176|AW774176 EST333259 KV3 Medicago truncatula cDNA clo... 105 4e-22
emb|AI894873|AI894873 EST264316 tomato callus, TAMU Lycopersicon... 103 2e-21
gb|U89256|LEU89256 Lycopersicon esculentum DNA-binding protein P... 103 2e-21
10 emb|AW030386|AW030386 EST273641 tomato callus, TAMU Lycopersicon... 103 2e-21
emb|AW030009|AW030009 EST273264 tomato callus, TAMU Lycopersicon... 103 2e-21
emb|AI782381|AI782381 EST263260 tomato susceptible, Cornell Lyco... 100 1e-20
emb|AW980654|AW980654 EST391807 GVN Medicago truncatula cDNA clo... 100 2e-20
emb|AV422393|AV422393 AV422393 Lotus japonicus young plants (two... 100 2e-20
15 emb|AI484961|AI484961 EST243224 tomato ovary, TAMU Lycopersicon ... 100 3e-20
emb|AW781602|AW781602 sl82d06.y1 Gm-cl037 Glycine max cDNA clone... 100 3e-20
emb|AW443265|AW443265 EST308195 tomato mixed elicitor, BTI Lycop... 100 3e-20
emb|AI440657|AI440657 sa63d09.y1 Gm-cl004 Glycine max cDNA clone... 99 4e-20
gb|U81157|NTU81157 Nicotiana tabacum S25-XP1 DNA binding protein... 98 8e-20
20 emb|AJ238740|CRO238740 Catharanthus roseus mRNA for AP2-domain D... 98 8e-20
emb|AW840611|AW840611 00057 leafy spurge Lambda HybriZAP 2.1 two... 97 1e-19
emb|AW559315|AW559315 EST306358 DSIR Medicago truncatula cDNA cl... 97 2e-19
emb|AV421566|AV421566 AV421566 Lotus japonicus young plants (two... 97 2e-19
emb|AI966559|AI966559 sc52a04.y1 Gm-cl015 Glycine max cDNA clone... 97 2e-19
25 emb|AI495036|AI495036 sa90a09.y1 Gm-cl004 Glycine max cDNA clone... 95 5e-19
emb|AI442716|AI442716 sa85d10.y1 Gm-cl004 Glycine max cDNA clone... 95 5e-19
emb|AI055252|AI055252 coau0003H16 Cotton Boll Abscission Zone cD... 67 8e-19
emb|AI967551|AI967551 Ljirmp05-400-d11 Ljirmp Lambda HybriZap... 95 1e-18
emb|AI896308|AI896308 EST265751 tomato callus, TAMU Lycopersicon... 94 1e-18
30 emb|AI776626|AI776626 EST257726 tomato resistant, Cornell Lycope... 93 3e-18
emb|AW686013|AW686013 NF033D04NR1F1000 Nodulated root Medicago t... 92 5e-18
emb|AW981323|AW981323 EST392476 DSIL Medicago truncatula cDNA cl... 92 5e-18
emb|AV417552|AV417552 AV417552 Lotus japonicus young plants (two... 92 5e-18
emb|AW618246|AW618246 EST314296 L. pennellii trichome, Cornell U... 92 5e-18
35 emb|AW685077|AW685077 NF024H04NR1F1000 Nodulated root Medicago t... 90 2e-17
emb|AW573782|AW573782 EST316373 GVN Medicago truncatula cDNA clo... 90 2e-17
emb|AW308784|AW308784 sf71h01.y1 Gm-cl013 Glycine max cDNA clone... 88 1e-16
emb|AW782252|AW782252 sm03d11.y1 Gm-cl027 Glycine max cDNA clone... 59 1e-16
emb|AW980481|AW980481 EST391634 GVN Medicago truncatula cDNA clo... 87 2e-16
40 gb|BE023264|BE023264 sm80a11.y1 Gm-cl015 Glycine max cDNA clone... 87 2e-16
emb|AW458901|AW458901 sh16c12.y1 Gm-cl016 Glycine max cDNA clone... 86 4e-16
emb|AW348322|AW348322 GM210001B23F6R Gm-r1021 Glycine max cDNA 3... 85 8e-16
emb|AW685799|AW685799 NF030D09NR1F1000 Nodulated root Medicago t... 53 1e-15
emb|AW775819|AW775819 EST334884 DSIL Medicago truncatula cDNA cl... 84 2e-15
45 emb|AI731242|AI731242 BNLGHi9002 Six-day Cotton fiber Gossypium ... 84 2e-15
emb|AI898992|AI898992 EST268435 tomato ovary, TAMU Lycopersicon ... 84 2e-15
emb|AI736796|AI736796 sb33f06.y1 Gm-cl012 Glycine max cDNA clone... 83 3e-15
emb|AW560968|AW560968 EST316016 DSIR Medicago truncatula cDNA cl... 57 4e-15
emb|AW560196|AW560196 EST315244 DSIR Medicago truncatula cDNA cl... 57 4e-15
50 emb|AI489709|AI489709 EST248048 tomato ovary, TAMU Lycopersicon ... 56 6e-15
emb|AW759236|AW759236 sl38f08.y1 Gm-cl027 Glycine max cDNA clone... 80 2e-14
gb|BE057468|BE057468 sm58e08.y1 Gm-cl028 Glycine max cDNA clone ... 55 7e-14
gb|T14923|T14923 crs406 lambdaZAPST Ricinus communis cDNA clone ... 56 9e-14
emb|AI489199|AI489199 EST247538 tomato ovary, TAMU Lycopersicon ... 52 1e-13
55 emb|AI486929|AI486929 EST245251 tomato ovary, TAMU Lycopersicon ... 52 1e-13
emb|AI483636|AI483636 EST249507 tomato ovary, TAMU Lycopersicon ... 52 1e-13
emb|AW033743|AW033743 EST277314 tomato callus, TAMU Lycopersicon... 52 1e-13
emb|AI483510|AI483510 EST249359 tomato ovary, TAMU Lycopersicon ... 52 1e-13
emb|AI771755|AI771755 EST252855 tomato ovary, TAMU Lycopersicon ... 52 1e-13
60 emb|AI485175|AI485175 EST243479 tomato ovary, TAMU Lycopersicon ... 52 1e-13
emb|AI489919|AI489919 EST248258 tomato ovary, TAMU Lycopersicon ... 52 1e-13

emb|AI897787|AI897787 EST267230 tomato ovary, TAMU Lycopersicon ... 52 1e-13
 emb|AI771834|AI771834 EST252934 tomato ovary, TAMU Lycopersicon ... 52 1e-13
 emb|AI485460|AI485460 EST243781 tomato ovary, TAMU Lycopersicon ... 52 1e-13
 emb|AI771795|AI771795 EST252895 tomato ovary, TAMU Lycopersicon ... 52 1e-13

5

Query= athorf_s_at16649_s_at/id_source
 /description gb|aafl6576.1|ac012563_29 (ac012563) putative
 s-adenosyl-L-methionine:trans-caffeoyl-coenzyme a
 3-o-methyltransferase [arabidopsis thaliana] /blast_score 1.00e-121
 /ec_number /family /chip nova /gb_link /ncgi
 (965 letters)

10

Database: plantfungal

15

661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	(bits)	Value
20	Sequences producing significant alignments:			
	emb AB000408 AB000408	Populus kitakamiensis mRNA for caffeoyl-Co...	215	3e-73
	gb U20736 MSU20736	Medicago sativa S-adenosyl-L-methionine:trans...	142	2e-68
	emb AW624860 AW624860	EST313689 tomato radicle, 5 d post-imbibit...	139	2e-67
25	emb AF022775 AF022775	Nicotiana tabacum caffeoyl-CoA 3-O-methyltr...	138	2e-67
	emb Z54233 VVCCOAOMT	V.vinifera mRNA for caffeoyl-CoA O-methyltr...	136	9e-67
	gb M69184 PUMCCOAMT	Petroselinum crispum caffeoyl-CoA 3-O-methyl...	133	2e-66
	gb U27116 PTU27116	Populus tremuloides caffeoyl-CoA 3-O-methyltr...	135	3e-66
	emb AJ224894 PBT AJ4894	Populus balsamifera subsp. trichocarpa mR...	135	3e-66
30	gb U13151 ZEU13151	Zinnia elegans S-adenosyl-L-methionine:trans-...	136	4e-66
	emb AI489305 AI489305	EST247644 tomato ovary, TAMU Lycopersicon ...	139	4e-66
	emb AJ224895 PBT AJ4895	Populus balsamifera subsp. trichocarpa mR...	136	6e-66
	emb AJ224896 PBT AJ4896	Populus balsamifera subsp. trichocarpa mR...	136	6e-66
	emb AF168780 AF168780	Eucalyptus globulus caffeoyl-CoA O-methyltr...	133	8e-66
35	emb AF053553 AF053553	Mesembryanthemum crystallinum caffeoyl-CoA...	132	1e-65
	emb AF240466 AF240466	Populus tomentosa caffeoyl-CoA O-methyltra...	135	1e-65
	emb A22706 A22706	Caffeoyl-CoA-3-O-Methyltransferase gene.	129	3e-65
	gb U62734 NTU62734	Nicotiana tabacum caffeoyl-CoA O-methyltransf...	134	5e-65
	emb Z56282 NTCCOAOMT	N.tabacum mRNA for caffeoyl-CoA O-methyltra...	132	5e-65
40	gb U62736 NTU62736	Nicotiana tabacum caffeoyl-CoA O-methyltransf...	136	5e-65
	gb U38612 NTU38612	Nicotiana tabacum caffeoyl-coenzymeA O-methyl...	136	5e-65
	emb Y12228 EG12228	E.gunnii mRNA for caffeoyl-CoA O-methyltransf...	133	7e-65
	gb L22203 SLASADEN	Stellaria longipes S-adenosyl-L-methionine:tr...	124	8e-65
	emb AF046122 AF046122	Eucalyptus globulus caffeoyl-CoA 3-O-methy...	133	9e-65
45	gb U62735 NTU62735	Nicotiana tabacum caffeoyl-CoA O-methyltransf...	134	3e-64
	emb AF036095 AF036095	Pinus taeda caffeoyl-CoA O-methyltransfera...	130	6e-64
	emb AF060180 AF060180	Nicotiana tabacum caffeoyl-coenzyme A trun...	90	9e-60
	emb AW102353 AW102353	sd86f04.y1 Gm-c1009 Glycine max cDNA clone...	139	5e-58
	emb AJ130841 PBA130841	Populus balsamifera subsp. trichocarpa mR...	133	2e-57
50	emb AJ001447 FVAJ1447	Fragaria vesca mRNA for putative caffeoyl-...	137	3e-57
	gb BE124003 BE124003	EST394128 DSIL Medicago truncatula cDNA clo...	127	9e-57
	emb AW775400 AW775400	EST334465 DSIL Medicago truncatula cDNA cl...	142	2e-56
	emb AW030189 AW030189	EST273444 tomato callus, TAMU Lycopersicon...	133	4e-56
	emb AW695080 AW695080	NF091D11ST1F1093 Developing stem Medicago ...	142	6e-56
55	emb AW348485 AW348485	GM210002B12A10R Gm-r1021 Glycine max cDNA ...	131	2e-55
	emb AI486500 AI486500	EST244821 tomato ovary, TAMU Lycopersicon ...	139	2e-55
	emb AI166541 AI166541	xylem.est.363 Poplar xylem Lambda ZAPII li...	135	7e-55
	gb BE034896 BE034896	ML05H01 ML Mesembryanthemum crystallinum cD...	132	1e-54
60	emb AW306951 AW306951	sf50h03.y1 Gm-c1009 Glycine max cDNA clone...	133	2e-54
	emb AW278810 AW278810	sf98g06.y1 Gm-c1019 Glycine max cDNA clone...	135	3e-54

- emb|AI939180|AI939180 sc67h02.y1 Gm-c1016 Glycine max cDNA clone... 125 3e-54
emb|AW102461|AW102461 sd88d11.y1 Gm-c1009 Glycine max cDNA clone... 133 3e-54
emb|AW776700|AW776700 EST335765 DSIL Medicago truncatula cDNA cl... 127 4e-54
emb|AW757356|AW757356 sl32c10.y1 Gm-c1027 Glycine max cDNA clone... 133 2e-53
5 emb|AW030736|AW030736 EST273991 tomato callus, TAMU Lycopersicon... 133 8e-53
emb|AI898029|AI898029 EST267472 tomato ovary, TAMU Lycopersicon ... 133 8e-53
emb|AW625527|AW625527 EST319434 tomato radicle, 5 d post-imbibit... 133 8e-53
emb|AW218547|AW218547 EST303730 tomato radicle, 5 d post-imbibit... 133 8e-53
emb|AW733300|AW733300 sk71f10.y1 Gm-c1016 Glycine max cDNA clone... 134 1e-52
10 emb|AW442463|AW442463 EST307393 tomato mixed elicitor, BTI Lycop... 133 1e-52
emb|AW094365|AW094365 EST287545 tomato mixed elicitor, BTI Lycop... 133 1e-52
gb|BE021597|BE021597 sm60a04.y1 Gm-c1028 Glycine max cDNA clone ... 135 1e-52
emb|AW034347|AW034347 EST277918 tomato callus, TAMU Lycopersicon... 133 2e-52
emb|AI443130|AI443130 sa84g01.y1 Gm-c1004 Glycine max cDNA clone... 131 2e-51
15 emb|AI898952|AI898952 EST268395 tomato ovary, TAMU Lycopersicon ... 139 2e-51
emb|AW424002|AW424002 sh59c10.y1 Gm-c1015 Glycine max cDNA clone... 115 2e-51
emb|AW707192|AW707192 sk22a02.y1 Gm-c1028 Glycine max cDNA clone... 132 3e-50
emb|AI899227|AI899227 EST268670 tomato ovary, TAMU Lycopersicon ... 139 3e-50
emb|AW980337|AW980337 EST391490 GVN Medicago truncatula cDNA clo... 127 3e-50
20 emb|AW648499|AW648499 EST326953 tomato germinating seedlings, TA... 99 7e-50
emb|AW690185|AW690185 NF029D09ST1F1000 Developing stem Medicago ... 142 1e-49
emb|AI895091|AI895091 EST264534 tomato callus, TAMU Lycopersicon... 99 3e-49
emb|AW306980|AW306980 sf51c05.y1 Gm-c1009 Glycine max cDNA clone... 135 8e-48
emb|AW695176|AW695176 NF092D12ST1F1101 Developing stem Medicago ... 142 1e-47
25 emb|AW684885|AW684885 NF022F07NR1F1000 Nodulated root Medicago t... 142 2e-47
emb|AA660318|AA660318 00189 MtrHE Medicago truncatula cDNA 5' si... 144 2e-47
emb|AW703717|AW703717 sk23e07.y1 Gm-c1028 Glycine max cDNA clone... 132 4e-47
emb|AW776435|AW776435 EST335500 DSIL Medicago truncatula cDNA cl... 142 5e-47
emb|AI486948|AI486948 EST245270 tomato ovary, TAMU Lycopersicon ... 100 1e-46
30 emb|AW620537|AW620537 sj06d09.y1 Gm-c1032 Glycine max cDNA clone... 133 1e-46
emb|AI775483|AI775483 EST256583 tomato resistant, Cornell Lycope... 139 2e-46
gb|BE124333|BE124333 EST393368 GVN Medicago truncatula cDNA clon... 125 3e-46
emb|AW704578|AW704578 sk38h08.y1 Gm-c1028 Glycine max cDNA clone... 140 3e-46
emb|AW350997|AW350997 GM210010A10C11R Gm-r1021 Glycine max cDNA ... 97 6e-46
35 emb|AW707224|AW707224 sk22c12.y1 Gm-c1028 Glycine max cDNA clone... 140 9e-46
emb|AW625126|AW625126 EST313943 tomato radicle, 5 d post-imbibit... 133 6e-45
emb|AI974778|AI974778 T113251e KV2 Medicago truncatula cDNA clon... 142 6e-45
emb|AI898101|AI898101 EST267544 tomato ovary, TAMU Lycopersicon ... 98 8e-45
gb|BE124175|BE124175 EST394300 DSIL Medicago truncatula cDNA clo... 127 1e-44
40 emb|AW686370|AW686370 NF040G10NR1F1000 Nodulated root Medicago t... 127 4e-44
emb|AI166314|AI166314 xylem.est.159 Poplar xylem Lambda ZAPII li... 136 4e-44
emb|AW256836|AW256836 EST304973 KV2 Medicago truncatula cDNA clo... 144 5e-44
emb|AW559274|AW559274 EST306110 DSIR Medicago truncatula cDNA cl... 142 5e-44
emb|AW278618|AW278618 sf46h04.y1 Gm-c1009 Glycine max cDNA clone... 139 1e-43
45 gb|BE059325|BE059325 sn31c09.y1 Gm-c1016 Glycine max cDNA clone ... 140 3e-43
emb|AW831448|AW831448 sm23c03.y1 Gm-c1028 Glycine max cDNA clone... 140 6e-43
emb|AI938893|AI938893 sc62d08.y1 Gm-c1016 Glycine max cDNA clone... 134 2e-42
emb|AW257069|AW257069 EST305206 KV2 Medicago truncatula cDNA clo... 142 2e-42
emb|AW695899|AW695899 NF100E02ST1F1017 Developing stem Medicago ... 125 5e-42
50 emb|AW774697|AW774697 EST333848 KV3 Medicago truncatula cDNA clo... 84 8e-42
emb|AW683492|AW683492 NF012H09LF1F1079 Developing leaf Medicago ... 134 2e-41
emb|AW152892|AW152892 se32d04.y1 Gm-c1015 Glycine max cDNA clone... 82 2e-41
gb|BE125749|BE125749 DG1_55_H11.b1_A002 Dark Grown 1 (DG1) Sorgh... 127 2e-41
gb|BE022002|BE022002 sm65c10.y1 Gm-c1028 Glycine max cDNA clone ... 137 3e-41
55 emb|AI488060|AI488060 EST246382 tomato ovary, TAMU Lycopersicon ... 100 7e-41
emb|AW622558|AW622558 EST313358 tomato root during/after fruit s... 139 1e-40
emb|AW625461|AW625461 EST319368 tomato radicle, 5 d post-imbibit... 99 1e-40
emb|AW625476|AW625476 EST319383 tomato radicle, 5 d post-imbibit... 139 3e-40
emb|AI960196|AI960196 sc80a08.y1 Gm-c1018 Glycine max cDNA clone... 132 5e-40
60 emb|Z82982|NTZ82982 N.tabacum mRNA for caffeoyl-CoA O-methyltran... 136 1e-39
emb|AW218486|AW218486 EST303669 tomato radicle, 5 d post-imbibit... 136 1e-39

Query= atu05206_s_at 17014_s_at /id_source genbank /description
 gb|aac48925.1| (u05206) ribonuclease [arabidopsis thaliana]
 5 /blast_score 1.00e-115 /ec_number /family /chip nova /gb_link /ncgi

(925 letters)

Database: plantfungal
 10 661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	
15	Sequences producing significant alignments:			(bits) Value
	emb AJ012689 CAR012689 Cicer arietinum mRNA for ribonuclease T2.	384	e-106	
	gb U13256 NAU13256 Nicotiana alata RNase NE mRNA, complete cds.	361	4e-99	
	gb U19924 ZEU19924 Zinnia elegans wounding-induced ribonuclease ...	358	4e-98	
20	emb AB034638 AB034638 Nicotiana tabacum mRNA for RNase, complete...	353	1e-96	
	emb X79337 LERNAL L.esculentum mRNA for ribonuclease le.	212	2e-93	
	dbj D49529 D49529 Pyrus pyrifolia mRNA for ribonuclease, complet...	335	4e-91	
	emb AI486253 AI486253 EST244574 tomato ovary, TAMU Lycopersicon ...	212	2e-89	
	emb AI485206 AI485206 EST243510 tomato ovary, TAMU Lycopersicon ...	212	1e-81	
25	gb U19923 ZEU19923 Zinnia elegans ribonuclease mRNA, complete cds.	232	3e-80	
	emb X79338 LERNALX L.esculentum mRNA for ribonuclease lx.	177	1e-73	
	emb AB032257 AB032257 Nicotiana glutinosa NGR3 mRNA for RNase NG...	176	7e-70	
	emb AI484830 AI484830 EST243091 tomato ovary, TAMU Lycopersicon ...	212	7e-70	
	emb AW684365 AW684365 NF016B03NR1F1000 Nodulated root Medicago t...	251	7e-66	
30	emb AI489460 AI489460 EST247799 tomato ovary, TAMU Lycopersicon ...	212	3e-63	
	emb Y17444 LES17444 Lycopersicon esculentum RNALE gene, exons 1 ...	152	2e-57	
	emb AI772676 AI772676 EST253776 tomato resistant, Cornell Lycope...	152	2e-57	
	emb AI775352 AI775352 EST256452 tomato resistant, Cornell Lycope...	212	3e-56	
	gb BE037115 BE037115 MP15C03 MP Mesembryanthemum crystallinum cD...	153	4e-55	
35	emb AF000939 AF000939 Hordeum vulgare aleurone ribonuclease mRNA...	89	7e-55	
	gb M83668 NELSTORAGE Nelumbo nucifera storage protein mRNA, comp...	127	2e-54	
	emb AI812905 AI812905 22D1 Pine Lambda Zap Xylem library Pinus t...	165	3e-54	
	emb AI488432 AI488432 EST246771 tomato ovary, TAMU Lycopersicon ...	211	5e-54	
	emb AW775298 AW775298 EST334363 DSIL Medicago truncatula cDNA cl...	200	7e-54	
40	emb AW279538 AW279538 sf90h05.y1 Gm-c1019 Glycine max cDNA clone...	188	6e-47	
	emb AF000940 AF000940 Hordeum vulgare ribonuclease gene, complet...	116	2e-44	
	gb BE060583 BE060583 HVSMEg0012L03f Hordeum vulgare pre-anthesis...	74	5e-42	
	emb Y17445 LES17445 Lycopersicon esculentum RNALE gene, exons 1 ...	122	6e-42	
	emb AI777654 AI777654 EST258449 tomato susceptible, Cornell Lyco...	152	2e-41	
45	emb AW596890 AW596890 sj84b03.y1 Gm-c1034 Glycine max cDNA clone...	162	3e-39	
	gb BE060118 BE060118 HVSMEg0011I10f Hordeum vulgare pre-anthesis...	89	6e-37	
	gb BE060590 BE060590 HVSMEg0012L10f Hordeum vulgare pre-anthesis...	89	2e-36	
	emb AW704136 AW704136 sk16e03.y1 Gm-c1028 Glycine max cDNA clone...	145	4e-34	
	emb AW289659 AW289659 NXNV003D07F Nsf Xylem Normal wood Vertical...	109	8e-32	
50	gb U19794 MDU19794 Malus domestica S-like RNase gene, partial cds.	76	2e-25	
	emb AI967855 AI967855 Ljimpest14-054-a9 Ljirnp Lambda HybriZap ...	109	4e-23	
	emb Y17446 LES17446 Lycopersicon esculentum RNALX gene, exons 1 ...	104	1e-21	
	dbj D64012 LUFRNLC2 Luffa cylindrica mRNA for ribonuclease (RNas...	95	1e-20	
	emb AW053670 AW053670 L30-1447T3 Ice plant Lambda Uni-Zap XR exp...	45	2e-20	
55	gb BE020073 BE020073 sm38f09.y1 Gm-c1028 Glycine max cDNA clone ...	45	7e-20	
	emb AW039494 AW039494 EST281775 tomato mixed elicitor, BTI Lycop...	43	6e-19	
	emb AW216541 AW216541 EST295255 tomato callus, TAMU Lycopersicon...	43	6e-19	
	dbj D64011 LUFRNLC1 Luffa cylindrica mRNA for ribonuclease (RNas...	89	8e-19	
	emb AB026836 AB026836 Prunus dulcis mRNA for Sa-RNase, complete ...	76	1e-18	
60	emb AW980478 AW980478 EST391631 GVN Medicago truncatula cDNA clo...	44	4e-18	
	gb BE124916 BE124916 EST393951 GVN Medicago truncatula cDNA clon...	44	4e-18	

	emb AB032256 AB032256 <i>Nicotiana glutinosa</i> NGR2 mRNA for RNase NG...	41	9e-18
	emb AW775880 AW775880 EST334945 <i>DSIL Medicago truncatula</i> cDNA cl...	44	9e-18
	emb AW775566 AW775566 EST334631 <i>DSIL Medicago truncatula</i> cDNA cl...	44	1e-17
	emb AW926310 AW926310 HVSMEg0006001 <i>Hordeum vulgare</i> pre-anthesis...	52	4e-17
5	emb AB034248 AB034248 <i>Volvox carteri</i> vrn1 mRNA for S-like RNase,...	58	8e-17
	emb AF176533 AF176533 <i>Solanum chacoense</i> self-incompatibility rib...	82	2e-16
	emb AI416638 AI416638 sal7c06.y1 <i>Gm-c1004 Glycine max</i> cDNA clone...	45	6e-16
	emb X96465 AHS2RNASE <i>A.hispanicum</i> mRNA for S2-Rnase.	60	2e-15
	emb AB028153 AB028153 <i>Prunus avium</i> mRNA for S1-RNase, complete cds.	56	3e-15
10	emb AW223027 AW223027 EST299838 tomato fruit red ripe, TAMU Lyco...	43	4e-15
	emb AW224120 AW224120 EST300931 tomato fruit red ripe, TAMU Lyco...	43	5e-15
	emb AW223831 AW223831 EST300642 tomato fruit red ripe, TAMU Lyco...	43	5e-15
	emb AF191732 AF191732 <i>Solanum chacoense</i> self-incompatibility rib...	82	6e-15
	emb AB010306 AB010306 <i>Prunus avium</i> mRNA for S3-RNase, complete cds.	57	2e-14
15	emb X76065 LPSRNASE <i>L.peruvianum</i> mRNA for S-RNase S3.	60	2e-14
	emb AB010304 AB010304 <i>Prunus avium</i> mRNA for S2-RNase, partial cds.	60	4e-14
	emb AI729649 AI729649 BNLGHi13860 Six-day Cotton fiber <i>Gossypium</i> ...	45	9e-14
	emb AI729386 AI729386 BNLGHi13239 Six-day Cotton fiber <i>Gossypium</i> ...	45	1e-13
	emb AW671991 AW671991 LG1_353_B05.b1_A002 Light Grown 1 (LG1) So...	45	1e-13
20	gb S61768 S61768 S (S5)=self-incompatibility {3' region} [Lycopersicon...	60	1e-13
	emb X56897 SCSIAP3 <i>S.chacoense</i> mRNA for self-incompatibility ass...	63	1e-13
	emb AW563386 AW563386 LG1_214_C01.b1_A002 Light Grown 1 (LG1) So...	45	1e-13
	emb AB011470 AB011470 <i>Prunus dulcis</i> mRNA for Sc-RNase, complete ...	60	3e-13
	emb AB011469 AB011469 <i>Prunus dulcis</i> mRNA for Sb-RNase, complete ...	57	4e-13
25	emb AW623083 AW623083 EST321028 tomato flower buds 3-8 mm, Corne...	43	8e-13
	emb AW034883 AW034883 EST279112 tomato callus, TAMU Lycopersicon...	43	8e-13
	emb AF232304 AF232304 <i>Solanum chacoense</i> gametophytic self-incomp...	58	1e-12
	emb Z26583 LPSLGS6 <i>L.peruvianum</i> (Mill) self-incompatibility glyc...	56	1e-12
	emb AB011471 AB011471 <i>Prunus dulcis</i> mRNA for Sd-RNase; partial cds.	57	1e-12
30	emb AV427528 AV427528 AV427528 <i>Lotus japonicus</i> young plants (two...	74	2e-12
	emb AF148465 AF148465 <i>Prunus dulcis</i> Sa-S-RNase gene, partial cds.	73	3e-12
	emb AB026982 AB026982 <i>Prunus salicina</i> mRNA for Sb-RNase, partial...	60	5e-12
	dbj E01266 E01266 cDNA encoding S2-protein linked to part of its...	56	1e-11
	gb M24600 TOBGPS <i>N.alata stylar</i> glycoprotein 2 mRNA, complete cds.	56	1e-11
35	dbj E01267 E01267 cDNA encoding S2-protein linked to its signal ...	56	1e-11
	emb X03803 NASINCS2 <i>Nicotiana alata</i> mRNA for S2 self-incompatibi...	56	1e-11
	gb L25930 TOBRNASESB <i>Nicotiana alata</i> RNase S mRNA.	56	1e-11
	emb AV410016 AV410016 AV410016 <i>Lotus japonicus</i> young plants (two...	44	1e-11
	emb AI724132 AI724132 RHIZ1_7_B07.y2_A001 Rhizome1 <i>Sorghum halep...</i>	70	2e-11
40	emb AJ271062 PHY271062 <i>Petunia hybrida</i> mRNA for Sv-ribonuclease ...	62	2e-11
	emb AB016522 AB016522 <i>Petunia x hybrida</i> mRNA for SB1-ribonucleas...	62	2e-11
	emb AB026981 AB026981 <i>Prunus salicina</i> mRNA for Sa-RNase, partial...	56	3e-11
	emb X96464 AHS5RNASE <i>A.hispanicum</i> mRNA for S5-Rnase.	57	4e-11
	gb U19791 MDU19791 <i>Malus domestica</i> S5-RNase (S) mRNA, partial cds.	38	4e-11
45	emb X96466 AHS4RNASE <i>A.hispanicum</i> mRNA for S4-Rnase.	46	7e-11
	gb M81686 PETSXPLOB <i>Petunia hybrida</i> Sx-protein (self-incompatibi...	58	1e-10
	emb Z26581 LPSLGS7 <i>L.peruvianum</i> (Mill) mRNA for self-incompatabi...	51	2e-10
	emb X56896 SCSIAP <i>S.chacoense</i> mRNA for self-incompatibility asso...	62	3e-10
	gb L40544 POTFSCS <i>Solanum carolinense</i> self-incompatibility ribon...	67	3e-10
50	emb AI460477 AI460477 sa79g07.y1 <i>Gm-c1004 Glycine max</i> cDNA clone...	42	3e-10
	emb Z26582 LPSLGS7 <i>L.peruvianum</i> (Mill) self-incompatibility glyc...	61	3e-10
	dbj D63887 D63887 <i>Nicotiana alata</i> mRNA for ribonuclease, complet...	61	3e-10
	emb AF105363 AF105363 <i>Lycium andersonii</i> self-incompatibility rib...	66	4e-10
	gb U07362 PHU07362 <i>Petunia hybrida</i> S1 self-incompatibility ribon...	62	4e-10
55	gb L40542 POTDSCS <i>Solanum carolinense</i> self-incompatibility ribon...	65	7e-10

Query= af098947_s_at 17051_s_at /id_source genbank /description
gb|aad09952.1| (af098947) ctf2b [arabidopsis thaliana] /blast_score 0
(1480 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments: (bits) Value

	emb AI782831 AI782831 EST263710 tomato susceptible, Cornell Lyco...	270	1e-71
10	emb AW093706 AW093706 EST286886 tomato mixed elicitor, BTI Lycop...	256	4e-67
	emb AW279194 AW279194 sf67g10.y1 Gm-cl013 Glycine max cDNA clone...	205	2e-53
	emb AI776928 AI776928 EST258028 tomato resistant, Cornell Lycope...	174	1e-42
	emb AW441294 AW441294 EST310690 tomato fruit red ripe, TAMU Lyco...	88	9e-42
	emb AW035369 AW035369 EST280931 tomato callus, TAMU Lycopersicon...	88	3e-35
15	gb BE037451 BE037451 MP21C02 MP Mesembryanthemum crystallinum cD...	88	2e-34
	gb BE058288 BE058288 sn14b07.y1 Gm-cl016 Glycine max cDNA clone ...	88	2e-34
	emb AI895992 AI895992 EST265435 tomato callus, TAMU Lycopersicon...	80	3e-34
	emb AW441248 AW441248 EST310644 tomato fruit red ripe, TAMU Lyco...	88	2e-33
	emb AW223990 AW223990 EST300801 tomato fruit red ripe, TAMU Lyco...	88	2e-33
20	emb AW761120 AW761120 sl63e05.y1 Gm-cl027 Glycine max cDNA clone...	127	9e-32
	gb BE037096 BE037096 MP14H01 MP Mesembryanthemum crystallinum cD...	86	2e-30
	emb AW038060 AW038060 EST279717 tomato mixed elicitor, BTI Lycop...	84	1e-29
	emb AW030010 AW030010 EST273265 tomato callus, TAMU Lycopersicon...	84	1e-29
	emb AW035432 AW035432 EST281170 tomato callus, TAMU Lycopersicon...	83	1e-29
25	emb AW221846 AW221846 EST298657 tomato fruit red ripe, TAMU Lyco...	80	2e-28
	emb AW907125 AW907125 EST343157 potato stolon, Cornell Universit...	127	3e-28
	emb AW306189 AW306189 se47b02.y1 Gm-cl017 Glycine max cDNA clone...	112	4e-27
	emb AW686451 AW686451 NF038B03NR1F1000 Nodulated root Medicago t...	57	1e-24
	emb AW934306 AW934306 EST360149 tomato fruit mature green, TAMU ...	80	4e-22
30	emb AI896882 AI896882 EST266325 tomato callus, TAMU Lycopersicon...	84	6e-22
	emb AW030032 AW030032 EST273287 tomato callus, TAMU Lycopersicon...	80	8e-22
	emb AW216521 AW216521 EST295235 tomato callus, TAMU Lycopersicon...	80	8e-22
	emb AW216877 AW216877 EST295591 tomato callus, TAMU Lycopersicon...	84	2e-21
	emb AI895032 AI895032 EST264475 tomato callus, TAMU Lycopersicon...	98	2e-19
35	emb AI054656 AI054656 coau0001K05 Cotton Boll Abscission Zone cD...	95	2e-18
	emb AW350604 AW350604 GM210008B20C3R Gm-r1021 Glycine max cDNA 3...	89	1e-16
	emb AW985224 AW985224 NXNV_132_F08_F Nsf Xylem Normal wood Verti...	84	2e-15
	emb AW782240 AW782240 sm03c06.y1 Gm-cl027 Glycine max cDNA clone...	80	2e-15
	emb AI894672 AI894672 EST264115 tomato callus, TAMU Lycopersicon...	80	3e-14
40	emb AW034079 AW034079 EST277574 tomato callus, TAMU Lycopersicon...	77	3e-13
	emb AW991119 AW991119 SsS0174 Suaeda salsa ZAP cDNA library Suae...	58	7e-10
	emb X95732 NPZEAXANT N.plumbaginifolia mRNA for zeaxanthin epoxi...	63	6e-09
	emb AV418279 AV418279 AV418279 Lotus japonicus young plants (two...	48	8e-09
	emb X91491 CAXANEPOX C.annuum mRNA for xanthophyll epoxidase.	61	2e-08
45	emb Z83835 LEZEAXAN L.esculentum mRNA for zeaxanthin epoxidase.	59	1e-07
	emb AI966377 AI966377 sc38a10.y1 Gm-cl014 Glycine max cDNA clone...	49	6e-07
	emb AF159948 AF159948 Prunus armeniaca zeaxanthin epoxidase (ZEA...	54	3e-06
	emb AF071888 AF071888 Prunus armeniaca zeaxanthin epoxidase (ZEA...	54	3e-06
	dbj D38415 AED4ABH Agaricus bisporus DNA for 4-aminobenzoate hyd...	47	3e-04
50	emb AQ274524 AQ274524 mgxb0022E01r CUGI Rice Blast BAC Library P...	47	3e-04
	emb AW982239 AW982239 HVSMEg0002G20f Hordeum vulgare pre-anthesi...	36	5e-04
	emb AJ274152 AJ274152 AJ274152 Metarhizium anisopliae ARSEF 2575...	41	0.018
	emb Z35859 SCYBL098W S.cerevisiae chromosome II reading frame OR...	39	0.12
	emb X79489 SCDNCH2 S.cerevisiae genomic DNA, chromosome II from ...	39	0.12
55	emb AW265977 AW265977 L30-2632T3 Ice plant Lambda Uni-Zap XR exp...	39	0.12
	emb AQ936092 AQ936092 Gm_UMb001_014_G18F UMN Soybean BAC Library...	38	0.16
	emb AA786833 AA786833 m6d11a1.r1 Aspergillus nidulans 24hr asexu...	38	0.23
	emb AV425826 AV425826 AV425826 Lotus japonicus young plants (two...	37	0.42
	emb AB017765 AB017765 Trypanosoma cruzi genes for GATase-CPSase,...	36	0.80
60	emb AL115728 CNS01CMW Botrytis cinerea strain T4 cDNA library un...	36	0.80
	gb U35892 NHU35892 Nectria haematococca maackiain detoxification...	36	0.80

emb|AI496271|AI496271 sb01f06.y1 Gm-c1004 Glycine max cDNA clone... 36 0.80
 emb|AJ223325|CRAJ3325 Chlamydomonas reinhardtii mRNA for ascorba... 35 1.1
 emb|AW185727|AW185727 se58h04.y1 Gm-c1019 Glycine max cDNA clone... 35 1.5
 emb|AW279175|AW279175 sf67d04.y1 Gm-c1013 Glycine max cDNA clone... 35 1.5
 5 emb|AF211986|AF211986 Acleisanthes anisophylla 18S ribosomal RNA... 35 1.5
 emb|AW348744|AW348744 GM210003A22C7R Gm-r1021 Glycine max cDNA 3... 35 2.1
 emb|AZ217020|AZ217020 Sheared DNA-75G4.TF Sheared DNA Trypanosom... 35 2.1
 emb|X80690|SCDNASEQ S.cerevisiae DNA sequence. 35 2.1
 emb|Z73040|SCYGR255C S.cerevisiae chromosome VII reading frame O... 35 2.1
 10 emb|AW680385|AW680385 WS1_52_D05.g1_A002 Water-stressed 1 (WS1) ... 35 2.1
 gb|N83134|N83134 TgESTzy73d09.r1 TgRH Tachyzoite cDNA Toxoplasma... 35 2.1
 emb|X99228|SCCHRVII S.cerevisiae genomic sequence from chromosom... 35 2.1
 emb|AW311010|AW311010 sg31e02.x1 Gm-c1024 Glycine max cDNA clone... 35 2.1
 emb|AL114377|CNS01BLD Botrytis cinerea strain T4 cDNA library un... 35 2.1
 15 gb|BE122310|BE122310 894019A08.y1 C. reinhardtii CC-1690, normal... 35 2.1
 emb|AF003698|AF003698 Saccharomyces cerevisiae COQ6 monooxygenas... 35 2.1
 emb|AW460022|AW460022 si07g06.y1 Gm-c1029 Glycine max cDNA clone... 27 2.5
 emb|AI855502|AI855502 sc20a03.y1 Gm-c1013 Glycine max cDNA clone... 34 2.9
 emb|AJ011587|KLA011587 Kluyveromyces lactis muf1 gene. 34 2.9
 20 emb|AI068756|AI068756 mgae0004aD11f Magnaporthe grisea Appressor... 34 2.9
 emb|AW286092|AW286092 LG1_261_C09.b1_A002 Light Grown 1 (LG1) So... 34 2.9
 emb|AW925351|AW925351 HVSMEg0001B14 Hordeum vulgare pre-anthesis... 34 2.9
 emb|AW760781|AW760781 sl36h06.y1 Gm-c1027 Glycine max cDNA clone... 34 2.9
 emb|AW063028|AW063028 SBcD23 Sugar beet leaf cDNA library Beta v... 34 2.9
 25 emb|AV429219|AV429219 AV429219 Lotus japonicus young plants (two... 34 2.9
 emb|AF068686|AF068686 Glycine max geranylgeranyl hydrogenase (Gg... 34 2.9
 emb|AQ447995|AQ447995 mgxb0015N12r CUGI Rice Blast BAC Library P... 30 3.2
 emb|AI398631|AI398631 NCW06C8T7 Westergaards Neurospora crassa c... 29 3.3
 emb|Z74950|BO13G6IC B.oleracea mRNA (unknown). 34 3.9
 30 emb|AW477291|AW477291 ga44f01.y1 Moss EST library PPU Physcomitr... 34 3.9
 emb|AW187125|AW187125 BNLGHi10212 Six-day Cotton fiber Gossypium... 34 3.9
 gb|L04488|TORPHD Trichosporon cutaneum phenol hydroxylase mRNA, ... 34 3.9
 emb|Z74962|BO13G6IG B.oleracea mRNA (unknown). 34 3.9
 emb|AA519702|AA519702 TgESTzz27g11.r1 TgME49 invivo Bradyzoite c... 34 3.9
 35 emb|AF008953|AF008953 Octomeles sumatrana 18S ribosomal RNA gene... 34 3.9
 emb|AL096797|SPBC146 S.pombe chromosome II cosmid c146. 30 4.4
 gb|M62862|TRBRTE Trypanosoma cruzi retrotransposon encoding gag ... 33 5.4
 emb|AQ411986|AQ411986 CpG0944B CpIOWAgDNA1 Cryptosporidium parvu... 33 5.4
 emb|AV389573|AV389573 AV389573 Chlamydomonas reinhardtii C9 Chla... 33 5.4
 40 emb|AC004145|AC004145 Leishmania major chromosome 3 clone L5801 ... 33 5.4
 emb|AI065213|AI065213 TENU2096 T. cruzi epimastigote normalized ... 33 5.4
 emb|AI075591|AI075591 TENU3013 T. cruzi epimastigote normalized ... 33 5.4
 emb|Z93115|MAZ93115 M.acuminata mRNA; clone pBAN UU131. 33 5.4
 gb|U11583|YSCH9196 Saccharomyces cerevisiae chromosome VIII cosm... 33 5.4
 45 emb|AL160727|P417R Leishmania major Friedlin PAC P417 right end-... 33 5.4
 emb|AW745646|AW745646 WS1_36_D09.b1_A002 Water-stressed 1 (WS1) ... 33 5.4
 emb|AA901886|AA901886 NCM4A1T3 Mycelial Neurospora crassa cDNA c... 29 6.0

50 Query= athrlpka_s_at 17068_s_at /id_source genbank /description
 gb|aaa32857.1| (m84658) receptor-like protein kinase [arabidopsis
 thaliana] /blast_score 0
 (2746 letters)

55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

60 Score E
 Sequences producing significant alignments: (bits) Value

- emb|AI896318|AI896318 EST265761 tomato callus, TAMU Lycopersicon... 182 5e-65
 emb|A67797|A67797 Sequence 2 from Patent WO9743427. 128 5e-51
 gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor-... 128 5e-51
 5 emb|AW432288|AW432288 sh71g05.y1 Gm-cl015 Glycine max cDNA clone... 200 5e-50
 emb|AI730535|AI730535 BNLGHi7007 Six-day Cotton fiber Gossypium ... 152 1e-49
 emb|AF085168|AF085168 Triticum aestivum receptor-like protein ki... 77 2e-46
 emb|AF085166|AF085166 Hordeum vulgare receptor-like kinase gene,... 86 2e-45
 emb|AF085167|AF085167 Hordeum vulgare receptor-like kinase ARK1A... 85 3e-45
 10 gb|U51330|TAU51330 Triticum aestivum leaf rust resistance kinase... 82 8e-45
 emb|AF100771|AF100771 Hordeum vulgare receptor-like kinase (Hv3A... 100 2e-44
 gb|U78762|TAU78762 Triticum aestivum receptor-like kinase ARK1AS... 86 2e-44
 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 129 7e-44
 emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 129 1e-43
 15 emb|AF085164|AF085164 Hordeum vulgare receptor-like kinase LRK10... 82 2e-43
 emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 80 7e-43
 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 77 3e-42
 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 86 4e-42
 emb|AI771630|AI771630 EST252730 tomato ovary, TAMU Lycopersicon ... 86 5e-42
 20 emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 123 8e-42
 emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 87 2e-41
 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 84 2e-41
 emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 126 2e-41
 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 75 3e-41
 25 dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 82 9e-41
 gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 76 3e-40
 emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 72 5e-40
 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 108 2e-39
 emb|AF220602|AF220602 Lycopersicon pimpinellifolium Rio Grande 7... 91 3e-39
 30 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 78 5e-39
 emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 86 5e-39
 emb|AW930866|AW930866 EST356709 tomato fruit mature green, TAMU ... 126 1e-38
 emb|AW621706|AW621706 EST312504 tomato root during/after fruit s... 122 1e-38
 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 77 2e-38
 35 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 84 2e-38
 emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 84 2e-38
 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 68 2e-38
 gb|BE057261|BE057261 sm99f12.y1 Gm-cl015 Glycine max cDNA clone ... 86 3e-38
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 74 3e-38
 40 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 82 3e-38
 emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 83 4e-38
 emb|AQ989326|AQ989326 Gm_ISb001_058_O23R ISU Soybean BAC Library... 94 5e-38
 dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 75 5e-38
 dbj|E05046|E05046 DNA encoding ZmPK1 homologue protein in tobacco. 75 5e-38
 45 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 81 6e-38
 emb|AF220603|AF220603 Lycopersicon esculentum VFNT Cherry Pto lo... 91 1e-37
 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 76 2e-37
 gb|BE060160|BE060160 HVSMEg0011B12f Hordeum vulgare pre-anthesis... 111 2e-37
 emb|AF131222|AF131222 Lophopyrum elongatum protein serine/threon... 110 3e-37
 50 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 78 5e-37
 emb|AI486547|AI486547 EST244868 tomato ovary, TAMU Lycopersicon ... 100 6e-37
 emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 100 7e-37
 emb|AW617954|AW617954 EST314028 L. pennellii trichome, Cornell U... 100 9e-37
 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 78 1e-36
 55 emb|AW030223|AW030223 EST273478 tomato callus, TAMU Lycopersicon... 92 2e-36
 emb|AW929662|AW929662 EST338450 tomato flower buds 8 mm to pre-a... 118 2e-36
 emb|AW704997|AW704997 sk41c03.y1 Gm-cl019 Glycine max cDNA clone... 89 2e-36
 emb|AI967314|AI967314 Ljirnp00-017 Ljirnp Lambda HybriZap two... 69 2e-36
 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 78 2e-36
 60 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 82 4e-36
 emb|Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 122 8e-36

emb|AW687349|AW687349 NF008F08RT1F1074 Developing root Medicago ... 80 9e-36
emb|AI487456|AI487456 EST245778 tomato ovary, TAMU Lycopersicon ... 97 1e-35
emb|AW668493|AW668493 GA__Ea0014C20 Gossypium arboreum 7-10 dpa ... 73 2e-35
emb|AI731504|AI731504 BNLGHi9991 Six-day Cotton fiber Gossypium ... 64 2e-35
5 emb|AW565461|AW565461 LG1_344_F11.g1_A002 Light Grown 1 (LG1) So... 106 4e-35
emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 76 4e-35
gb|BE059471|BE059471 sn32d11.y1 Gm-c1016 Glycine max cDNA clone ... 115 5e-35
emb|AA738546|AA738546 SbRLK4 Sorghum bicolor cv. TX430 leaf Sorg... 120 1e-34
emb|AW760240|AW760240 sl59g07.y1 Gm-c1027 Glycine max cDNA clone... 76 1e-34
10 emb|AW597214|AW597214 si71g06.y1 Gm-c1031 Glycine max cDNA clone... 126 2e-34
emb|AW092144|AW092144 EST285240 tomato mixed elicitor, BTI Lycop... 122 2e-34
emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 74 2e-34
emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 74 3e-34
emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 74 3e-34
15 emb|AW934655|AW934655 EST353547 tomato flower buds 0-3 mm, Corne... 93 3e-34
emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 67 3e-34
emb|AI896277|AI896277 EST265720 tomato callus, TAMU Lycopersicon... 111 3e-34
emb|AW666082|AW666082 sk31h04.y1 Gm-c1028 Glycine max cDNA clone... 116 3e-34
emb|AW233982|AW233982 sf32g05.y1 Gm-c1028 Glycine max cDNA clone... 130 3e-34
20 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 74 5e-34
emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 77 6e-34
emb|AB030083|AB030083 Populus nigra PnLPK mRNA for lectin-like p... 71 6e-34
emb|AW329840|AW329840 N201116e rootphos(-) Medicago truncatula c... 119 9e-34
emb|AW679172|AW679172 WS1_23_D02.b1_A002 Water-stressed 1 (WS1) ... 145 1e-33
25 emb|AA738547|AA738547 SbRLK5 Sorghum bicolor cv. TX430 leaf Sorg... 115 2e-33
emb|AW267961|AW267961 EST306183 DSIR Medicago truncatula cDNA cl... 76 2e-33
emb|AI736063|AI736063 sb22d04.y1 Gm-c1007 Glycine max cDNA clone... 68 8e-33
emb|AI967315|AI967315 Ljirmp00-018 Ljirmp Lambda HybriZap two... 75 2e-32
emb|AI823209|AI823209 L30-1092T3 Ice plant Lambda Uni-Zap XR exp... 85 3e-32
30 emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 72 4e-32
emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 79 4e-32
emb|AW329560|AW329560 N200811e rootphos(-) Medicago truncatula c... 95 4e-32
emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 78 5e-32
gb|BE058691|BE058691 sn19e05.y1 Gm-c1016 Glycine max cDNA clone ... 108 5e-32
35 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 76 7e-32
emb|AW694732|AW694732 NF079D07ST1F1061 Developing stem Medicago ... 118 7e-32
emb|AI727531|AI727531 BNLGHi8333 Six-day Cotton fiber Gossypium ... 125 7e-32
emb|AW649958|AW649958 EST328412 tomato germinating seedlings, TA... 79 2e-31
emb|AW279355|AW279355 sf65g10.y1 Gm-c1013 Glycine max cDNA clone... 118 3e-31
40 emb|AW040672|AW040672 EST283536 tomato mixed elicitor, BTI Lycop... 111 3e-31

Query= atu18770_s_at 17083_s_at /id_source
/description gb|aad25838.1|ac006951_17 (ac006951) putative
45 indole-3-glycerol phosphate synthase [arabidopsis thaliana]
/blast_score 0
(1362 letters)

Database: plantfungal
50 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
55 Sequences producing significant alignments: (bits) Value

emb|AI483399|AI483399 EST241520 tomato shoot, Cornell Lycopersic... 289 2e-89
emb|AW728148|AW728148 GA__Ea0014F23 Gossypium arboreum 7-10 dpa ... 247 1e-84
emb|AW200814|AW200814 se93h01.y1 Gm-c1027 Glycine max cDNA clone... 212 3e-78
60 emb|AI490817|AI490817 EST241526 tomato shoot, Cornell Lycopersic... 189 3e-71
emb|AW757393|AW757393 sl32g05.y1 Gm-c1027 Glycine max cDNA clone... 185 8e-63

- emb|AI731648|AI731648 BNLGHi10360 Six-day Cotton fiber *Gossypium*... 182 2e-61
emb|AW458591|AW458591 sh11b01.y1 *Gm-c1016 Glycine max cDNA clone*... 138 1e-59
emb|AW033644|AW033644 EST277215 tomato callus, TAMU *Lycopersicon*... 144 1e-51
emb|AW704608|AW704608 sk54c06.y1 *Gm-c1019 Glycine max cDNA clone*... 153 5e-51
5 emb|AW458875|AW458875 sh16b06.y1 *Gm-c1016 Glycine max cDNA clone*... 113 3e-49
emb|AW648549|AW648549 EST327003 tomato germinating seedlings, TA... 116 3e-48
gb|BE125163|BE125163 DG1_13_H04.b1_A002 Dark Grown 1 (DG1) *Sorgh*... 180 2e-44
gb|BE053284|BE053284 GA_Ea0007G10f *Gossypium arboreum* 7-10 dpa ... 123 1e-43
emb|AW648007|AW648007 EST326461 tomato germinating seedlings, TA... 100 2e-38
10 emb|AI773256|AI773256 EST254356 tomato resistant, Cornell *Lycopersicon*... 99 5e-38
gb|BE052703|BE052703 GA_Ea0031N16f *Gossypium arboreum* 7-10 dpa ... 86 1e-36
emb|AW676692|AW676692 DG1_13_H04.g1_A002 Dark Grown 1 (DG1) *Sorgh*... 105 4e-31
emb|AW758260|AW758260 874006H11.y1 *C. reinhardtii* CC-1690, *Lambd*... 132 6e-30
emb|AW564868|AW564868 LG1_310_H09.b1_A002 Light Grown 1 (LG1) *So*... 104 3e-29
15 emb|AL096874|SPBC1539 *S.pombe* chromosome II cosmid c1539. 57 5e-29
emb|AW696155|AW696155 NF103A11ST1F1084 Developing stem *Medicago* ... 76 6e-29
emb|Y09137|SPTRP1 *S.pombe* trp-1 mRNA. 57 1e-28
emb|AW618611|AW618611 EST320597 *L. pennellii* trichome, Cornell U... 82 4e-24
emb|AV420994|AV420994 AV420994 *Lotus japonicus* young plants (two... 106 3e-22
20 emb|AI490823|AI490823 EST241532 tomato shoot, Cornell *Lycopersicon*... 104 2e-21
emb|AW432225|AW432225 sh70g02.y1 *Gm-c1015 Glycine max cDNA clone*... 95 2e-18
gb|BE059030|BE059030 sn24c03.y1 *Gm-c1016 Glycine max cDNA clone* ... 78 1e-13
emb|AU012336|AU012336 AU012336 *Schizosaccharomyces pombe* late lo... 48 1e-10
emb|X53576|ANTRPCA *Aspergillus niger* trpC gene for glutamine ami... 64 3e-09
25 emb|X07071|ANTRPC *Aspergillus niger* trpC gene. 64 3e-09
emb|X05033|PCTRPC *Penicillium chrysogenum* trpC gene for put. tri... 62 7e-09
emb|X02390|ANTRPC1 *Aspergillus nidulans* trpC gene. 62 7e-09
gb|M23177|PBLTRPX1A *Phycomyces blakesleeanus* (TRP1) gene, comple... 61 3e-08
dbj|E00783|E00783 DNA encoding for structural gene MOX(alcoholox... 58 1e-07
30 emb|A11156|A11156 MOX structural gene and it's 5'and 3'-flanking... 58 1e-07
emb|X02425|HPMOXG *Hansenula polymorpha* MOX gene for methanol oxi... 58 1e-07
emb|X70035|CHTRP1 *C.heterostrophus* gene for trifunctional trypto... 58 2e-07
gb|M64473|PHTTRP1 *Phytophthora parasitica* N-(5'-phosphoribosyl)a... 57 3e-07
gb|J01252|NEUTRP1 *n.crassa* trifunctional tryptophan biosynthesis... 57 3e-07
35 emb|X56047|PDTRPC *P. chrysosporium* trpC gene for trifunctional p... 55 1e-06
emb|X75951|SC6ORF *S.cerevisiae* URA1, SAC1, RSD1 and TRP3 genes a... 50 1e-06
gb|K01386|YSCTRP3 *Yeast (S.cerevisiae)* TRP3 gene coding for anth... 50 1e-06
emb|Z28211|SCYKL211C *S.cerevisiae* chromosome XI reading frame OR... 50 1e-06
emb|A86135|A86135 Sequence 794 from Patent EP0866129. 35 0.002
40 gb|M74901|CPCTRP1 *Cryptococcus neoformans* phosphoribosyl anthran... 40 0.042
emb|X75652|ALRIBT *A.longa* plastid genes for tRNAs, ribosomal pro... 36 0.74
emb|X14385|ALCRPEF *Astasia longa* chloroplast rps7 and tufA genes... 36 0.74
emb|X51672|SCRSD1 *Saccharomyces cerevisiae* rsd1 gene. 35 1.0
emb|AL049180|PFMAL13P1 *Plasmodium falciparum* chromosome 13 strai... 34 2.6
45 gb|U33057|SCD9717 *Saccharomyces cerevisiae* chromosome IV cosmids... 34 2.6
emb|AV423493|AV423493 AV423493 *Lotus japonicus* young plants (two... 34 3.6
emb|AL353822|NC15E6 *Neurospora crassa* DNA linkage group V Cosmid... 34 3.6
emb|AW180222|AW180222 MgA0308f MgA Library *Mycosphaerella gramin*... 34 3.6
emb|AJ133598|PSA133598 *Pisum sativum* chloroplast gF16P gene, exo... 33 5.0
50 emb|AI054479|AI054479 coau0001B20 Cotton Boll Abscission Zone cD... 33 5.0
gb|L34806|PEAFRUBISP *Pisum sativum* fructose-1,6-bisphosphate mRN... 33 5.0
emb|X68826|PSF16B *P.sativum* mRNA for fructose 1,6 biphosphatase. 33 5.0
emb|AV391683|AV391683 AV391683 *Chlamydomonas reinhardtii* C9 Chla... 33 5.0
emb|AJ231281|BSAJ1281 *Brachythecium salebrosum* partial mRNA for ... 33 6.8
55 emb|AQ902358|AQ902358 LMAJFV1_lm85h07.x1 *Leishmania major* FV1 ra... 33 6.8
emb|AQ654520|AQ654520 Sheared DNA-10A10.TF Sheared DNA *Trypanoso*... 32 9.3
emb|AF180022|AF180022 *Adiantum capillus-veneris* photosystem I P7... 32 9.3
emb|AQ649354|AQ649354 Sheared DNA-30F1.TF Sheared DNA *Trypanosom*... 32 9.3
gb|L44013|BLYCH *Hordeum vulgare* (clone WG241) STS mRNA, sequence... 32 9.3
60 emb|AA451566|AA451566 AOB168f Onion seedling leaf cDNA library A... 32 9.3
dbj|D87301|D87301 D87301 *Trypanosoma cruzi* Y (Tomoo Tanaka) Tryp... 28 10.0

Query= atu66345_s_at 17097_s_at /id_source genbank /description
gb|aac49697.1| (u66345) calreticulin [arabidopsis thaliana]
/blast_score 0

5 (1424 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

10 Searching.....done

	Score	E	
	(bits) Value		
Sequences producing significant alignments:			
15	emb AJ002057 BVMRNAC Beta vulgaris mRNA for calreticulin.	577 e-163	
	emb Z71395 NPCAL1MNR N.plumbaginifolia mRNA for calreticulin.	575 e-163	
	gb U74630 RCU74630 Ricinus communis calreticulin mRNA, complete ...	575 e-163	
	emb AF052040 AF052040 Berberis stolonifera calreticulin mRNA, co...	571 e-162	
	emb X85382 NTRNATCAL N.tabacum mRNA for calreticulin.	570 e-161	
20	emb AF134733 AF134733 Prunus armeniaca calcium-binding protein c...	565 e-160	
	gb L27349 BLYCRH2A Hordeum vulgare calreticulin (CRH2) mRNA, par...	560 e-159	
	gb L27348 BLYCRH1A Hordeum vulgare calreticulin (CRH1) mRNA, par...	560 e-159	
	emb AF019376 AF019376 Brassica napus calreticulin mRNA, complete...	465 e-156	
	emb X80756 CAPCRTC C.annuum PCRTC mRNA.	344 e-154	
25	gb U74631 RCU74631 Ricinus communis calreticulin gene, complete ...	149 e-123	
	emb AJ000765 CRAJ765 Chlamydomonas reinhardtii mRNA for calretic...	369 e-122	
	emb AI728389 AI728389 BNLGHi10665 Six-day Cotton fiber Gossypium...	438 e-122	
	emb AI782264 AI782264 EST263143 tomato susceptible, Cornell Lyco...	418 e-116	
	emb AB018243 AB018243 Solanum melongena EEF22 mRNA for calreticu...	402 e-111	
30	emb AW667951 AW667951 GA_Ea0012A11 Gossypium arboreum 7-10 dpa ...	402 e-111	
	emb AW216727 AW216727 EST295441 tomato callus, TAMU Lycopersicon...	391 e-108	
	emb AW509432 AW509432 si37b03.y1 Gm-r1030 Glycine max cDNA clone...	389 e-107	
	emb AW039860 AW039860 EST282333 tomato mixed elicitor, BTI Lycop...	382 e-105	
	emb AW624478 AW624478 EST322423 tomato flower buds 3-8 mm, Corne...	378 e-104	
35	emb AW626316 AW626316 EST320223 tomato radicle, 5 d post-imbibit...	375 e-103	
	emb AW727433 AW727433 GA_Ea0012B12 Gossypium arboreum 7-10 dpa ...	374 e-103	
	emb AW622049 AW622049 EST312847 tomato root during/after fruit s...	363 3e-99	
	emb AW568477 AW568477 si59c07.y1 Gm-r1030 Glycine max cDNA clone...	361 9e-99	
	emb AW441195 AW441195 EST310591 tomato fruit red ripe, TAMU Lyco...	359 2e-98	
40	gb BE059929 BE059929 sn38h08.y1 Gm-cl016 Glycine max cDNA clone ...	350 1e-95	
	emb AW944954 AW944954 EST337004 tomato flower buds 3-8 mm, Corne...	349 3e-95	
	emb AW932476 AW932476 EST358319 tomato fruit mature green, TAMU ...	348 5e-95	
	emb AW930392 AW930392 EST340945 tomato fruit mature green, TAMU ...	348 7e-95	
	emb AW649196 AW649196 EST327650 tomato germinating seedlings, TA...	347 2e-94	
45	emb AW650460 AW650460 EST328914 tomato germinating seedlings, TA...	344 8e-94	
	emb AW560421 AW560421 EST315469 DSIR Medicago truncatula cDNA cl...	330 1e-93	
	emb AW650947 AW650947 EST329401 tomato germinating seedlings, TA...	343 2e-93	
	emb AW685878 AW685878 NF031C11NR1F1000 Nodulated root Medicago t...	341 6e-93	
	emb AW756722 AW756722 sl26d08.y1 Gm-cl027 Glycine max cDNA clone...	336 2e-91	
50	emb AW934135 AW934135 EST359978 tomato fruit mature green, TAMU ...	333 2e-90	
	emb AW621571 AW621571 EST312369 tomato root during/after fruit s...	333 2e-90	
	emb Y09816 EGCALRPR E.gracilis mRNA for calreticulin precursor.	257 3e-89	
	emb AW731454 AW731454 GA_Ea0030H17 Gossypium arboreum 7-10 dpa ...	329 4e-89	
	emb AI960982 AI960982 sc93e09.y1 Gm-cl019 Glycine max cDNA clone...	328 6e-89	
55	emb AW725609 AW725609 GA_Ea0018P14 Gossypium arboreum 7-10 dpa ...	326 3e-88	
	emb AW725587 AW725587 GA_Ea0018N14 Gossypium arboreum 7-10 dpa ...	326 3e-88	
	emb AW033447 AW033447 EST277018 tomato callus, TAMU Lycopersicon...	323 2e-87	
	emb AW668560 AW668560 GA_Ea0014K06 Gossypium arboreum 7-10 dpa ...	317 2e-85	
	emb AW201052 AW201052 se97c10.y1 Gm-cl027 Glycine max cDNA clone...	316 2e-85	
60	emb AW773947 AW773947 EST332933 KV3 Medicago truncatula cDNA clo...	316 2e-85	
	emb AI726591 AI726591 BNLGHi6198 Six-day Cotton fiber Gossypium ...	312 5e-84	

- emb|AI735991|AI735991 sb21e08.y1 Gm-cl007 Glycine max cDNA clone... 309 3e-83
emb|AI812952|AI812952 22G9 Pine Lambda Zap Xylem library Pinus t... 247 9e-82
emb|AW219282|AW219282 EST301764 tomato root during/after fruit s... 303 2e-81
emb|AW035959|AW035959 EST282818 tomato callus, TAMU Lycopersicon... 303 3e-81
5 emb|Y09078|DBCALLKPR D.bioculata mRNA for calreticulin-like prot... 225 7e-81
emb|AA660877|AA660877 00772 MtrHE Medicago truncatula cDNA 5' si... 207 8e-80
emb|AW509028|AW509028 si39c02.y1 Gm-r1030 Glycine max cDNA clone... 297 1e-79
emb|AW306403|AW306403 se50b10.y1 Gm-cl017 Glycine max cDNA clone... 296 3e-79
emb|AW773889|AW773889 EST332875 KV3 Medicago truncatula cDNA clo... 295 7e-79
10 emb|AW727696|AW727696 GA__Ea0015K01 Gossypium arboreum 7-10 dpa ... 258 8e-79
emb|AW705880|AW705880 sk52a09.y1 Gm-cl019 Glycine max cDNA clone... 293 2e-78
emb|AW299150|AW299150 EST305824 KV2 Medicago truncatula cDNA clo... 293 2e-78
emb|AI898214|AI898214 EST267657 tomato ovary, TAMU Lycopersicon ... 292 6e-78
emb|AW738476|AW738476 EST339903 tomato flower buds, anthesis, Co... 291 1e-77
15 emb|AW933869|AW933869 EST359712 tomato fruit mature green, TAMU ... 287 1e-76
emb|AW695765|AW695765 NF098D02ST1F1016 Developing stem Medicago ... 286 4e-76
emb|AW220942|AW220942 EST297411 tomato fruit mature green, TAMU ... 285 5e-76
emb|AW649817|AW649817 EST328271 tomato germinating seedlings, TA... 285 5e-76
emb|AA660477|AA660477 00363 MtrHE Medicago truncatula cDNA 5' si... 281 7e-75
20 emb|AW184893|AW184893 se82a03.y1 Gm-cl023 Glycine max cDNA clone... 281 1e-74
emb|AW309216|AW309216 sg05g07.y1 Gm-cl019 Glycine max cDNA clone... 281 1e-74
emb|AW979917|AW979917 EST341567 tomato root deficiency, Cornell ... 279 3e-74
emb|AW132963|AW132963 se12f08.y1 Gm-cl013 Glycine max cDNA clone... 278 6e-74
emb|AW277466|AW277466 sf82d10.y1 Gm-cl019 Glycine max cDNA clone... 276 3e-73
25 emb|AW033083|AW033083 EST276642 tomato callus, TAMU Lycopersicon... 275 8e-73
emb|AI899646|AI899646 EST269089 tomato susceptible, Cornell Lyco... 272 5e-72
emb|AW773817|AW773817 EST332803 KV3 Medicago truncatula cDNA clo... 271 1e-71
emb|AW727636|AW727636 GA__Ea0015E17 Gossypium arboreum 7-10 dpa ... 270 2e-71
emb|AI973534|AI973534 sc88a04.y1 Gm-cl019 Glycine max cDNA clone... 270 3e-71
30 emb|AW648010|AW648010 EST326464 tomato germinating seedlings, TA... 268 7e-71
emb|AI495184|AI495184 sa89b11.y1 Gm-cl004 Glycine max cDNA clone... 267 1e-70
emb|AI437497|AI437497 sa34a12.y1 Gm-cl004 Glycine max cDNA clone... 265 6e-70
emb|AI489195|AI489195 EST247534 tomato ovary, TAMU Lycopersicon ... 264 2e-69
emb|AI771812|AI771812 EST252912 tomato ovary, TAMU Lycopersicon ... 264 2e-69
35 emb|AW728940|AW728940 GA__Ea0018J21 Gossypium arboreum 7-10 dpa ... 262 6e-69
emb|AW043340|AW043340 ST32B12 Pine TriplEx shoot tip library Pin... 260 1e-68
emb|AW596414|AW596414 sj12b07.y1 Gm-cl032 Glycine max cDNA clone... 256 3e-67
emb|AW731131|AW731131 GA__Ea0008P21 Gossypium arboreum 7-10 dpa ... 256 3e-67
emb|AW933031|AW933031 EST358874 tomato fruit mature green, TAMU ... 254 9e-67
40 emb|AW649360|AW649360 EST327814 tomato germinating seedlings, TA... 254 1e-66
emb|AW266258|AW266258 L30-2972T3 Ice plant Lambda Uni-Zap XR exp... 253 3e-66
emb|AW907386|AW907386 EST343509 potato stolon, Cornell Universit... 252 4e-66
emb|AW035234|AW035234 EST280496 tomato callus, TAMU Lycopersicon... 252 6e-66
emb|AI779884|AI779884 EST260763 tomato susceptible, Cornell Lyco... 151 7e-66
45 emb|AW587738|AW587738 ST66B09 Pine TriplEx shoot tip library Pin... 248 6e-65
gb|BE055451|BE055451 GA__Ea0033B14f Gossypium arboreum 7-10 dpa ... 247 1e-64
emb|AI166964|AI166964 xylem.est.744 Poplar xylem Lambda ZAPII li... 247 2e-64
emb|AW720057|AW720057 LjNEST13b1r Lotus japonicus nodule library... 246 4e-64
emb|AV419506|AV419506 AV419506 Lotus japonicus young plants (two... 242 7e-63
50 emb|AW760501|AW760501 sl51b04.y1 Gm-cl027 Glycine max cDNA clone... 239 3e-62
emb|AF107115|AF107115 Trypanosoma cruzi calreticulin (clr) gene,... 143 9e-61
emb|AF162779|AF162779 Trypanosoma cruzi Tc45-calreticulin precur... 143 2e-60
emb|AW725203|AW725203 GA__Ea0015H01 Gossypium arboreum 7-10 dpa ... 232 4e-60

55

Query= athrprp1a_s_at 17128_s_at/id_source
/description gb|aac69381.1| (ac005398) pathogenesis-related
pr-1-like protein [arabidopsis /blast_score 1.00e-94 /ec_number
/family /chip nova /gb_link /ncgi

60

(757 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments: (bits) Value

	gb U70666 BNU70666 Brassica napus pathogenesis-related protein P...	323	3e-89
10	gb U21849 BNU21849 Brassica napus PR-1a (LSC94) mRNA, complete cds.	323	3e-89
	gb U64806 BNU64806 Brassica napus pathogenesis-related protein P...	209	4e-86
	emb AI352851 AI352851 MB69-8A PZ204.BNlib Brassica napus cDNA cl...	311	5e-84
	emb AI352893 AI352893 MB72-6D PZ204.BNlib Brassica napus cDNA cl...	165	3e-62
	emb AW217013 AW217013 EST295727 tomato callus, TAMU Lycopersicon...	152	4e-60
15	emb AW219671 AW219671 EST302153 tomato root during/after fruit s...	151	1e-59
	emb AW092403 AW092403 EST285583 tomato mixed elicitor, BTI Lycop...	151	1e-59
	emb AI895090 AI895090 EST264533 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW625930 AW625930 EST319825 tomato radicle, 5 d post-imbibit...	151	1e-59
	emb AW032514 AW032514 EST276073 tomato callus, TAMU Lycopersicon...	151	1e-59
20	emb AW034260 AW034260 EST277831 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW040983 AW040983 EST283847 tomato mixed elicitor, BTI Lycop...	151	1e-59
	emb AW034206 AW034206 EST277777 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW219480 AW219480 EST301878 tomato root during/after fruit s...	151	1e-59
	emb AW092623 AW092623 EST285803 tomato mixed elicitor, BTI Lycop...	151	1e-59
25	emb AW040954 AW040954 EST283818 tomato mixed elicitor, BTI Lycop...	151	1e-59
	emb AW034454 AW034454 EST278025 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW032723 AW032723 EST276282 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW033873 AW033873 EST277444 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AI894650 AI894650 EST264093 tomato callus, TAMU Lycopersicon...	151	1e-59
30	emb AW033593 AW033593 EST277164 tomato callus, TAMU Lycopersicon...	151	3e-59
	emb AW034724 AW034724 EST278526 tomato callus, TAMU Lycopersicon...	148	7e-59
	emb AW041033 AW041033 EST283897 tomato mixed elicitor, BTI Lycop...	148	7e-59
	emb X66942 NTPRB1B N.tabacum prb-1b gene.	146	9e-59
	emb AW559895 AW559895 EST314943 DSIR Medicago truncatula cDNA cl...	160	1e-58
35	emb AW329241 AW329241 N200453e rootphos(-) Medicago truncatula c...	160	1e-58
	emb AI352771 AI352771 MB58-5G PZ204.BNlib Brassica napus cDNA cl...	220	2e-58
	emb AW559894 AW559894 EST314942 DSIR Medicago truncatula cDNA cl...	159	5e-58
	emb AW035820 AW035820 EST281974 tomato callus, TAMU Lycopersicon...	145	6e-58
	emb AW032139 AW032139 EST275593 tomato callus, TAMU Lycopersicon...	145	6e-58
40	emb AW034330 AW034330 EST277901 tomato callus, TAMU Lycopersicon...	144	2e-57
	emb AW622143 AW622143 EST312941 tomato root during/after fruit s...	149	2e-57
	emb AW032749 AW032749 EST276308 tomato callus, TAMU Lycopersicon...	149	3e-57
	emb AI894391 AI894391 EST263846 tomato callus, TAMU Lycopersicon...	142	4e-57
	emb AI896249 AI896249 EST265692 tomato callus, TAMU Lycopersicon...	142	6e-57
45	emb AI782621 AI782621 EST263500 tomato susceptible, Cornell Lyco...	144	8e-57
	emb AW126362 AW126362 N100469e rootphos(-) Medicago truncatula c...	160	3e-56
	emb AW981257 AW981257 EST392410 DSIL Medicago truncatula cDNA cl...	128	1e-55
	emb AW033687 AW033687 EST277258 tomato callus, TAMU Lycopersicon...	149	2e-55
	emb AI352783 AI352783 MB59-12D PZ204.BNlib Brassica napus cDNA c...	198	3e-55
50	emb X14065 NTPRP1 Nicotiana tabacum gene for basic form of patho...	140	5e-55
	emb AW625666 AW625666 EST319573 tomato radicle, 5 d post-imbibit...	135	6e-55
	emb AW032727 AW032727 EST276286 tomato callus, TAMU Lycopersicon...	147	1e-53
	emb X52555 NTW381 Tobacco W38/1 gene for PR-1 pathogenesis-relat...	116	1e-52
	gb BE034214 BE034214 MH01C07 MH Mesembryanthemum crystallinum cD...	112	4e-52
55	emb AW053720 AW053720 L30-1612T3 Ice plant Lambda Uni-Zap XR exp...	112	4e-52
	emb AW559969 AW559969 EST315017 DSIR Medicago truncatula cDNA cl...	81	4e-52
	emb AI352801 AI352801 MB61-9C PZ204.BNlib Brassica napus cDNA cl...	194	1e-51
	emb X17681 NTPR1CA Tobacco gene for pathogenesis-related protein...	111	2e-51
	emb X05454 NTPR1CR Nicotiana tabacum mRNA for PR-1c protein.	111	2e-51
60	emb X12487 NTPR1C Tobacco mRNA fragment for pathogenesis-related...	111	2e-51
	emb AJ011520 LES011520 Lycopersicon esculentum pr1a (P4) gene.	98	1e-50

- gb|M69247|TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat... 98 1e-50
 emb|A22634|LEPI4GENE L.esculentum P14 gene. 98 1e-50
 emb|AJ250136|STU250136 Solanum tuberosum mRNA for pathogenesis r... 99 2e-50
 emb|AW218808|AW218808 EST301288 tomato root during/after fruit s... 116 3e-50
 5 emb|AI896011|AI896011 EST265454 tomato callus, TAMU Lycopersicon... 116 3e-50
 emb|AW094536|AW094536 EST287716 tomato mixed elicitor, BTI Lycop... 116 3e-50
 emb|AW038553|AW038553 EST280236 tomato mixed elicitor, BTI Lycop... 116 3e-50
 dbj|D90196|TOBPR1A Nicotiana tabacum mRNA for PR1a protein precu... 104 3e-50
 emb|X05959|NTPR1AG Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
 10 emb|X12737|NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
 emb|X06361|NTPR1AG1 Nicotiana tabacum gene for pathogenesis-rela... 104 4e-50
 emb|X12485|NTPR1A Tobacco mRNA fragment for pathogenesis-related... 104 4e-50
 emb|AW033469|AW033469 EST277040 tomato callus, TAMU Lycopersicon... 116 5e-50
 emb|X06930|NTPR1AG2 Tobacco PR-1a gene for pathogenesis-related ... 104 7e-50
 15 emb|AI352858|AI352858 MB70-10D PZ204.BNlib Brassica napus cDNA c... 197 7e-50
 emb|AI782416|AI782416 EST263295 tomato susceptible, Cornell Lyco... 95 7e-50
 emb|AW034882|AW034882 EST279111 tomato callus, TAMU Lycopersicon... 95 1e-49
 emb|AW031086|AW031086 EST274393 tomato callus, TAMU Lycopersicon... 116 1e-49
 emb|X74939|HVPR1AR H.vulgare HvPR-1a mRNA for a basic PR-1-type... 114 2e-49
 20 emb|AF136636|AF136636 Glycine max PR1a precursor (PR1a) mRNA, co... 110 2e-49
 emb|AW034167|AW034167 EST277738 tomato callus, TAMU Lycopersicon... 94 2e-49
 emb|X17680|NTPR1BA Tobacco gene for pathogenesis-related protein... 103 4e-49
 emb|X03465|NTPRPR Nicotiana tabacum mRNA for pathogenesis-relate... 103 4e-49
 dbj|D90197|TOBPR1B1 Nicotiana tabacum mRNA for PR1b protein. 103 4e-49
 25 emb|Y08804|LEPR1B1 L.esculentum mRNA for PR protein. 92 7e-49
 gb|M69248|TOMPRP6 Lycopersicon esculentum PR (pathogenesis relat... 92 7e-49
 emb|X68738|LEP1P14A L.esculentum mRNA for ethylene-induced P1(pl... 92 7e-49
 emb|AI781499|AI781499 EST262378 tomato susceptible, Cornell Lyco... 92 7e-49
 emb|AI779424|AI779424 EST260303 tomato susceptible, Cornell Lyco... 92 7e-49
 30 emb|AW031093|AW031093 EST274400 tomato callus, TAMU Lycopersicon... 92 7e-49
 emb|AI779425|AI779425 EST260304 tomato susceptible, Cornell Lyco... 92 7e-49
 emb|AI782545|AI782545 EST263424 tomato susceptible, Cornell Lyco... 92 7e-49
 emb|AI782822|AI782822 EST263701 tomato susceptible, Cornell Lyco... 92 7e-49
 emb|AI778686|AI778686 EST259565 tomato susceptible, Cornell Lyco... 92 7e-49
 35 emb|AI778680|AI778680 EST259559 tomato susceptible, Cornell Lyco... 92 7e-49
 emb|AI899514|AI899514 EST268957 tomato susceptible, Cornell Lyco... 92 7e-49
 emb|AI779287|AI779287 EST260166 tomato susceptible, Cornell Lyco... 92 7e-49
 emb|AI773130|AI773130 EST254230 tomato resistant, Cornell Lycope... 92 7e-49
 emb|AI778790|AI778790 EST259669 tomato susceptible, Cornell Lyco... 92 7e-49
 40 emb|AI778791|AI778791 EST259670 tomato susceptible, Cornell Lyco... 92 7e-49
 emb|AI778985|AI778985 EST259864 tomato susceptible, Cornell Lyco... 92 7e-49
 emb|AW032026|AW032026 EST275480 tomato callus, TAMU Lycopersicon... 92 7e-49
 emb|AI782288|AI782288 EST263167 tomato susceptible, Cornell Lyco... 92 7e-49
 emb|AI779013|AI779013 EST259892 tomato susceptible, Cornell Lyco... 92 7e-49
 45 emb|AI781431|AI781431 EST262298 tomato susceptible, Cornell Lyco... 92 7e-49
 emb|AI780973|AI780973 EST261852 tomato susceptible, Cornell Lyco... 92 7e-49
 emb|AI895236|AI895236 EST264679 tomato callus, TAMU Lycopersicon... 92 7e-49

50 Query= af107726_s_at 17499_s_at /id_source genbank /description
 gb|aad19610.1| (af107726) cyclic nucleotide gated channel [arabidopsis
 thaliana] /blast_score 0
 (2208 letters)

55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

60 Score E
 Sequences producing significant alignments: (bits) Value

	emb AF079872 AF079872 <i>Nicotiana tabacum</i> cyclic nucleotide-gated ...	380	0.0
	emb AF079871 AF079871 <i>Nicotiana tabacum</i> cyclic nucleotide-gated ...	373	0.0
	emb AJ002610 HVAJ2610 <i>Hordeum vulgare</i> mRNA for putative calmodul...	331	0.0
5	emb AW625647 AW625647 EST319554 tomato radicle, 5 d post-imbibit...	255	6e-82
	emb AW038928 AW038928 EST280884 tomato mixed elicitor, BTI Lycop...	190	2e-80
	emb AI782780 AI782780 EST263659 tomato susceptible, Cornell Lyco...	259	4e-77
	emb AI486671 AI486671 EST244993 tomato ovary, TAMU Lycopersicon ...	241	4e-70
	emb AW725576 AW725576 GA_Ea0018M08 <i>Gossypium arboreum</i> 7-10 dpa ...	196	3e-69
10	emb AW265987 AW265987 L30-2643T3 Ice plant Lambda Uni-Zap XR exp...	150	3e-69
	emb AW033272 AW033272 EST276843 tomato callus, TAMU Lycopersicon...	260	2e-68
	emb AW126067 AW126067 N100263e rootphos(-) <i>Medicago truncatula</i> c...	258	1e-67
	gb U65390 NTU65390 <i>Nicotiana tabacum</i> CaMB-channel protein mRNA, ...	162	1e-65
	emb AI898047 AI898047 EST267490 tomato ovary, TAMU Lycopersicon ...	241	2e-62
15	emb AI487755 AI487755 EST246077 tomato ovary, TAMU Lycopersicon ...	241	2e-62
	emb AI776725 AI776725 EST257825 tomato resistant, Cornell Lycope...	240	3e-62
	emb AI729234 AI729234 BNLGHi12947 Six-day Cotton fiber <i>Gossypium</i> ...	176	3e-57
	emb AW705372 AW705372 sk48b11.y1 Gm-c1019 Glycine max cDNA clone...	133	4e-51
	emb AW029776 AW029776 EST273031 tomato callus, TAMU Lycopersicon...	156	4e-51
20	emb AW220952 AW220952 EST297421 tomato fruit mature green, TAMU ...	118	3e-50
	emb AW626197 AW626197 EST320104 tomato radicle, 5 d post-imbibit...	132	1e-49
	gb BE059468 BE059468 sn32d07.y1 Gm-c1016 Glycine max cDNA clone ...	133	5e-46
	emb AW029909 AW029909 EST273164 tomato callus, TAMU Lycopersicon...	122	5e-45
	emb AI729590 AI729590 BNLGHi13704 Six-day Cotton fiber <i>Gossypium</i> ...	180	4e-44
25	emb AI490589 AI490589 EST249143 tomato ovary, TAMU Lycopersicon ...	178	1e-43
	emb AW830981 AW830981 sm31b10.y1 Gm-c1028 Glycine max cDNA clone...	176	8e-43
	emb AV414437 AV414437 AV414437 <i>Lotus japonicus</i> young plants (two...	112	2e-41
	emb AI494870 AI494870 sb06e03.y1 Gm-c1004 Glycine max cDNA clone...	125	1e-40
	emb AI055360 AI055360 coau0003M11 Cotton Boll Abscission Zone cD...	123	8e-39
30	emb AW737921 AW737921 EST339348 tomato flower buds, anthesis, Co...	128	1e-37
	emb AI967361 AI967361 Ljirnp02-095-a3 Ljirnp Lambda HybriZap ...	94	2e-36
	emb AI776645 AI776645 EST257745 tomato resistant, Cornell Lycope...	70	3e-35
	emb AW775519 AW775519 EST334584 DSIL <i>Medicago truncatula</i> cDNA cl...	147	3e-34
	emb AI778171 AI778171 EST259050 tomato susceptible, Cornell Lyco...	76	4e-34
35	emb AW309771 AW309771 sf24f01.x1 Gm-c1028 Glycine max cDNA clone...	143	7e-33
	emb AI960258 AI960258 sc81a02.y1 Gm-c1018 Glycine max cDNA clone...	122	2e-32
	emb AW563840 AW563840 LG1_272_B06.b1_A002 Light Grown 1 (LG1) So...	113	1e-30
	emb AW774513 AW774513 EST333664 KV3 <i>Medicago truncatula</i> cDNA clo...	135	1e-30
	emb AI967666 AI967666 Ljirnp08-671-e8 Ljirnp Lambda HybriZap ...	116	2e-30
40	emb AW671345 AW671345 LG1_335_D05.b1_A002 Light Grown 1 (LG1) So...	100	2e-30
	gb C95565 C95565 C95565 <i>Citrus unshiu</i> Miyagawa-wase maturation s...	132	1e-29
	emb AW759050 AW759050 sl34a04.y1 Gm-c1027 Glycine max cDNA clone...	129	9e-29
	emb AW286638 AW286638 LG1_335_D05.g1_A002 Light Grown 1 (LG1) So...	127	2e-28
	emb AW831384 AW831384 sm24g05.y1 Gm-c1028 Glycine max cDNA clone...	87	9e-27
45	emb AW037755 AW037755 EST279384 tomato mixed elicitor, BTI Lycop...	122	1e-26
	emb AW508715 AW508715 si35e10.y1 Gm-r1030 Glycine max cDNA clone...	117	3e-25
	emb AW350588 AW350588 GM210009A10H2R Gm-r1021 Glycine max cDNA 3...	106	1e-24
50	emb AW350847 AW350847 GM210009B20G5R Gm-r1021 Glycine max cDNA 3...	106	2e-24
	emb AI776960 AI776960 EST251986 tomato callus, TAMU Lycopersicon...	111	2e-23
	emb AW781088 AW781088 sl88h09.y1 Gm-c1037 Glycine max cDNA clone...	111	3e-23
	emb AW039011 AW039011 EST280984 tomato mixed elicitor, BTI Lycop...	111	3e-23
	emb AW617273 AW617273 EST323684 <i>L. hirsutum</i> trichome, Cornell Un...	106	7e-22
55	gb BE022211 BE022211 sm72b10.y1 Gm-c1028 Glycine max cDNA clone ...	106	7e-22
	emb AW668188 AW668188 GA_Ea0013B18 <i>Gossypium arboreum</i> 7-10 dpa ...	105	2e-21
	emb AA824914 AA824914 CT202.SK Tomato Leaf cDNA from cv. VFNT ch...	93	6e-21
	emb AT000374 AT000374 AT000374 Apple peel cDNA library <i>Malus x d</i> ...	102	1e-20
	emb AW623583 AW623583 EST321528 tomato flower buds 3-8 mm, Corne...	69	7e-20
60	emb AI495394 AI495394 sa97d10.y1 Gm-c1004 Glycine max cDNA clone...	98	2e-19
	emb AI725563 AI725563 BNLGHi12127 Six-day Cotton fiber <i>Gossypium</i> ...	67	5e-18

emb|AW119379|AW119379 sd45d12.y1 Gm-c1016 Glycine max cDNA clone... 74 3e-17
emb|AW617083|AW617083 EST323494 L. hirsutum trichome, Cornell Un... 65 7e-17
emb|AW832684|AW832684 00046 leafy spurge Lambda HybriZAP 2.1 two... 60 4e-12
emb|AI776961|AI776961 EST251987 tomato callus, TAMU Lycopersicon... 67 5e-12
5 emb|AI894661|AI894661 EST264104 tomato callus, TAMU Lycopersicon... 68 3e-10
emb|AW217336|AW217336 EST296159 tomato flower buds 0-3 mm, Corne... 67 7e-10
emb|AW688833|AW688833 NF012B10ST1F1000 Developing stem Medicago ... 58 1e-09
emb|AW164084|AW164084 Ljirnp19-528-f6 Ljirnp Lambda HybriZap ... 56 1e-06
emb|AJ249962|DCA249962 Daucus carota mRNA for potassium channel ... 55 3e-06
10 emb|AW184978|AW184978 se85a09.y1 Gm-c1023 Glycine max cDNA clone... 54 4e-06
emb|AW091651|AW091651 EST284747 tomato mixed elicitor, BTI Lycop... 51 3e-05
emb|AW041519|AW041519 EST284383 tomato mixed elicitor, BTI Lycop... 51 3e-05
emb|AF145272|AF145272 Samanea saman pulvinus inward-rectifying c... 49 1e-04
gb|BE060413|BE060413 HVSMEg0012D21f Hordeum vulgare pre-anthesis... 38 2e-04
15 emb|AW928912|AW928912 EST337700 tomato flower buds 8 mm to pre-a... 48 2e-04
emb|AW756344|AW756344 sl19e03.y1 Gm-c1036 Glycine max cDNA clone... 47 6e-04
emb|AI494962|AI494962 sa93c01.y1 Gm-c1004 Glycine max cDNA clone... 40 0.001
emb|AW256509|AW256509 EST304646 KV2 Medicago truncatula cDNA clo... 45 0.003
gb|U19908|PTU19908 Paramecium tetraurelia K+ channel (PaK2) gene... 42 0.015
20 emb|AW256736|AW256736 EST304873 KV2 Medicago truncatula cDNA clo... 40 0.016
emb|AI488021|AI488021 EST246343 tomato ovary, TAMU Lycopersicon ... 42 0.020
emb|AI729515|AI729515 BNLGHi13574 Six-day Cotton fiber Gossypium... 41 0.027
emb|AW687023|AW687023 NF005B04RT1F1032 Developing root Medicago ... 39 0.13
emb|AL163552|LMFL5075 Leishmania major Friedlin chromosome 14 co... 38 0.25
25 emb|AQ847838|AQ847838 LMAJFV1_lm42a03.y1 Leishmania major FV1 ra... 38 0.25
emb|AI748348|AI748348 sb51d12.y1 Gm-c1016 Glycine max cDNA clone... 38 0.35
emb|AL031530|SPCC970 S.pombe chromosome III cosmid c970. 38 0.35
gb|U33057|SCD9717 Saccharomyces cerevisiae chromosome IV cosmids... 37 0.48
gb|M84796|YSCEUG1 Saccharomyces cerevisiae endoplasmic reticulum... 37 0.48
30 emb|AF099095|AF099095 Samanea saman pulvinus inward-rectifying c... 37 0.66
emb|AI775282|AI775282 EST256382 tomato resistant, Cornell Lycope... 36 0.90
emb|AF053314|AF053314 Exophiala dermatitidis chitin synthase 3 (... 36 1.2
emb|AQ947260|AQ947260 Sheared DNA-45L23.TR Sheared DNA Trypanoso... 31 1.5
emb|AC016528|AC016528 Leishmania major chromosome 35 clone L4123... 35 1.7
35 emb|AI781524|AI781524 EST262403 tomato susceptible, Cornell Lyco... 31 2.0
gb|U28374|YSCD9740 Saccharomyces cerevisiae chromosome IV cosmid... 35 2.3
emb|AW399566|AW399566 EST310066 L. pennellii trichome, Cornell U... 35 2.3
gb|BE034738|BE034738 ML03G05 ML Mesembryanthemum crystallinum cD... 35 2.3
emb|AW929752|AW929752 EST354022 tomato flower buds 8 mm to pre-a... 35 2.3
40 emb|AW648153|AW648153 EST326607 tomato germinating seedlings, TA... 35 2.3
gb|M74798|HEVHMGR3A Hevea brasiliensis 3-hydroxy-3-methylglutary... 34 4.4
emb|AW728887|AW728887 GA__Ea0018B11 Gossypium arboreum 7-10 dpa ... 34 4.4
Query= athcallga_s_at 17500_s_at/id_source
/description emb|cab42906.1| (al049862) calmodulin-like
45 protein [arabidopsis thaliana] /blast_score 6.00e-99
(827 letters)
Database: plantfungal
661,018 sequences; 426,114,510 total letters
50 Searching.....done
Score E
Sequences producing significant alignments: (bits) Value
55 emb|AI489346|AI489346 EST247685 tomato ovary, TAMU Lycopersicon ... 79 2e-28
emb|AW350323|AW350323 GM210007B20E12R Gm-r1021 Glycine max cDNA ... 80 2e-27
emb|AW509006|AW509006 si38h07.y1 Gm-r1030 Glycine max cDNA clone... 79 2e-26
emb|AW685404|AW685404 NF028H10NR1F1000 Nodulated root Medicago t... 74 2e-24
60 emb|AW781320|AW781320 sk68d07.y1 Gm-c1016 Glycine max cDNA clone... 86 2e-24
emb|AI897832|AI897832 EST267275 tomato ovary, TAMU Lycopersicon ... 78 1e-23

- emb|AW102460|AW102460 sd88d10.y1 Gm-c1009 Glycine max cDNA clone... 70 2e-22
emb|AI490284|AI490284 EST248610 tomato ovary, TAMU Lycopersicon ... 103 2e-22
emb|AI487362|AI487362 EST245684 tomato ovary, TAMU Lycopersicon ... 72 3e-20
gb|BE125690|BE125690 DG1_54_A02.g1_A002 Dark Grown 1 (DG1) Sorgh... 96 3e-19
5 emb|X80231|LTCAMA L.tarentolae CAM A gene for calmodulin. 73 1e-18
emb|AL115248|CNS01C9K Botrytis cinerea strain T4 cDNA library un... 65 4e-18
dbj|D10521|TETCALW T.pyriformis mRNA for calmodulin. 73 7e-18
gb|M76407|SLECALMODU Stylonychia lemnae calmodulin gene, complet... 74 9e-18
emb|AF007889|AF007889 Symbiodinium microadriaticum calmodulin (S... 74 1e-17
10 emb|AF078679|AF078679 Olea europaea calcium-binding protein (PCA... 57 2e-17
emb|X56511|TBCALUBG T. brucei genes for calmodulin, EFH5 and ubi... 77 2e-17
emb|X52096|TCCALB2 Trypanosoma cruzi CalA2 calmodulin gene. 77 2e-17
emb|AF030033|AF030033 Phaseolus vulgaris calmodulin (CaM) mRNA, ... 75 2e-17
emb|X90560|PPCAMPROT Physcomitrella patens mRNA for calmodulin. 71 2e-17
15 gb|U91642|POU91642 Pleurotus ostreatus calmodulin mRNA, complete... 75 2e-17
emb|AF078680|AF078680 Olea europaea calcium-binding protein (PCA... 57 2e-17
emb|X85091|MPCAM M.pyrifera mRNA for calmodulin. 74 2e-17
gb|M83535|PHTCALPIA P.infestans calmodulin (calA) gene, complete... 75 2e-17
emb|Y08373|TGCM T.gondii mRNA for calmodulin. 74 2e-17
20 gb|C96396|C96396 C96396 Marchantia polymorpha immature sex organ... 73 3e-17
emb|AL113315|CNS01ARV Botrytis cinerea strain T4 cDNA library un... 72 3e-17
emb|AB044286|AB044286 Chara corallina ccam mRNA for calmodulin, ... 75 4e-17
emb|AB041712|AB041712 Chara corallina cccam2 mRNA for calmodulin... 75 4e-17
emb|AB041711|AB041711 Chara corallina cccam1 mRNA for calmodulin... 75 4e-17
25 gb|J05116|ACKCAL A.klebsiana calmodulin gene, complete cds. 75 4e-17
emb|X70923|NCCALMOE N.crassa mRNA for calmodulin. 74 6e-17
emb|AI328739|AI328739 a6d02ne.fl Neurospora crassa evening cDNA ... 74 6e-17
emb|AF034964|AF034964 Glomerella cingulata calmodulin (cam) mRNA... 74 6e-17
gb|U12505|HCCMD Histoplasma capsulatum 186AS calmodulin mRNA, co... 74 8e-17
30 gb|M34540|PARCAM P.tetraurelia calmodulin gene, complete cds. 74 8e-17
gb|S68025|S68025 CAM=calmodulin [Paramecium tetraurelia, Genomic... 74 8e-17
emb|AW164773|AW164773 se77e12.y1 Gm-c1023 Glycine max cDNA clone... 64 8e-17
emb|AW719875|AW719875 LjNEST11d4r Lotus japonicus nodule library... 57 8e-17
emb|AW830090|AW830090 sm22a12.y1 Gm-c1028 Glycine max cDNA clone... 64 8e-17
35 emb|AW126204|AW126204 N100049e rootphos(-) Medicago truncatula c... 57 8e-17
emb|X52242|TTCALM T.thermophila mRNA for calmodulin. 73 1e-16
gb|L02963|NEUCLMDLN Neurospora crassa calmodulin mRNA, complete ... 74 1e-16
emb|AW625406|AW625406 EST319229 tomato radicle, 5 d post-imbibit... 62 1e-16
gb|K02944|TRBCMRSG Trypanosoma brucei gambiense calmodulin genes... 73 2e-16
40 gb|M88307|BNACALM Brassica juncea calmodulin mRNA, complete cds. 73 2e-16
gb|U10150|BNU10150 Brassica napus Naehan calmodulin (bcm1) mRNA,... 73 2e-16
emb|X89890|BPCALMGEN B.pilosa mRNA for calmodulin. 73 2e-16
emb|AW099396|AW099396 sd39h01.y1 Gm-c1016 Glycine max cDNA clone... 76 2e-16
emb|AW101324|AW101324 sd77e09.y1 Gm-c1009 Glycine max cDNA clone... 59 2e-16
45 emb|AL112713|CNS01AB5 Botrytis cinerea strain T4 cDNA library un... 73 2e-16
emb|AL114582|CNS01BR2 Botrytis cinerea strain T4 cDNA library un... 74 2e-16
emb|AL112170|CNS019W2 Botrytis cinerea strain T4 cDNA library un... 74 2e-16
emb|AL114124|CNS01BEC Botrytis cinerea strain T4 cDNA library un... 74 2e-16
emb|AL115056|CNS01C48 Botrytis cinerea strain T4 cDNA library un... 73 2e-16
50 emb|AL116760|CNS01DFK Botrytis cinerea strain T4 cDNA library un... 73 2e-16
emb|AW573768|AW573768 EST316359 GVN Medicago truncatula cDNA clo... 72 2e-16
emb|Y13784|MSCALMODU Mougeotia scalaris mRNA for calmodulin. 70 3e-16
emb|AI727960|AI727960 BNLGHi9833 Six-day Cotton fiber Gossypium ... 73 3e-16
emb|AA660367|AA660367 00239 MtrHE Medicago truncatula cDNA 5' si... 71 3e-16
55 emb|AW164628|AW164628 se74e01.y1 Gm-c1023 Glycine max cDNA clone... 60 3e-16
emb|AF150059|AF150059 Brassica napus calmodulin (CaM1) mRNA, com... 72 3e-16
emb|AW738989|AW738989 gb23c06.y1 Moss EST library PPN Physcomitr... 73 3e-16
gb|U48693|TAU48693 Triticum aestivum calmodulin TaCaM3-1 mRNA, c... 73 4e-16
gb|M27303|BLYCAMA Barley cam gene encoding calmodulin, complete ... 73 4e-16
60 gb|BE033450|BE033450 ME02B08 ME Mesembryanthemum crystallinum cD... 73 4e-16
emb|AF064552|AF064552 Apium graveolens calmodulin mRNA, complete... 73 4e-16

gb|S81594|S81594 auxin-regulated calmodulin [*Vigna radiata*=mung ... 73 4e-16
 gb|L20691|VIRCALMOD *Vigna radiata* calmodulin mRNA, complete cds. 73 4e-16
 emb|AW730911|AW730911 GA__Ea0029I11 *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 gb|BE036340|BE036340 MO23E04 *MO Mesembryanthemum crystallinum* cD... 73 4e-16
 5 emb|AF030032|AF030032 *Phaseolus vulgaris* calmodulin (CaM) mRNA, ... 73 4e-16
 gb|L01431|SOYSCAM2X Soybean calmodulin (SCaM-2) mRNA, complete cds. 73 4e-16
 emb|Y09853|CACAM *Cicer arietinum* mRNA for CaM protein. 73 4e-16
 gb|L01432|SOYSCAM3X Soybean calmodulin (SCaM-3) mRNA, complete cds. 73 4e-16
 gb|U49104|TAU49104 *Triticum aestivum* calmodulin TaCaM3-3 mRNA, c... 73 4e-16
 10 gb|U49105|TAU49105 *Triticum aestivum* calmodulin TaCaM4-1 mRNA, c... 73 4e-16
 emb|AF030034|AF030034 *Phaseolus vulgaris* calmodulin (CaM) mRNA, ... 73 4e-16
 emb|AW728030|AW728030 GA__Ea0029H21 *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 gb|L20507|VIRCALMODU *Vigna radiata* (clone pMBCaM-1) calmodulin m... 73 4e-16
 gb|U48242|TAU48242 *Triticum aestivum* calmodulin TaCaM1-1 mRNA, c... 73 4e-16
 15 gb|M80836|PETCAM81 *Petunia hybrida* CAM81 mRNA,. 73 4e-16
 gb|U49103|TAU49103 *Triticum aestivum* calmodulin TaCaM3-2 mRNA, c... 73 4e-16
 emb|X52398|MSCAL1 Alfalfa cal1 mRNA for calmodulin. 73 4e-16
 gb|U48688|TAU48688 *Triticum aestivum* calmodulin TaCaM1-2 mRNA, c... 73 4e-16
 gb|L01430|SOYSCAM1X Soybean calmodulin (SCaM-1) mRNA, complete cds. 73 4e-16
 20 emb|AW927068|AW927068 HVSMEg0009G21 *Hordeum vulgare* pre-anthesis... 73 4e-16
 gb|U48689|TAU48689 *Triticum aestivum* calmodulin TaCaM1-3 mRNA, c... 73 4e-16
 gb|M80831|PETCALPRO *Petunia hybrida* CAM53 mRNA, complete cds. 73 4e-16
 emb|AW348582|AW348582 GM210002B22C3R *Gm-r1021 Glycine max* cDNA 3... 73 4e-16
 emb|X59751|DCCAM1G Carrot Ccam-1 gene for calmodulin. 73 4e-16
 25 emb|AW775754|AW775754 EST334819 *DSIL Medicago truncatula* cDNA cl... 73 4e-16
 gb|BE052400|BE052400 GA__Ea0001L24f *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 emb|AW666735|AW666735 GA__Ea0005N08 *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 gb|U13882|PSU13882 *Pisum sativum* Alaska calmodulin mRNA, complet... 73 4e-16
 gb|BE051931|BE051931 GA__Ea0002G11f *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 30 emb|AW666619|AW666619 GA__Ea0005C16 *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 emb|AW108833|AW108833 gate0001L24f *Gossypium arboreum* 7-10 dpa f... 73 4e-16
 emb|Z12839|LLCALMOD *L.longiflorum* mRNA encoding calmodulin. 73 4e-16
 gb|L18912|LILCALMODU *Lilium longiflorum* calmodulin mRNA, complet... 73 4e-16

35

Query= af067605_s_at 17511_s_at /id_source genbank /description
 gb|aab71482.1| (ac002294) similar to s-linalool synthase
 gp|u58314|1491939 [*arabidopsis thaliana*] /blast_score 0
 (2661 letters)

40

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

45

Score E

Sequences producing significant alignments: (bits) Value

50 gb|U58314|CBU58314 *Clarkia breweri* S-linalool synthase (Lis) mRN... 146 e-171
 emb|AF067603|AF067603 *Clarkia breweri* linalool synthase 2 (LIS2)... 149 e-154
 emb|AF067602|AF067602 *Clarkia concinna* linalool synthase gene, c... 112 1e-53
 emb|AF097310|AF097310 *Stevia rebaudiana* kaurene synthase (KS1-1)... 88 5e-31
 emb|AF097311|AF097311 *Stevia rebaudiana* kaurene synthase (KS22-1... 88 5e-31
 emb|AF067604|AF067604 *Oenothera arizonica* linalool synthase-like... 75 5e-24
 55 emb|AF067601|AF067601 *Clarkia breweri* linalool synthase 1 (LIS1)... 86 1e-17
 gb|U43904|CMU43904 *Cucurbita maxima* ent-kaurene synthase B mRNA,... 63 5e-17
 emb|AI485628|AI485628 EST243949 tomato ovary, TAMU *Lycopersicon* ... 60 3e-15
 emb|AI485623|AI485623 EST243944 tomato ovary, TAMU *Lycopersicon* ... 55 9e-14
 gb|U92267|AGU92267 *Abies grandis* gamma-humulene synthase mRNA, c... 45 2e-10
 60 gb|U50768|AGU50768 *Abies grandis* abietadiene synthase (ac22) mRN... 58 6e-10
 emb|AW255432|AW255432 ML454 peppermint glandular trichome *Mentha*... 56 1e-08

	emb AW255334 AW255334 ML343 peppermint glandular trichome Mentha...	56	1e-08
	emb AF233894 AF233894 Perilla citriodora limonene synthase mRNA,...	62	2e-08
	gb U87909 AGU87909 Abies grandis pinene synthase (AG3.18) mRNA, ...	61	5e-08
	dbj D49368 D49368 Perilla frutescens mRNA for limonene cyclase, ...	61	5e-08
5	emb AF006195 AF006195 Abies grandis E-alpha-bisabolene synthase ...	55	7e-08
	emb AF006194 AF006194 Abies grandis E-alpha-bisabolene synthase ...	55	7e-08
	emb AI487110 AI487110 EST245432 tomato ovary, TAMU Lycopersicon ...	60	7e-08
	emb AW616561 AW616561 EST322972 L. hirsutum trichome, Cornell Un...	39	8e-08
	gb U63652 PSU63652 Pisum sativum ent-kaurene synthase A (LS) mRN...	60	1e-07
10	gb U92266 AGU92266 Abies grandis d-selinene synthase mRNA, compl...	60	1e-07
	emb AW738064 AW738064 EST339491 tomato flower buds, anthesis, Co...	38	1e-07
	emb AI491074 AI491074 EST241783 tomato shoot, Cornell Lycopersic...	38	1e-07
	emb AW617193 AW617193 EST323604 L. hirsutum trichome, Cornell Un...	40	2e-07
	emb AW616893 AW616893 EST323304 L. hirsutum trichome, Cornell Un...	40	2e-07
15	emb AF034545 AF034545 Stevia rebaudiana copalyl pyrophosphate sy...	59	2e-07
	emb AF271259 AF271259 Perilla frutescens terpene synthase mRNA, ...	59	2e-07
	emb AW616634 AW616634 EST323045 L. hirsutum trichome, Cornell Un...	39	3e-07
	emb AW616591 AW616591 EST323002 L. hirsutum trichome, Cornell Un...	39	3e-07
	emb AW616079 AW616079 EST296838 L. hirsutum trichome, Cornell Un...	39	3e-07
20	emb AW616201 AW616201 EST307240 L. hirsutum trichome, Cornell Un...	39	3e-07
	emb AW616573 AW616573 EST322984 L. hirsutum trichome, Cornell Un...	39	3e-07
	emb AW616493 AW616493 EST322904 L. hirsutum trichome, Cornell Un...	39	3e-07
	emb AW616908 AW616908 EST323319 L. hirsutum trichome, Cornell Un...	39	3e-07
	emb AW617347 AW617347 EST323758 L. hirsutum trichome, Cornell Un...	39	3e-07
25	emb AW617467 AW617467 EST323878 L. hirsutum trichome, Cornell Un...	39	3e-07
	emb AW617665 AW617665 EST324076 L. hirsutum trichome, Cornell Un...	39	3e-07
	emb AW617376 AW617376 EST323787 L. hirsutum trichome, Cornell Un...	39	3e-07
	emb AF049905 AF049905 Cucurbita maxima copalyl diphosphate synth...	58	3e-07
	emb AW616328 AW616328 EST322739 L. hirsutum trichome, Cornell Un...	38	5e-07
30	emb AW624730 AW624730 EST322675 tomato flower buds 3-8 mm, Corne...	37	6e-07
	emb AB042424 AB042424 Croton sublyratus cps mRNA for copalyl dip...	57	7e-07
	emb AW254843 AW254843 ML1265 peppermint glandular trichome Menth...	57	7e-07
	emb AW254789 AW254789 ML1071 peppermint glandular trichome Menth...	57	7e-07
	emb AW254821 AW254821 ML1244 peppermint glandular trichome Menth...	57	7e-07
35	emb AW255149 AW255149 ML145 peppermint glandular trichome Mentha...	57	7e-07
	emb AW255044 AW255044 ML1227 peppermint glandular trichome Menth...	57	7e-07
	emb AF139207 AF139207 Abies grandis (-)-limonene/(-)-alpha-pinen...	57	9e-07
	emb AW616366 AW616366 EST322777 L. hirsutum trichome, Cornell Un...	36	2e-06
	emb AW255042 AW255042 ML1225 peppermint glandular trichome Menth...	55	2e-06
40	emb AW255052 AW255052 ML1347 peppermint glandular trichome Menth...	55	2e-06
	emb AW254888 AW254888 ML1312 peppermint glandular trichome Menth...	55	2e-06
	emb AW687409 AW687409 NF009C09RT1F1069 Developing root Medicago ...	54	5e-06
	emb AB015675 AB015675 Lycopersicon esculentum CPS mRNA for copal...	54	5e-06
	emb AF051901 AF051901 Salvia officinalis (+)-sabinene synthase m...	54	5e-06
45	emb AF175323 AF175323 Mentha longifolia limonene synthase mRNA, ...	54	6e-06
	gb L13459 MHC4SLSP Mentha spicata 4S-limonene synthase mRNA, com...	54	6e-06
	emb AW255678 AW255678 ML735 peppermint glandular trichome Mentha...	53	1e-05
	emb AF139205 AF139205 Abies grandis beta-phellandrene synthase (...)	52	2e-05
	emb AW617714 AW617714 EST324125 L. hirsutum trichome, Cornell Un...	33	2e-05
50	emb AF154125 AF154125 Artemisia annua (3R)-linalool synthase (QH...	51	4e-05
	emb AF049906 AF049906 Cucurbita maxima copalyl diphosphate synth...	51	4e-05
	emb AW684730 AW684730 NF020C02NR1F1000 Nodulated root Medicago t...	51	4e-05
	gb U87908 AGU87908 Abies grandis myrcene synthase (AG2.2) mRNA, ...	51	6e-05
	emb AW255083 AW255083 ML1378 peppermint glandular trichome Menth...	51	6e-05
55	emb AW254876 AW254876 ML1300 peppermint glandular trichome Menth...	49	2e-04
	gb U48796 TBU48796 Taxus brevifolia taxadiene synthase (TDC1) mR...	49	2e-04
	emb AF051899 AF051899 Salvia officinalis 1,8-cineole synthase mR...	48	4e-04
	emb AF006193 AF006193 Abies grandis (-)-4S-limonene synthase mRN...	47	5e-04
	emb AF154124 AF154124 Artemisia annua (3R)-linalool synthase (QH...	46	0.001
60	emb AF139206 AF139206 Abies grandis terpinolene synthase (agc9) ...	45	0.004
	emb AW687308 AW687308 NF008C02RT1F1008 Developing root Medicago ...	44	0.005

	emb AF051900 AF051900 <i>Salvia officinalis</i> (+)-bornyl diphosphate ...	43	0.009
	emb AF212433 AF212433 <i>Capsicum annuum</i> UV-induced sesquiterpene c...	43	0.009
	emb AF061285 AF061285 <i>Capsicum annuum</i> sesquiterpene cyclase mRNA...	43	0.009
	emb AW685590 AW685590 NF029D03NR1F1000 Nodulated root <i>Medicago t...</i>	34	0.014
5	emb AW125997 AW125997 N100193e rootphos(-) <i>Medicago truncatula</i> c...	34	0.015
	emb AW622483 AW622483 EST313271 tomato root during/after fruit s...	42	0.018
	emb AW254970 AW254970 ML1141 peppermint glandular trichome <i>Menth...</i>	41	0.034
	emb AB006530 AB006530 <i>Citrullus lanatus</i> Sat gene for serine acet...	41	0.046
	emb AW559431 AW559431 EST314479 DSIR <i>Medicago truncatula</i> cDNA cl...	32	0.065
10	emb AW255471 AW255471 ML495 peppermint glandular trichome <i>Mentha...</i>	40	0.087
	emb AB005744 AB005744 <i>Perilla frutescens</i> DNA for 1-limonene synt...	40	0.087
	emb AW616571 AW616571 EST322982 <i>L. hirsutum</i> trichome, Cornell Un...	30	0.17
	emb AW617415 AW617415 EST323826 <i>L. hirsutum</i> trichome, Cornell Un...	30	0.17
	gb U20189 HMU20189 <i>Hyoscyamus muticus</i> clone cVS2 vetispiradiene ...	39	0.23
15	emb AF042382 AF042382 <i>Solanum tuberosum</i> vetispiradiene synthase ...	38	0.31
	emb AF043300 AF043300 <i>Solanum tuberosum</i> putative vetispiradiene ...	38	0.31
	emb AB022720 AB022720 <i>Solanum tuberosum</i> PVS3 mRNA for vetispirad...	38	0.31
	gb L32134 RCCCASSYNT <i>Ricinus communis</i> casbene synthase mRNA.	38	0.43
	emb AW043070 AW043070 ST28H10 Pine TriplEx shoot tip library Pin...	38	0.43
20	emb AI940878 AI940878 sb79b02.y1 Gm-c1010 Glycine max cDNA clone...	38	0.43
	emb AB022719 AB022719 <i>Solanum tuberosum</i> PVS2 mRNA for vetispirad...	37	0.58
	emb AF043298 AF043298 <i>Solanum tuberosum</i> putative vetispiradiene ...	37	0.58
	emb AF043299 AF043299 <i>Solanum tuberosum</i> putative vetispiradiene ...	37	0.58
	emb AJ001452 FVAJ1452 <i>Fragaria vesca</i> partial mRNA for putative s...	30	0.70
25	emb AB022598 AB022598 <i>Solanum tuberosum</i> PVS1 mRNA for vetispirad...	36	1.1
	emb AB023816 AB023816 <i>Solanum tuberosum</i> PVS4 mRNA for vetispirad...	36	1.1

30 Query= d78606_s_at 17522_s_at /id_source genbank /description
dbj|baa28538.1| (d78606) cytochrome p450 monooxygenase [arabidopsis
thaliana] /blast_score 0
(1580 letters)

35 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	
40	Sequences producing significant alignments:		(bits)	Value
	emb AB001379 AB001379 <i>Glycyrrhiza echinata</i> CYP81E1 mRNA for cyto...	376	e-149	
	emb AB022732 AB022732 <i>Glycyrrhiza echinata</i> CYP Ge-31 mRNA for cy...	376	e-149	
	emb AJ238439 CAR238439 <i>Cicer arietinum</i> mRNA for a cytochrome P45...	377	e-147	
45	emb AJ012581 CAR012581 <i>Cicer arietinum</i> mRNA for cytochrome P450.	376	e-147	
	emb AJ239051 CAR239051 <i>Cicer arietinum</i> mRNA for cytochrome P450 ...	255	e-145	
	emb AB025016 AB025016 <i>Lotus japonicus</i> mRNA for cytochrome P450, ...	340	e-142	
	emb AJ249800 CAR249800 <i>Cicer arietinum</i> partial mRNA for cytochro...	352	3e-96	
	emb AJ000478 HTCYP81L <i>Helianthus tuberosus</i> mRNA for cytochrome P...	225	4e-84	
50	emb AJ000477 HTCYP81C <i>Helianthus tuberosus</i> mRNA for cytochrome P...	225	4e-84	
	emb AW185361 AW185361 se90e02.y1 Gm-c1027 Glycine max cDNA clone...	302	5e-81	
	emb AJ249801 CAR249801 <i>Cicer arietinum</i> partial mRNA for cytochro...	298	6e-80	
	emb AF082028 AF082028 <i>Hemerocallis</i> hybrid cultivar senescence-as...	209	4e-76	
	emb AW733691 AW733691 sk83g07.y1 Gm-c1016 Glycine max cDNA clone...	277	2e-73	
55	emb AW307234 AW307234 sf54d12.y1 Gm-c1009 Glycine max cDNA clone...	275	6e-73	
	emb AW234443 AW234443 sf25c03.y1 Gm-c1028 Glycine max cDNA clone...	273	3e-72	
	emb AW775904 AW775904 EST334969 DSIL <i>Medicago truncatula</i> cDNA cl...	242	3e-71	
	emb AW171738 AW171738 N100632e rootphos(-) <i>Medicago truncatula</i> c...	265	7e-70	
	emb AI725744 AI725744 BNLGHi12803 Six-day Cotton fiber <i>Gossypium</i> ...	193	3e-63	
60	emb AI729126 AI729126 BNLGHi12694 Six-day Cotton fiber <i>Gossypium</i> ...	188	2e-62	
	emb AI495626 AI495626 sb11c08.y1 Gm-c1004 Glycine max cDNA clone...	236	5e-61	

- emb|AW329224|AW329224 N200436e rootphos(-) Medicago truncatula c... 228 1e-58
 emb|AW932147|AW932147 EST357990 tomato fruit mature green, TAMU ... 226 3e-58
 emb|AW100311|AW100311 sd22g12.y2 Gm-c1012 Glycine max cDNA clone... 218 8e-56
 emb|AF014802|AF014802 Eschscholzia californica (S)-N-methylcocla... 177 9e-56
 5 emb|AI774414|AI774414 EST255514 tomato resistant, Cornell Lycopen... 152 9e-56
 emb|AW171672|AW171672 N100566e rootphos(-) Medicago truncatula c... 216 3e-55
 emb|AF029856|AF029856 Sorghum bicolor cytochrome P450 CYP98A1 (C... 164 2e-54
 emb|AI776121|AI776121 EST257209 tomato resistant, Cornell Lycopen... 116 1e-51
 emb|AV412147|AV412147 AV412147 Lotus japonicus young plants (two... 204 2e-51
 10 dbj|E13663|E13663 cDNA encoding cytochrome P450 which is induced... 116 5e-50
 dbj|D83968|SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)... 116 5e-50
 emb|AW676742|AW676742 DG1_14_A08.g1_A002 Dark Grown 1 (DG1) Sorg... 116 1e-49
 emb|AI731081|AI731081 BNLGHi8648 Six-day Cotton fiber Gossypium ... 198 1e-49
 emb|AW257188|AW257188 EST305325 KV2 Medicago truncatula cDNA clo... 152 2e-49
 15 emb|AW309826|AW309826 sf25c03.x1 Gm-c1028 Glycine max cDNA clone... 196 5e-49
 emb|Y10492|GMC450CP5 G.max mRNA for putative cytochrome P450, cl... 117 5e-48
 emb|AF022461|AF022461 Glycine max cytochrome P450 monooxygenase ... 108 1e-47
 emb|AW736144|AW736144 EST332120 KV3 Medicago truncatula cDNA clo... 190 2e-47
 dbj|D86351|D86351 Glycine max CYP93A2 mRNA for cytochrome P-450,... 111 2e-47
 20 emb|X71657|SMCYPEG7 S.melongena CYP76A2 mRNA for hydroxylase. 160 4e-47
 emb|AI973839|AI973839 sd11c06.y1 Gm-c1020 Glycine max cDNA clone... 116 7e-47
 emb|AB015762|AB015762 Nicotiana tabacum mRNA for cytochrome P450... 150 7e-47
 emb|X71658|SMCYPEG8 S.melongena CYP76A1 mRNA. 161 7e-47
 emb|AW616170|AW616170 EST307209 L. hirsutum trichome, Cornell Un... 124 9e-47
 25 emb|Y10982|GMP450CP6 Glycine max mRNA for cytochrome P450-like p... 159 9e-47
 emb|Y09920|HT7EC0DET Helianthus tuberosus mRNA for 7-ethoxycouma... 156 1e-46
 emb|Y10098|HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... 156 1e-46
 emb|AF124372|AF124372 Nicotiana tabacum NT7 mRNA, partial cds. 145 1e-46
 emb|AW728802|AW728802 GA_Ea0028I12 Gossypium arboreum 7-10 dpa ... 168 2e-46
 30 emb|AF156976|AF156976 Gerbera hybrida flavone synthase II (CYP93... 103 2e-46
 emb|X96784|NTP450GEN N.tabacum cytochrome P-450 gene. 162 6e-46
 dbj|D14590|D14590 Campanula medium mRNA for flavonoid 3',5'-hydr... 157 1e-45
 emb|AW616482|AW616482 EST322893 L. hirsutum trichome, Cornell Un... 124 2e-45
 emb|AW617814|AW617814 EST324213 L. hirsutum trichome, Cornell Un... 124 2e-45
 35 emb|AF155332|AF155332 Petunia x hybrida flavonoid 3'-hydroxylase... 183 2e-45
 emb|AW616075|AW616075 EST296834 L. hirsutum trichome, Cornell Un... 124 5e-45
 gb|U72654|EGU72654 Eustoma grandiflorum flavonoid 3'5'-hydroxyla... 160 6e-45
 gb|M32885|AVOCYP Avocado cytochrome P-450LXXIA1 (cyp71A1) mRNA, ... 160 8e-45
 emb|AW679544|AW679544 WS1_29_D01.g1_A002 Water-stressed 1 (WS1) ... 101 8e-45
 40 emb|AW102198|AW102198 sd84f03.y1 Gm-c1009 Glycine max cDNA clone... 181 1e-44
 dbj|D14589|D14589 Eustoma russellianum mRNA for flavonoid 3',5'-... 160 2e-44
 emb|AJ011862|CRO011862 Catharanthus roseus mRNA for flavonoid 3'... 161 2e-44
 emb|AW034115|AW034115 EST277610 tomato callus, TAMU Lycopersicon... 119 6e-44
 emb|Y10491|GMC450CP4 G.max mRNA for putative cytochrome P450, cl... 149 7e-44
 45 emb|AW309498|AW309498 sf20c05.x1 Gm-c1028 Glycine max cDNA clone... 178 1e-43
 emb|AF135485|AF135485 Glycine max cytochrome P450 monooxygenaseC... 100 1e-43
 gb|U29333|PSU29333 Pisum sativum novel wound-inducible cytochrom... 157 1e-43
 emb|AW616143|AW616143 EST296912 L. hirsutum trichome, Cornell Un... 128 1e-43
 emb|AW616066|AW616066 EST296823 L. hirsutum trichome, Cornell Un... 122 1e-43
 50 emb|AW255096|AW255096 ML139 peppermint glandular trichome Mentha... 162 2e-43
 emb|AI779370|AI779370 EST260249 tomato susceptible, Cornell Lyco... 160 3e-43
 emb|AJ243804|CAR243804 Cicer arietinum mRNA for cytochrome P450 ... 104 7e-43
 emb|AW651341|AW651341 EST329795 tomato germinating seedlings, TA... 156 9e-43
 gb|L07634|PHVC4HYDRO Phaseolus aureus cinnamate 4-hydroxylase mR... 148 3e-42
 55 emb|AB023636|AB023636 Glycyrrhiza echinata CYP Ge-8 mRNA for cyt... 107 4e-42
 emb|AW728587|AW728587 GA_Ea0017C12 Gossypium arboreum 7-10 dpa ... 172 5e-42
 emb|Y10489|GMC450CP1 G.max mRNA for putative cytochrome P450, cl... 144 6e-42
 emb|X92437|GMCYP73 Glycine max mRNA for cinnamic acid 4-hydroxyl... 146 8e-42
 emb|AW668189|AW668189 GA_Ea0013B20 Gossypium arboreum 7-10 dpa ... 155 8e-42
 60 emb|AI731481|AI731481 BNLGHi9879 Six-day Cotton fiber Gossypium ... 171 9e-42
 emb|AB024931|AB024931 Lotus japonicus mRNA for cytochrome P450, ... 105 9e-42

dbj|D87520|D87520 Glycyrrhiza echinata suspension-cultured cells... 146 1e-41
 emb|AB006790|AB006790 Petunia x hybrida IMT-2 mRNA for cytochrom... 144 1e-41
 emb|AB001380|AB001380 Glycyrrhiza echinata CYP93B1 mRNA for cyto... 104 2e-41
 emb|AF195800|AF195800 Medicago sativa isoflavone synthase 1 (ifs... 101 3e-41
 5 emb|AB022733|AB022733 Glycyrrhiza echinata CYP Ge-51 mRNA for cy... 104 4e-41
 emb|AW560648|AW560648 EST315696 DSIR Medicago truncatula cDNA cl... 169 5e-41
 emb|AF195798|AF195798 Glycine max isoflavone synthase 1 (ifs1) m... 100 6e-41
 emb|AF135484|AF135484 Glycine max cytochrome P450 monooxygenase ... 100 6e-41
 emb|AF195811|AF195811 Trifolium pratense isoflavone synthase 2 (... 100 6e-41
 10 emb|AF195810|AF195810 Trifolium pratense isoflavone synthase 1 (... 100 6e-41
 emb|AF195808|AF195808 Vigna radiata isoflavone synthase 3 (ifs3)... 100 6e-41
 emb|AF195807|AF195807 Vigna radiata isoflavone synthase 2 (ifs2)... 100 6e-41
 emb|AF195802|AF195802 Medicago sativa isoflavone synthase 3 (ifs... 100 6e-41
 emb|AF188612|AF188612 Callistephus chinensis flavone synthase II... 94 8e-41
 15 emb|AF022458|AF022458 Glycine max cytochrome P450 monooxygenase ... 168 9e-41
 emb|AF195812|AF195812 Pisum sativum isoflavone synthase 1 (ifs1)... 100 2e-40
 emb|AF195817|AF195817 Beta vulgaris isoflavone synthase 2 (ifs2)... 100 2e-40
 emb|AW560673|AW560673 EST315721 DSIR Medicago truncatula cDNA cl... 167 2e-40
 emb|AW351157|AW351157 GM210010B20F8R Gm-r1021 Glycine max cDNA 3... 167 2e-40
 20

Query= atu40856_s_at 17544_s_at /id_source
 /description gb|aac49282.1| (u40856) aigl [arabidopsis
 thaliana] /blast_score 1.00e-150
 25 (1381 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

30 Searching.....done

		Score	E
	Sequences producing significant alignments:	(bits)	Value
35	gb U64925 NTU64925 Nicotiana tabacum geranylgeranylated protein ...	260	1e-68
	emb AW625701 AW625701 EST319608 tomato radicle, 5 d post-imbibit...	228	6e-59
	emb AW720227 AW720227 LjNEST17c4r Lotus japonicus nodule library...	219	4e-56
	emb AW220184 AW220184 EST302667 tomato root during/after fruit s...	208	7e-53
	emb AI774580 AI774580 EST255680 tomato resistant, Cornell Lycopersicon...	173	2e-42
40	emb AW685484 AW685484 NF030E02NR1F1000 Nodulated root Medicago t...	171	2e-41
	emb AI443867 AI443867 sa44d09.y1 Gm-c1004 Glycine max cDNA clone...	170	3e-41
	emb AW397252 AW397252 sg76f06.y1 Gm-c1007 Glycine max cDNA clone...	168	1e-40
	emb AW033368 AW033368 EST276939 tomato callus, TAMU Lycopersicon...	162	5e-39
	emb AV417858 AV417858 AV417858 Lotus japonicus young plants (two...	153	4e-36
45	emb AI780050 AI780050 EST260929 tomato susceptible, Cornell Lyco...	138	9e-32
	emb AW039095 AW039095 EST281068 tomato mixed elicitor, BTI Lycop...	111	2e-23
	emb AI780139 AI780139 EST261018 tomato susceptible, Cornell Lyco...	86	7e-16
	emb AW164180 AW164180 Ljirnpes21-672-c8 Ljirnp Lambda HybriZap ...	84	2e-15
	emb AI781596 AI781596 EST262475 tomato susceptible, Cornell Lyco...	75	1e-12
50	emb AW774764 AW774764 EST333915 KV3 Medicago truncatula cDNA clo...	62	7e-09
	emb AW348781 AW348781 GM210003A22H11R Gm-r1021 Glycine max cDNA ...	54	2e-06
	emb AI491210 AI491210 EST241919 tomato shoot, Cornell Lycopersic...	29	0.010
	emb AW651526 AW651526 EST329980 tomato germinating seedlings, TA...	29	0.011
	emb AW220594 AW220594 EST296979 tomato fruit mature green, TAMU ...	29	0.011
55	emb AW926585 AW926585 HVSMEg0007J19 Hordeum vulgare pre-anthesis...	29	0.025
	emb AW032321 AW032321 EST275775 tomato callus, TAMU Lycopersicon...	28	0.026
	emb AW736598 AW736598 EST333090 KV3 Medicago truncatula cDNA clo...	37	0.39
	emb AW736597 AW736597 EST333089 KV3 Medicago truncatula cDNA clo...	37	0.39
	emb AW713727 AW713727 h1f12ne.fl Neurospora crassa evening cDNA ...	35	1.0
60	emb AW711542 AW711542 f3g07ne.fl Neurospora crassa evening cDNA ...	35	1.0
	emb AB009972 AB009972 Aspergillus oryzae gene for beta-1,4-xylos...	35	1.0

	emb AW713709 AW713709 hle09ne.fl Neurospora crassa evening cDNA ...	35	1.0
	emb AW712721 AW712721 g3a07ne.fl Neurospora crassa evening cDNA ...	35	1.0
	emb AW709185 AW709185 d3e02ne.fl Neurospora crassa evening cDNA ...	35	1.0
	emb Y09354 SPABC1 S.pombe ABC1 gene.	35	1.4
5	emb Z99262 SPAC9E9 S.pombe chromosome I cosmid c9E9.	35	1.4
	emb AJ225108 STA225108 Solanum tuberosum (cultivar Bintje) mitoc...	35	1.4
	emb AW933326 AW933326 EST359169 tomato fruit mature green, TAMU ...	26	1.5
	emb Z25870 CACDC10G C.albicans CDC10 gene for cell division cycl...	31	1.5
	emb AC008368 AC008368 Trypanosoma brucei chromosome II clone RPC...	35	1.9
10	emb AQ942780 AQ942780 Sheared DNA-42B15.TR Sheared DNA Trypanoso...	35	1.9
	emb AQ953508 AQ953508 Sheared DNA-33G8.TR Sheared DNA Trypanosom...	35	1.9
	emb AC009463 AC009463 Trypanosoma brucei chromosome II clone RPC...	35	1.9
	emb AQ950237 AQ950237 Sheared DNA-39C11.TF Sheared DNA Trypanoso...	35	1.9
	emb AQ643883 AQ643883 RPCI93-DpnII-26C13.TV RPCI93-DpnII Trypano...	35	1.9
15	emb AQ948491 AQ948491 Sheared DNA-49H2.TF Sheared DNA Trypanosom...	35	1.9
	emb AW729536 AW729536 GA__Ea0025E24 Gossypium arboreum 7-10 dpa ...	35	1.9
	emb AW727289 AW727289 GA__Ea0011H24 Gossypium arboreum 7-10 dpa ...	35	1.9
	gb L36856 PEAIAP34A Pisum sativum GTP-binding protein (IAP34) mR...	28	2.1
	emb Z28341 PSCLOEP P.sativum (miranda) mRNA for chloroplast oute...	28	2.1
20	emb AW776020 AW776020 EST335085 DSIL Medicago truncatula cDNA cl...	28	2.2
	emb AW685649 AW685649 NF032G04NR1F1000 Nodulated root Medicago t...	28	2.2
	emb AW690755 AW690755 NF037H10ST1F1000 Developing stem Medicago ...	28	2.2
	emb AW256896 AW256896 EST305033 KV2 Medicago truncatula cDNA clo...	28	2.3
	emb AV422565 AV422565 AV422565 Lotus japonicus young plants (two...	28	2.3
25	emb AW832303 AW832303 sm07c04.y1 Gm-c1027 Glycine max cDNA clone...	27	2.3
	emb AL136538 SPAC30 S.pombe chromosome I cosmid c30.	34	2.6
	emb AI724721 AI724721 RHIZ1_26_C05.y2_A001 Rhizome1 Sorghum hale...	34	2.6
	emb AW256609 AW256609 EST304746 KV2 Medicago truncatula cDNA clo...	34	2.6
	emb AI775696 AI775696 EST256796 tomato resistant, Cornell Lycopen...	28	3.1
30	emb Z71682 SCYNR067C S.cerevisiae chromosome XIV reading frame O...	34	3.6
	emb AI776315 AI776315 EST257415 tomato resistant, Cornell Lycopen...	34	3.6
	emb AF230371 AF230371 Lycopersicon esculentum allene oxide synth...	34	3.6
	emb AA741645 AA741645 LmLv39p3/255A Leishmania major promastigot...	34	3.6
	gb U08843 PPU08843 Porphyra purpurea putative polysaccharide bin...	34	3.6
35	emb AF124792 AF124792 Sporothrix schenckii protein kinase C (PCK...	29	4.7
	emb AQ399149 AQ399149 mgxb0019C01f CUGI Rice Blast BAC Library P...	33	5.0
	emb AW615911 AW615911 EST325409 tomato flower buds 0-3 mm, Corne...	33	5.0
	emb AW035453 AW035453 EST281191 tomato callus, TAMU Lycopersicon...	33	5.0
	emb AF051695 AF051695 Trypanosoma cruzi sialidase homolog (P85.1...	33	5.0
40	emb Z37538 LTGRR4 L.tarentolae mRNA encoding putative NADH subun...	28	5.5
	emb X85021 SCXLTORFS S.cerevisiae DNA from left arm of chromosom...	33	6.8
	gb L25088 YSCMEF2MIT Saccharomyces cerevisiae nuclear-encoded mi...	33	6.8
	emb AQ443826 AQ443826 GSSTc01287 Trypanosoma cruzi random genom...	33	6.8
	emb AQ502942 AQ502942 V47H4 mTn-3xHA/lacZ Insertion Library Sacc...	33	6.8
45	emb Z85962 MSZ85962 Musa sp. DNA for sequence tagged microsatell...	33	6.8
	emb Z49377 SCYJL102W S.cerevisiae chromosome X reading frame ORF...	33	6.8
	emb AW224537 AW224537 EST302980 tomato root, plants pre-anthesis...	31	7.5
	emb AW257183 AW257183 EST305320 KV2 Medicago truncatula cDNA clo...	32	9.4
	emb AQ642922 AQ642922 RPCI93-DpnII-27E7.TV RPCI93-DpnII Trypanos...	32	9.4
50	emb AW738509 AW738509 EST339936 tomato flower buds, anthesis, Co...	32	9.4
	emb AW217351 AW217351 EST296174 tomato flower buds 0-3 mm, Corne...	32	9.4
	emb AW219255 AW219255 EST301737 tomato root during/after fruit s...	32	9.4
	emb AC007865 AC007865 Trypanosoma brucei chromosome II clone RPC...	32	9.4
	emb AW684118 AW684118 NF012F02NR1F1000 Nodulated root Medicago t...	32	9.4
55	emb AW622239 AW622239 EST313037 tomato root during/after fruit s...	32	9.4
	emb AQ651543 AQ651543 Sheared DNA-7C22.TF Sheared DNA Trypanosom...	32	9.4
	emb Y11565 NC11565 N.crassa acu-15 gene.	32	9.4
	emb AW775944 AW775944 EST335009 DSIL Medicago truncatula cDNA cl...	32	9.4
	emb AB014493 AB014493 Gibberella zeae gene for reductase, partia...	32	9.4
60			

Query= AJ002295_s_at 18012_s_at /id_source genbank /description

"emb|cab59428.1| (aj002295) inositol-1,4,5-trisphosphate 5-phosphatase
[arabidopsis thaliana]" /blast_score 0
(2083 letters)

5 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

10	Score	E	
	Sequences producing significant alignments:	(bits)	Value
	emb AI898446 AI898446 EST267889 tomato ovary, TAMU Lycopersicon ...	209	e-107
	emb AW217248 AW217248 EST295962 tomato callus, TAMU Lycopersicon...	245	1e-88
15	emb AI485780 AI485780 EST244101 tomato ovary, TAMU Lycopersicon ...	242	1e-85
	emb AI485695 AI485695 EST244016 tomato ovary, TAMU Lycopersicon ...	261	3e-85
	emb AI485239 AI485239 EST243543 tomato ovary, TAMU Lycopersicon ...	291	1e-77
	emb AI899197 AI899197 EST268640 tomato ovary, TAMU Lycopersicon ...	161	1e-77
	emb AW034573 AW034573 EST278257 tomato callus, TAMU Lycopersicon...	272	8e-72
20	emb AI488812 AI488812 EST247151 tomato ovary, TAMU Lycopersicon ...	251	1e-65
	emb AW687082 AW687082 NF005G09RT1F1071 Developing root Medicago ...	182	6e-65
	emb AI898248 AI898248 EST267691 tomato ovary, TAMU Lycopersicon ...	204	1e-63
	emb AI483614 AI483614 EST249464 tomato ovary, TAMU Lycopersicon ...	238	1e-61
	emb AI897089 AI897089 EST266532 tomato ovary, TAMU Lycopersicon ...	226	7e-58
25	emb AW774994 AW774994 EST334145 KV3 Medicago truncatula cDNA clo...	182	2e-56
	emb AW559604 AW559604 EST314652 DSIR Medicago truncatula cDNA cl...	177	3e-53
	emb AI485284 AI485284 EST243588 tomato ovary, TAMU Lycopersicon ...	204	3e-51
	emb AI485664 AI485664 EST243985 tomato ovary, TAMU Lycopersicon ...	195	8e-49
	emb AW774741 AW774741 EST333892 KV3 Medicago truncatula cDNA clo...	90	2e-48
30	emb AI487608 AI487608 EST245930 tomato ovary, TAMU Lycopersicon ...	187	3e-46
	emb AI483438 AI483438 EST249259 tomato ovary, TAMU Lycopersicon ...	169	6e-41
	emb AW775688 AW775688 EST334753 DSIL Medicago truncatula cDNA cl...	157	2e-37
	emb AI485008 AI485008 EST243271 tomato ovary, TAMU Lycopersicon ...	157	2e-37
	emb AI938737 AI938737 sb58c06.y1 Gm-cl018 Glycine max cDNA clone...	151	2e-35
35	emb AI967736 AI967736 Ljirmp11-837-a7 Ljirmp Lambda HybriZap ...	147	4e-34
	emb Z50161 SCC14ORFS S.cerevisiae orfs and LEU4, MET4, POL1, RAS...	60	1e-33
	emb Z71382 SCYNL106C S.cerevisiae chromosome XIV reading frame O...	60	1e-33
	emb AI973618 AI973618 sd07d04.y1 Gm-cl020 Glycine max cDNA clone...	141	2e-32
	emb AI485392 AI485392 EST243713 tomato ovary, TAMU Lycopersicon ...	138	2e-31
40	emb X94335 SC130KBXV S.cerevisiae 130kb DNA fragment from chromo...	51	1e-29
	emb Z75017 SCYOR109W S.cerevisiae chromosome XV reading frame OR...	51	1e-29
	emb AL022103 SPBC2G2 S.pombe chromosome II cosmid c2G2.	79	1e-27
	emb X79743 SCBPPS S.cerevisiae BET1, PAN1 PRI1 and STS1 genes.	72	2e-27
	emb Z38062 SC9687 S.cerevisiae chromosome IX cosmid 9687.	72	2e-27
45	emb AI488810 AI488810 EST247149 tomato ovary, TAMU Lycopersicon ...	121	3e-26
	gb BE020060 BE020060 sm38e06.y1 Gm-cl028 Glycine max cDNA clone ...	119	9e-26
	emb AW685248 AW685248 NF028A10NR1F1000 Nodulated root Medicago t...	116	2e-24
	emb AW257207 AW257207 EST305344 KV2 Medicago truncatula cDNA clo...	75	2e-24
	emb AV406995 AV406995 AV406995 Lotus japonicus young plants (two...	67	2e-23
50	emb AW034093 AW034093 EST277588 tomato callus, TAMU Lycopersicon...	111	3e-23
	emb Z98763 SPAC9G1 S.pombe chromosome I cosmid c9G1.	59	8e-23
	emb AQ502761 AQ502761 V84A11 mTn-3xHA/lacZ Insertion Library Sac...	52	2e-22
	emb AI897134 AI897134 EST266577 tomato ovary, TAMU Lycopersicon ...	107	4e-22
	emb AI771644 AI771644 EST252744 tomato ovary, TAMU Lycopersicon ...	104	3e-21
55	emb AW731056 AW731056 GA_Ea0008D13 Gossypium arboreum 7-10 dpa ...	102	1e-20
	emb AV413397 AV413397 AV413397 Lotus japonicus young plants (two...	100	8e-20
	emb AW616540 AW616540 EST322951 L. hirsutum trichome, Cornell Un...	98	2e-19
	emb AL110506 SPBC577 S.pombe chromosome II cosmid c577.	74	1e-18
	emb AW126841 AW126841 ga16f04.y1 Moss EST library PPU Physcomitr...	94	4e-18
60	emb AI780067 AI780067 EST260946 tomato susceptible, Cornell Lyco...	94	5e-18
	emb AW687035 AW687035 NF005C05RT1F1037 Developing root Medicago ...	73	2e-17

- emb|AW685930|AW685930 NF036F03NR1F1000 Nodulated root Medicago t... 73 2e-17
 emb|AV415287|AV415287 AV415287 Lotus japonicus young plants (two... 90 4e-17
 gb|BE124605|BE124605 EST393640 GVN Medicago truncatula cDNA clon... 65 5e-15
 emb|AW220291|AW220291 EST302774 tomato root during/after fruit s... 68 1e-14
 5 emb|AQ644913|AQ644913 RPCI93-EcoRI-2C7.TV RPCI93-EcoRI Trypanoso... 53 1e-13
 emb|AA495505|AA495505 c430 Zhou and Ragan 1993 Gracilaria gracil... 49 4e-13
 emb|AW830613|AW830613 sm04c07.y1 Gm-c1027 Glycine max cDNA clone... 77 4e-13
 emb|AW666237|AW666237 sk34b04.y1 Gm-c1028 Glycine max cDNA clone... 77 4e-13
 emb|AW285758|AW285758 LG1_223_C03.b1_A002 Light Grown 1 (LG1) So... 74 4e-12
 10 emb|AQ658256|AQ658256 Sheared DNA-13C5.TR Sheared DNA Trypanosom... 73 1e-11
 emb|AW704333|AW704333 sk18a03.y1 Gm-c1028 Glycine max cDNA clone... 71 4e-11
 emb|AV390446|AV390446 AV390446 Chlamydomonas reinhardtii C9 Chla... 70 5e-11
 emb|AL160371|LMFLCHR15 Leishmania major Friedlin assembled chrom... 64 7e-11
 emb|AZ048449|AZ048449 PSB67 Barley PstI genomic clones Hordeum v... 69 1e-10
 15 emb|AW695904|AW695904 NF099H04ST1F1043 Developing stem Medicago ... 49 2e-10
 emb|AW760518|AW760518 sl51d02.y1 Gm-c1027 Glycine max cDNA clone... 66 9e-10
 emb|AW332143|AW332143 S4G7 AGS-1 Pneumocystis carinii f. sp. car... 36 1e-09
 emb|AW687790|AW687790 NF013E04RT1F1034 Developing root Medicago ... 65 2e-09
 emb|AI486692|AI486692 EST245014 tomato ovary, TAMU Lycopersicon ... 54 3e-09
 20 emb|AW333870|AW333870 S27C11 AGS-1 Pneumocystis carinii f. sp. c... 36 4e-09
 emb|AQ850639|AQ850639 LMAJFV1_lm41a04.x1 Leishmania major FV1 ra... 44 5e-09
 emb|AW127178|AW127178 M110117 GVN Medicago truncatula cDNA clone... 63 8e-09
 emb|AW399291|AW399291 EST309791 L. pennellii trichome, Cornell U... 62 2e-08
 emb|AW616547|AW616547 EST322958 L. hirsutum trichome, Cornell Un... 62 2e-08
 25 emb|AW693686|AW693686 NF068A05ST1F1036 Developing stem Medicago ... 62 2e-08
 emb|AW208046|AW208046 M111077e DSIR Medicago truncatula cDNA clo... 61 4e-08
 emb|AQ642482|AQ642482 RPCI93-EcoRI-1A17.TV RPCI93-EcoRI Trypanos... 53 6e-08
 emb|AW686583|AW686583 NF039G02NR1F1000 Nodulated root Medicago t... 45 5e-07
 emb|AQ849089|AQ849089 LMAJFV1_lm41a04.y1 Leishmania major FV1 ra... 44 5e-06
 30 emb|AI781410|AI781410 EST262277 tomato susceptible, Cornell Lyco... 52 2e-05
 emb|AW617564|AW617564 EST323975 L. hirsutum trichome, Cornell Un... 49 2e-04
 emb|AQ946427|AQ946427 Sheared DNA-49M8.TF Sheared DNA Trypanosom... 47 4e-04
 emb|AW099113|AW099113 sd34f04.y1 Gm-c1012 Glycine max cDNA clone... 46 0.001
 emb|Z74807|SCYOL065C S.cerevisiae chromosome XV reading frame OR... 29 0.002
 35 emb|AQ655271|AQ655271 Sheared DNA-27A17.TR Sheared DNA Trypanoso... 38 0.004
 emb|AW685854|AW685854 NF031A06NR1F1000 Nodulated root Medicago t... 43 0.007
 emb|AW437996|AW437996 ST83C09 Pine TriplEx shoot tip library Pin... 42 0.014
 emb|AI440709|AI440709 sa62e11.y1 Gm-c1004 Glycine max cDNA clone... 31 0.021
 emb|AW979881|AW979881 EST341528 tomato root deficiency, Cornell ... 37 0.45
 40 gb|M28064|PFAHRKP Plasmodium brasilianum DNA homologous to the h... 37 0.45
 emb|AF263282|AF263282 Filobasidiella neoformans var. neoformans ... 34 0.54
 emb|AW702543|AW702543 TgESTzz85a12.y1 TgRH*-Tachyzoite cDNA Toxo... 32 0.58
 emb|AQ651205|AQ651205 Sheared DNA-30N15.TF Sheared DNA Trypanoso... 37 0.62
 emb|AQ945454|AQ945454 Sheared DNA-54H22.TF Sheared DNA Trypanoso... 37 0.62
 45 emb|AZ214873|AZ214873 Sheared DNA-109E2.TR Sheared DNA Trypanoso... 37 0.62
 emb|AQ939979|AQ939979 Sheared DNA-42A15.TF Sheared DNA Trypanoso... 37 0.62
 emb|AL049180|PFMAL13P1 Plasmodium falciparum chromosome 13 strai... 36 1.2
 emb|Z74892|BO15H11 B.oleracea mRNA for glycine-rich protein. 36 1.2
 emb|AW774740|AW774740 EST333891 KV3 Medicago truncatula cDNA clo... 36 1.2
 50 emb|Z38060|SC5610 S.cerevisiae chromosome IX sequence derived fr... 36 1.2
 emb|AL031745|PFMAL1P2 Plasmodium falciparum chromosome 1 strain ... 35 2.2

Query= AJ010971_at18022_at /id_source genbank /description
 55 emb|cab52675.1| (aj010971) glucose-6-phosphate 1-dehydrogenase
 [arabidopsis thaliana] /blast_score 0
 (1690 letters)

Database: plantfungal
 60 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	
	(bits)		Value
Sequences producing significant alignments:			
5	emb X74421 STG6PDH	S.tuberosum mRNA for glucose-6-phosphate dehy...	911 0.0
	emb AF012862 AF012862	Petroselinum crispum cytosolic glucose-6-p...	841 0.0
	emb AJ001770 NTTCG9	Nicotiana tabacum mRNA for cytosolic glucose...	893 0.0
	gb U18238 MSU18238	Medicago sativa glucose-6-phosphate dehydroge...	900 0.0
10	emb AF012863 AF012863	Petroselinum crispum cytosolic glucose-6-p...	887 0.0
	emb AJ001769 NTTCG6	Nicotiana tabacum mRNA cytosolic glucose-6-p...	895 0.0
	emb AF097663 AF097663	Mesembryanthemum crystallinum cytoplasmic ...	754 0.0
	emb AB011441 AB011441	Triticum aestivum WESR5 mRNA for glucose-6...	500 e-141
	emb X70373 KLLTZWF	K.lactis LET1 gene and ZWF gene for glucose-...	231 e-138
15	emb Z69381 SCCXIV39K	S.cerevisiae 38,855 bp segment of chromosom...	244 e-136
	gb M34709 YSCG6PD	S.cerevisiae glucose-6-phosphate dehydrogenase...	244 e-136
	emb X57336 SCMET19	S. cerevisiae MET19 gene for glucose-6-phosph...	244 e-136
	emb Z71517 SCYNL241C	S.cerevisiae chromosome XIV reading frame O...	244 e-136
	emb AJ010712 STU010712	Solanum tuberosum mRNA for glucose-6-phos...	240 e-136
20	emb X99405 NTG6PD	N.tabacum mRNA for chloroplast glucose-6-phosp...	242 e-135
	emb AF012861 AF012861	Petroselinum crispum plastidic glucose-6-p...	248 e-135
	emb AI730607 AI730607	BNLGH17371 Six-day Cotton fiber Gossypium ...	481 e-135
	emb X87942 ANG6PDHSE	A.niger mRNA for glucose-6-phosphate dehydr...	225 e-132
	emb AW686120 AW686120	NF038D09NR1F1000 Nodulated root Medicago t...	472 e-132
25	emb AJ132346 DBI132346	Dunaliella bioculata mRNA for plastidic g...	235 e-132
	emb AW925642 AW925642	HVSMEg0005C04 Hordeum vulgare pre-anthesis...	465 e-130
	emb AJ001772 NTTPG18	Nicotiana tabacum mRNA for plastidic glucos...	243 e-129
	emb AW930385 AW930385	EST340938 tomato fruit mature green, TAMU ...	444 e-124
	emb AW831416 AW831416	sm22g09.y1 Gm-c1028 Glycine max cDNA clone...	434 e-121
30	emb X83923 STG6PDHPI	S.tuberosum mRNA for glucose-6-phosphate de...	249 e-118
	emb AJ000182 SO000182	Spinacia oleracea mRNA for glucose-6-phosp...	242 e-117
	emb AJ001771 NTTPG16	Nicotiana tabacum mRNA for plastidic glucos...	247 e-116
	emb AI491202 AI491202	EST241911 tomato shoot, Cornell Lycopersic...	368 e-116
	emb AL121764 SPAC9	S.pombe chromosome I cosmid c9.	196 e-116
35	emb AW233801 AW233801	sf26h03.y1 Gm-c1028 Glycine max cDNA clone...	415 e-115
	emb Z95395 SPAC3A12	S.pombe chromosome I cosmid c3A12.	196 e-108
	emb AW288048 AW288048	N100892e rootphos(-) Medicago truncatula c...	387 e-106
	emb AW685333 AW685333	NF027C04NR1F1000 Nodulated root Medicago t...	356 e-105
	emb X77830 ANWGGSDA	A.nidulans (WG096) gsdA gene.	130 e-102
40	emb AJ006246 CCA6246	Cyanidium caldarium mRNA for glucose-6-phos...	239 e-102
	emb AJ000184 SO000184	Spinacia oleracea mRNA for glucose-6-phosp...	242 e-100
	emb AJ000183 SO000183	Spinacia oleracea mRNA for glucose-6-phosp...	190 3e-99
	emb X84001 ANDNAG6PD	A.nidulans g6pd gene.	130 2e-98
	emb AW744917 AW744917	LG1_384_F04.b1_A002 Light Grown 1 (LG1) So...	356 3e-97
45	emb AW761534 AW761534	sl68h05.y1 Gm-c1027 Glycine max cDNA clone...	356 4e-97
	emb X74988 PFGPLP	P.falciparum gene for glucose-6-phosphate dehy...	192 5e-89
	emb AW560329 AW560329	EST315377 DSIR Medicago truncatula cDNA cl...	323 2e-87
	gb M80655 PFAG6PD	Plasmodium falciparum glucose-6-phosphate dehy...	192 1e-86
	emb AW497059 AW497059	ga53c08.y1 Moss EST library PPU Physcomitr...	319 5e-86
50	emb AW216550 AW216550	EST295264 tomato callus, TAMU Lycopersicon...	188 6e-84
	emb AW219903 AW219903	EST302386 tomato root during/after fruit s...	305 7e-82
	emb AW180861 AW180861	MgA1030f MgA Library Mycosphaerella gramin...	226 5e-80
	emb AW616585 AW616585	EST322996 L. hirsutum trichome, Cornell Un...	175 7e-80
	emb AW309937 AW309937	sf26h03.x1 Gm-c1028 Glycine max cDNA clone...	294 1e-78
55	emb AW031447 AW031447	EST274901 tomato callus, TAMU Lycopersicon...	166 6e-78
	emb AI894720 AI894720	EST264163 tomato callus, TAMU Lycopersicon...	291 1e-77
	emb AW690515 AW690515	NF030E09ST1F1000 Developing stem Medicago ...	174 3e-77
	emb AW736245 AW736245	EST332231 KV3 Medicago truncatula cDNA clo...	278 7e-76
	emb AW455246 AW455246	EST311906 tomato root during/after fruit s...	155 6e-75
60	emb AW980010 AW980010	EST310488 tomato root deficiency, Cornell ...	153 3e-74
	emb AL023595 SPCC794	S.pombe chromosome III cosmid c794.	177 1e-73

- emb|AW255521|AW255521 ML551 peppermint glandular trichome Mentha... 270 3e-71
 emb|AW567621|AW567621 si65f02.y1 Gm-r1030 Glycine max cDNA clone... 264 1e-69
 emb|AW689492|AW689492 NF019H04ST1F1000 Developing stem Medicago ... 128 3e-69
 emb|AW737104|AW737104 EST338531 tomato flower buds, anthesis, Co... 141 1e-64
 5 emb|AW255222|AW255222 ML216 peppermint glandular trichome Mentha... 142 2e-64
 emb|AW737079|AW737079 EST338506 tomato flower buds, anthesis, Co... 141 3e-64
 emb|AW565200|AW565200 LG1_328_D07.b1_A002 Light Grown 1 (LG1) So... 119 1e-60
 emb|AW684970|AW684970 NF023F11NR1F1000 Nodulated root Medicago t... 128 1e-60
 emb|AQ952407|AQ952407 Sheared DNA-32N19.TF Sheared DNA Trypanoso... 84 2e-60
 10 emb|AA787466|AA787466 n3f11a1.r1 Aspergillus nidulans 24hr asexu... 229 4e-59
 emb|AW254983|AW254983 ML1164 peppermint glandular trichome Menth... 134 2e-58
 emb|AW617385|AW617385 EST323796 L. hirsutum trichome, Cornell Un... 141 2e-57
 emb|AI773327|AI773327 EST254427 tomato resistant, Cornell Lycopen... 222 5e-57
 emb|AW704079|AW704079 sk27e10.y1 Gm-c1028 Glycine max cDNA clone... 219 6e-56
 15 emb|X77829|ANNGSDA A.niger (N400) gsdA gene. 131 4e-55
 emb|AW286177|AW286177 LG1_328_D07.g1_A002 Light Grown 1 (LG1) So... 216 4e-55
 emb|AW617091|AW617091 EST323502 L. hirsutum trichome, Cornell Un... 138 5e-55
 emb|AI777244|AI777244 EST258209 tomato resistant, Cornell Lycopen... 150 1e-54
 emb|AV424412|AV424412 AV424412 Lotus japonicus young plants (two... 205 9e-52
 20 emb|AQ875204|AQ875204 V123H11 mTn-3xHA/lacZ Insertion Library, s... 192 1e-49
 emb|AV416113|AV416113 AV416113 Lotus japonicus young plants (two... 196 4e-49
 emb|Z99568|SPAC3C7 S.pombe chromosome I cosmid c3C7. 95 1e-48
 emb|AQ500574|AQ500574 V36G4 mTn-3xHA/lacZ Insertion Library Sacc... 127 6e-48
 emb|AI187687|AI187687 p280 Porphyra yezoensis in Lambda UniZAP P... 87 1e-47
 25 emb|AJ279688|BPE279688 Betula pendula partial mRNA for Glucose-6... 93 7e-47
 emb|AW700124|AW700124 gb34g09.y1 Moss EST library PPN Physcomitr... 187 3e-46
 emb|AW223852|AW223852 EST300663 tomato fruit red ripe, TAMU Lyco... 141 6e-46
 emb|AW774199|AW774199 EST333350 KV3 Medicago truncatula cDNA clo... 143 3e-45
 emb|AW621290|AW621290 EST312088 tomato root during/after fruit s... 138 3e-43
 30 emb|AW980083|AW980083 EST341594 tomato root deficiency, Cornell ... 133 2e-42
 emb|AZ217409|AZ217409 Sheared DNA-90C8.TR Sheared DNA Trypanosom... 90 3e-42
 emb|AI941197|AI941197 sb85g11.y1 Gm-c1010 Glycine max cDNA clone... 169 7e-41
 emb|AW224136|AW224136 EST300947 tomato fruit red ripe, TAMU Lyco... 141 3e-40
 emb|AW616535|AW616535 EST322946 L. hirsutum trichome, Cornell Un... 139 2e-38
 35 emb|AU036687|AU036687 Schizosaccharomyces pombe genomic clone ha... 98 3e-38
 emb|AI416414|AI416414 NCW07G12T3 Westergaards Neurospora crassa ... 103 3e-38
 emb|AW286271|AW286271 LG1_329_F06.g1_A002 Light Grown 1 (LG1) So... 149 4e-35
 emb|AI055328|AI055328 coau0003K24 Cotton Boll Abscission Zone cD... 78 3e-32
 emb|AW698775|AW698775 r358 non-glandular-haired subtracted cDNA ... 133 5e-30
 40 emb|AJ130773|LDI130773 Laminaria digitata mRNA for glucose-6-pho... 131 2e-29
 emb|AI974714|AI974714 T113172e KV2 Medicago truncatula cDNA clon... 118 2e-28
 emb|AF173650|AF173650 Beta vulgaris clone GPD109UNI glucose-6-ph... 77 1e-27
 emb|AJ004900|GMJ004900 Glycine max mRNA for glucose-6-phosphate-... 121 1e-26
 emb|AW831248|AW831248 sm13f09.y1 Gm-c1027 Glycine max cDNA clone... 104 8e-26
 45

Query= AJ238846_at 18054_at /id_source genbank /description
 emb|cab54517.1| (aj238846) sgp1 monomeric g-protein [arabidopsis
 thaliana] /blast_score 1.00e-150
 50 (887 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

55 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

- 60 emb|AW725454|AW725454 GA_Ea0018A14 Gossypium arboreum 7-10 dpa ... 238 8e-81
 emb|Z38114|SC9745 S.cerevisiae chromosome XIII cosmid 9745. 122 2e-33

	gb U34860 SCU34860 <i>Saccharomyces cerevisiae</i> origin recognition c...	122	2e-33
	dbj D38172 YSCTEM1P Yeast gene for GTP-binding protein Tem1p, co...	122	2e-33
	emb AI988573 AI988573 sd04c11.y1 Gm-cl020 Glycine max cDNA clone...	142	3e-33
	emb Y12314 SPSPG1GEN <i>S.pombe</i> spg1 gene.	67	9e-20
5	emb AJ001587 SPAJ1587 <i>Schizosaccharomyces pombe</i> sid3 gene.	67	9e-20
	emb AW776339 AW776339 EST335404 <i>DSIL</i> <i>Medicago truncatula</i> cDNA cl...	67	5e-14
	emb AI416417 AI416417 NCW07E2T3 <i>Westergaards Neurospora crassa</i> c...	55	1e-06
	gb U17243 YSCL8003 <i>Saccharomyces cerevisiae</i> chromosome XII cosmi...	32	2e-06
	emb Z75093 SCYOR185C <i>S.cerevisiae</i> chromosome XV reading frame OR...	32	2e-06
10	gb L08690 YSCGSP1X Yeast GTP-binding protein (GSP1) gene, comple...	32	2e-06
	gb L08691 YSCGSP2X Yeast GTP-binding protein (GSP2) gene, comple...	32	2e-06
	emb X71946 SCCNR2A <i>S.cerevisiae</i> CNR2 gene.	32	2e-06
	emb X71945 SCCNR1A <i>S.cerevisiae</i> CNR1 gene.	32	2e-06
	dbj D17748 TETTRAN <i>Tetrahymena thermophila</i> mRNA for Ran/TC4, com...	33	3e-06
15	dbj D21825 TETPRAN <i>Tetrahymena pyriformis</i> mRNA for Ran/TC4, comp...	33	3e-06
	gb U17086 TBU17086 <i>Trypanosoma brucei rhodesiense</i> RAN/TC4 GTPase...	30	6e-05
	emb AC008031 AC008031 <i>Trypanosoma brucei</i> chromosome II clone RPC...	35	0.001
	emb AQ661102 AQ661102 Sheared DNA-15E18.TF Sheared DNA <i>Trypanoso...</i>	32	0.002
20	emb AW671770 AW671770 LG1_351_B08.b1_A002 Light Grown 1 (LG1) So...	42	0.005
	emb W68882 W68882 T2862 MVAT4 bloodstream form of serodeme WRATa...	30	0.009
	emb AW685566 AW685566 NF031H02NR1F1000 Nodulated root <i>Medicago t...</i>	36	0.037
	emb AB024996 AB024996 <i>Cicer arietinum</i> mRNA for rac-type small GT...	36	0.091
	emb AW832298 AW832298 sm07b06.y1 Gm-cl027 Glycine max cDNA clone...	38	0.13
	emb AW218480 AW218480 EST303663 tomato radicle, 5 d post-imbibit...	36	0.13
25	emb AI437767 AI437767 sa39c11.y1 Gm-cl004 Glycine max cDNA clone...	37	0.17
	emb AV413867 AV413867 AV413867 <i>Lotus japonicus</i> young plants (two...	35	0.17
	emb AW690945 AW690945 NF034H11ST1F1000 Developing stem <i>Medicago ...</i>	35	0.23
	emb AW621657 AW621657 EST312455 tomato root during/after fruit s...	37	0.24
	emb AI775563 AI775563 EST256663 tomato resistant, Cornell Lycoper...	37	0.24
30	emb AW738459 AW738459 EST339886 tomato flower buds, anthesis, Co...	36	0.33
	emb AI731040 AI731040 BNLGHi8453 Six-day Cotton fiber <i>Gossypium ...</i>	36	0.33
	emb AI727570 AI727570 BNLGHi8420 Six-day Cotton fiber <i>Gossypium ...</i>	36	0.33
	emb AV419645 AV419645 AV419645 <i>Lotus japonicus</i> young plants (two...	36	0.33
	emb Z49191 BVRHO1 <i>B.vulgaris</i> mRNA for small G protein (clone 1S5).	36	0.33
35	emb AW930158 AW930158 EST340615 tomato fruit mature green, TAMU ...	36	0.33
	gb U17085 TBU17085 <i>Trypanosoma brucei brucei</i> RAN/TC4 GTPase homo...	29	0.43
	emb AI440994 AI440994 sa63e10.y1 Gm-cl004 Glycine max cDNA clone...	36	0.45
	gb U03624 PTU03624 <i>Paramecium tetraurelia</i> clone plg-14 guanine n...	36	0.45
	gb U64924 NTU64924 <i>Nicotiana tabacum</i> geranylgeranylated protein ...	35	0.55
40	emb AW040005 AW040005 EST282496 tomato mixed elicitor, BTI Lycop...	35	0.56
	emb AW039993 AW039993 EST282484 tomato mixed elicitor, BTI Lycop...	35	0.56
	emb AW705028 AW705028 sk41f03.y1 Gm-cl019 Glycine max cDNA clone...	35	0.57
	emb AW929161 AW929161 EST337949 tomato flower buds 8 mm to pre-a...	35	0.57
	emb AW705209 AW705209 sk43a11.y1 Gm-cl019 Glycine max cDNA clone...	35	0.57
45	emb AV414769 AV414769 AV414769 <i>Lotus japonicus</i> young plants (two...	35	0.62
	gb U64923 NTU64923 <i>Nicotiana tabacum</i> geranylgeranylated protein ...	35	0.62
	emb Z73962 LJRAC2 <i>L.japonicus</i> mRNA for small GTP-binding protein...	35	0.62
	gb BE021064 BE021064 sm47d01.y1 Gm-cl028 Glycine max cDNA clone ...	35	0.62
	emb AW573660 AW573660 EST316251 <i>GVN</i> <i>Medicago truncatula</i> cDNA clo...	35	0.62
50	emb AV413108 AV413108 AV413108 <i>Lotus japonicus</i> young plants (two...	35	0.62
	emb AW202293 AW202293 sf13c10.y1 Gm-cl027 Glycine max cDNA clone...	35	0.62
	emb AI937960 AI937960 sc06b11.y1 Gm-cl012 Glycine max cDNA clone...	35	0.62
	emb Z73961 LJRAC1 <i>L.japonicus</i> mRNA for small GTP-binding protein...	35	0.62
	emb AI162198 AI162198 A013P52U Hybrid aspen plasmid library Popu...	35	0.62
55	emb AW694335 AW694335 NF075C06ST1F1049 Developing stem <i>Medicago ...</i>	35	0.62
	emb AW109094 AW109094 gate0002P07f <i>Gossypium arboreum</i> 7-10 dpa f...	35	0.62
	gb L19093 PEARHOGTPP <i>Pisum sativum</i> rho (ras-related) GTP-binding...	35	0.62
	emb AW565277 AW565277 LG1_332_G03.b1_A002 Light Grown 1 (LG1) So...	35	0.62
	emb AV412205 AV412205 AV412205 <i>Lotus japonicus</i> young plants (two...	35	0.62
60	gb BE054534 BE054534 GA_Ea0033M19f <i>Gossypium arboreum</i> 7-10 dpa ...	35	0.62
	emb AW108667 AW108667 gate0001G03f <i>Gossypium arboreum</i> 7-10 dpa f...	35	0.62

	emb AI495724 AI495724 sb15e06.y1 Gm-c1004 Glycine max cDNA clone...	35	0.62
	gb S79309 S79309 Rac9=21.5 kda GTP-binding protein [Gossypium hi...	35	0.62
	gb S79308 S79308 Rac13=21.8 kda GTP-binding protein [Gossypium h...	35	0.62
	emb AJ250174 NTA250174 Nicotiana tabacum mRNA for putative rac p...	35	0.62
5	gb BE055015 BE055015 GA__Ea0001G03f Gossypium arboreum 7-10 dpa ...	35	0.62
	emb AW690086 AW690086 NF028B10ST1F1000 Developing stem Medicago ...	35	0.62
	emb AW573665 AW573665 EST316256 GVN Medicago truncatula cDNA clo...	35	0.62
	emb AW559248 AW559248 EST306084 DSIR Medicago truncatula cDNA cl...	35	0.62
	emb AI460950 AI460950 sa78f02.y1 Gm-c1004 Glycine max cDNA clone...	35	0.62
10	emb AW692052 AW692052 NF047B03ST1F1000 Developing stem Medicago ...	35	0.62
	emb AW394676 AW394676 sh34a02.y1 Gm-c1017 Glycine max cDNA clone...	35	0.62
	gb BE054555 BE054555 GA__Ea0002P07f Gossypium arboreum 7-10 dpa ...	35	0.62
	emb AF146340 AF146340 Physcomitrella patens Rac-like GTP binding...	35	0.85
	emb AF233446 AF233446 Physcomitrella patens rac 1 protein (rac1)...	35	0.85
15	emb AF115476 AF115476 Physcomitrella patens rac-like GTP binding...	35	0.85
	gb U06051 PFU06051 Plasmodium falciparum Dd2 Ran/TC4 nuclear GTP...	35	0.85
	emb AW729788 AW729788 GA__Ea0026A18 Gossypium arboreum 7-10 dpa ...	35	0.85
	emb AF146341 AF146341 Physcomitrella patens Rac-like GTP binding...	35	0.85
	emb AI731831 AI731831 BNLGHi11032 Six-day Cotton fiber Gossypium...	35	0.85
20	emb AF051223 AF051223 Picea mariana Rac-like GTP binding protein...	35	0.85
	gb BE055583 BE055583 GA__Ea0001I02f Gossypium arboreum 7-10 dpa ...	35	0.85
	emb AW108575 AW108575 gate0001I02f Gossypium arboreum 7-10 dpa f...	35	0.85
	emb X73954 PFRAN1 P.falciparum gene for ras-related nuclear prot...	35	0.85
	emb AW056772 AW056772 ST55F07 Pine TriplEx shoot tip library Pin...	35	1.2
25	emb AW559842 AW559842 EST314890 DSIR Medicago truncatula cDNA cl...	34	1.6
	emb AW217581 AW217581 EST296295 tomato flower buds 3-8 mm, Corne...	34	1.6
	emb AW217573 AW217573 EST296287 tomato flower buds 3-8 mm, Corne...	34	1.6
	emb Z36133 SCYBR264C S.cerevisiae chromosome II reading frame OR...	34	1.6
	emb X70529 SCCIIORF S. cerevisiae chromosome II sequence for ORF...	34	1.6
30	emb AI778114 AI778114 EST258993 tomato susceptible, Cornell Lyco...	34	1.6
	emb AF042330 AF042330 Brassica rapa rac-like small GTP binding p...	34	1.6
	emb AW625569 AW625569 EST319476 tomato radicle, 5 d post-imbibit...	34	1.6
	emb AW931490 AW931490 EST357333 tomato fruit mature green, TAMU ...	34	1.6
35	gb BE033825 BE033825 MG04D04 MG Mesembryanthemum crystallinum cD...	34	2.2
	gb BE036577 BE036577 MP01F02 MP Mesembryanthemum crystallinum cD...	34	2.2
	emb AQ399302 AQ399302 mgxb0015O18f CUGI Rice Blast BAC Library P...	34	2.2
	emb AW697756 AW697756 Str1-D6 Sugar Beet germination cDNA librar...	34	2.2
40	Query= X91916_at 18716_at /id_source genbank /description gb aaf26754.1 ac007396_3 (ac007396) t4o12.6 [arabidopsis thaliana] /blast_score 3.00e-36 (403 letters)		
45	Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching.....done		
50	Score E Sequences producing significant alignments: (bits) Value		
	gb U18557 RSU18557 Raphanus sativus antifungal protein 1 preprot...	166	7e-43
	emb A26875 A26875 R.sativus AFP1 gene.	166	7e-43
55	emb X97318 RSAFP4 R.sativus mRNA for antifungal protein 4.	162	6e-42
	gb U18556 RSU18556 Raphanus sativus antifungal protein 2 preprot...	160	1e-38
	emb X97319 RSEFP3 R.sativus mRNA for antifungal protein 3.	133	8e-37
	gb U59459 BNU59459 Brassica napus antifungal protein mRNA, compl...	135	2e-36
	emb AT001728 AT001728 AT001728 Flower bud cDNA Brassica rapa sub...	82	2e-15
60	gb L47901 L47901 BNAF1712 Mustard flower buds Brassica rapa cDNA...	81	5e-15
	emb A26963 A26963 D.merkii AMP1 sequence.	74	5e-13

	emb A27062 A27062 C.benedictus AMP2 sequence.	73 1e-12
	emb X53375 HASF18 Sunflower anther-specific mRNA SF18.	72 3e-12
	emb A26906 A26906 C.benedictus AMP1 sequence.	72 3e-12
	emb AT001738 AT001738 AT001738 Flower bud cDNA Brassica rapa sub...	69 2e-11
5	emb A27064 A27064 C.ternatea AMP1 sequence.	58 8e-10
	emb X91487 PASPI1GEN P.abies mRNA for gamma-thionin protein (put...	40 1e-05
	emb AW870017 AW870017 NXNV_122_A10_F Nsf Xylem Normal wood Verti...	35 6e-05
	emb AW064751 AW064751 ST35D04 Pine TriplEx shoot tip library Pin...	36 7e-05
	emb AW775186 AW775186 EST331908 GVN Medicago truncatula cDNA clo...	41 0.001
10	dbj D29679 TOBPIT1A Tobacco pit1 mRNA (which expression is induc...	41 0.003
	emb AW621708 AW621708 EST312506 tomato root during/after fruit s...	36 0.007
	emb AW220215 AW220215 EST302698 tomato root during/after fruit s...	36 0.007
	emb AW623112 AW623112 EST321057 tomato flower buds 3-8 mm, Corne...	40 0.008
	emb AW220231 AW220231 EST302714 tomato root during/after fruit s...	36 0.008
15	emb AW219164 AW219164 EST301646 tomato root during/after fruit s...	36 0.008
	emb AW219793 AW219793 EST302275 tomato root during/after fruit s...	36 0.009
	emb AI487824 AI487824 EST246146 tomato ovary, TAMU Lycopersicon ...	40 0.009
	emb AI483999 AI483999 EST249870 tomato ovary, TAMU Lycopersicon ...	40 0.010
	gb U20591 SLU20591 Solanum lycopersicum flower-specific gamma-th...	40 0.010
20	emb AW622923 AW622923 EST306993 tomato flower buds 3-8 mm, Corne...	40 0.010
	emb AW929929 AW929929 EST354199 tomato flower buds 8 mm to pre-a...	40 0.010
	emb AW929939 AW929939 EST354209 tomato flower buds 8 mm to pre-a...	40 0.010
	emb AW217552 AW217552 EST296266 tomato flower buds 3-8 mm, Corne...	40 0.012
	emb AI490062 AI490062 EST248401 tomato ovary, TAMU Lycopersicon ...	40 0.012
25	emb AW217379 AW217379 EST296063 tomato flower buds 0-3 mm, Corne...	40 0.012
	emb AI484887 AI484887 EST243150 tomato ovary, TAMU Lycopersicon ...	40 0.012
	emb AI485550 AI485550 EST243871 tomato ovary, TAMU Lycopersicon ...	40 0.012
	emb AI898009 AI898009 EST267452 tomato ovary, TAMU Lycopersicon ...	40 0.012
	emb AI897456 AI897456 EST266899 tomato ovary, TAMU Lycopersicon ...	40 0.012
30	emb AI483612 AI483612 EST249462 tomato ovary, TAMU Lycopersicon ...	40 0.012
	emb AI489818 AI489818 EST248157 tomato ovary, TAMU Lycopersicon ...	40 0.012
	emb AI487398 AI487398 EST245720 tomato ovary, TAMU Lycopersicon ...	40 0.012
	emb AI487859 AI487859 EST246181 tomato ovary, TAMU Lycopersicon ...	40 0.012
	emb AI484497 AI484497 EST242507 tomato ovary, TAMU Lycopersicon ...	40 0.012
35	emb AI490243 AI490243 EST248569 tomato ovary, TAMU Lycopersicon ...	40 0.012
	emb AI897392 AI897392 EST266835 tomato ovary, TAMU Lycopersicon ...	40 0.012
	emb AW219347 AW219347 EST301829 tomato root during/after fruit s...	33 0.014
	emb AW621529 AW621529 EST312327 tomato root during/after fruit s...	35 0.025
	emb AW622375 AW622375 EST313174 tomato root during/after fruit s...	35 0.026
40	emb AW622390 AW622390 EST313189 tomato root during/after fruit s...	35 0.029
	emb AI486656 AI486656 EST244977 tomato ovary, TAMU Lycopersicon ...	38 0.031
	emb AW399651 AW399651 EST310151 L. pennellii trichome, Cornell U...	38 0.043
	emb AW621171 AW621171 EST311969 tomato root during/after fruit s...	34 0.048
	emb AW622051 AW622051 EST312849 tomato root during/after fruit s...	34 0.053
45	emb AI485044 AI485044 EST243324 tomato ovary, TAMU Lycopersicon ...	37 0.059
	emb AW622079 AW622079 EST312877 tomato root during/after fruit s...	33 0.061
	emb AW621330 AW621330 EST312128 tomato root during/after fruit s...	33 0.061
	emb AW220086 AW220086 EST302569 tomato root during/after fruit s...	33 0.065
	emb AW621962 AW621962 EST312760 tomato root during/after fruit s...	33 0.070
50	emb AF153353 AF153353 Dimocarpus longan ribulose 1,5-bisphosphat...	36 0.15
	emb A26964 A26964 D.merkii AMP2-sequence.	35 0.21
	emb AW621634 AW621634 EST312432 tomato root during/after fruit s...	31 0.32
	emb AW255597 AW255597 ML641 peppermint glandular trichome Mentha...	35 0.40
	emb Y15150 GMY15150 Gonystylus macrophyllus rbcL gene.	34 0.54
55	emb Y15139 BOY15139 Bixa orellana chloroplast rbcL gene.	34 0.54
	emb Y15149 ABY15149 Aquilaria beccariana rbcL gene.	34 0.54
	emb AF022128 AF022128 Bixa orellana ribulose 1,5-bisphosphate ca...	34 0.54
	emb AF022125 AF022125 Theobroma cacao ribulose 1,5-bisphosphate ...	34 0.54
	gb L12568 AKARBC Akania bidwillii ribulosebisphosphate carboxyla...	34 0.54
60	emb A27063 A27063 L.cicera AFP sequence.	34 0.54
	gb M95753 BCNCPRBCL Bretschneidera sinensis chloroplast ribulose...	34 0.54

	gb BE124525 BE124525 EST393560 GVN Medicago truncatula cDNA clon...	31	0.68
	emb AW725876 AW725876 GA__Ea0020A08 Gossypium arboreum 7-10 dpa ...	34	0.75
	gb L01579 PEADRR230B Pea (pi39) disease resistance response prot...	34	0.75
	emb AJ757757 AJ757757 EtESTea34d02.y1 Eimeria S5-2 Sporozoite st...	34	0.75
5	gb L14293 HDOCPRBCL Hydrolea ovata chloroplast ribulosebisphosph...	33	1.0
	emb AL138618 LMFL2954 Leishmania major Friedlin chromosome 23 co...	33	1.4
	emb AJ233156 PPAJ3156 Pentace polyantha chloroplast rbcL gene, p...	33	1.4
	gb L01961 TEPCPRBCL Thespesia populnea ribulose 1,5-bisphosphate...	33	1.4
	emb AJ233137 RTAJ3137 Reevesia thyrsoidea chloroplast rbcL gene,...	33	1.4
10	emb AJ233145 ATAJ3145 Apeiba tibourbou chloroplast rbcL gene, pa...	33	1.4
	emb AJ233117 MCAJ3117 Matisia cordata chloroplast rbcL gene, par...	33	1.4
	emb AJ233116 CSAJ3116 Chorisia speciosa chloroplast rbcL gene, p...	33	1.4
	emb AJ233127 HBAJ3127 Helicteres baruensis chloroplast rbcL gene...	33	1.4
	gb M77700 COTRBCLA Gossypium hirsutum ribulosebiphosphate carbox...	33	1.4
15	emb AJ012208 AAU012208 Abroma angusta chloroplast rbcL gene.	33	1.4
	emb AF022127 AF022127 Tilia americana ribulose 1,5-bisphosphate ...	33	1.4
	emb AF022126 AF022126 Sterculia tragacantha ribulose 1,5-bisphos...	33	1.4
	emb AF022121 AF022121 Quararibea gomeziana ribulose 1,5-bisphosp...	33	1.4
	emb AF022120 AF022120 Camptostemon schultzei ribulose 1,5-bispho...	33	1.4
20	emb AF022119 AF022119 Durio zibethinus ribulose 1,5-bisphosphate...	33	1.4
	emb AF022118 AF022118 Bombax buonopozense ribulose 1,5-bisphosph...	33	1.4
	gb L13186 COTCPRBCLA Gossypium ronbinsonii chloroplast ribuloseb...	33	1.4
	emb AJ233155 MAAJ3155 Mortoniodendron anisophyllum chloroplast r...	33	1.4
	emb AJ233131 HBAJ3131 Hildegardia barteri chloroplast rbcL gene,...	33	1.4
25	gb U38925 QAU38925 Quassia amara ribulose 1,5-bisphosphate carbo...	33	1.4
	emb AJ233134 LPAJ3134 Leptonychia pallida chloroplast rbcL gene,...	33	1.4
	emb AJ233151 GMAJ3151 Goethalsia meiantha chloroplast rbcL gene,...	33	1.4
	emb AJ233150 CFAJ3150 Colona floribunda chloroplast rbcL gene, p...	33	1.4
	emb AJ233149 CAAJ3149 Christiana africana chloroplast rbcL gene,...	33	1.4
30	emb AJ233157 PDAJ3157 Pentaplaris doroteae chloroplast rbcL gene...	33	1.4

Query= AC006577.16_i_at 12777_i_at /id_source genbank /description
 "gb|aad25772.1|ac006577_8 (ac006577) belongs to the pf|00657
 35 lipase/acylhydrolase with gds1-motif family. ests gb|t44453,
 gb|t04815, gb|t45993, gb|r30138, gb|ai099570 and gb|t22281 come from
 this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family
 /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 40 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006577|/ncgi
 http://www.ncgr.org/cgi-bin/ff?ac006577
 (1194 letters)

Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	
50	Sequences producing significant alignments:	(bits)	Value
	emb Y10156 BNMYAP12 B.napus for myrosinase-associated protein, c...	224	e-163
	emb Y10155 BNMYAP9 B.napus for myrosinase-associated protein, cl...	224	e-160
	gb U39289 BNU39289 Brassica napus myrosinase-associated protein ...	227	e-156
55	gb U39319 BNU39319 Brassica napus myrosinase-associated protein ...	176	e-127
	emb AJ223307 BNAJ3307 Brassica napus gene encoding induced myros...	176	6e-99
	emb AW568594 AW568594 si78g03.y1 Gm-c1031 Glycine max cDNA clone...	47	1e-13
	emb AW288014 AW288014 N100858e rootphos(-) Medicago truncatula c...	67	3e-13
	emb AW774945 AW774945 EST334096 KV3 Medicago truncatula cDNA clo...	46	5e-13
60	emb AW685185 AW685185 NF025E06NR1F1000 Nodulated root Medicago t...	62	1e-10
	emb AW922141 AW922141 LG1_323_G11.b1_A002 Light Grown 1 (LG1) So...	65	5e-10

	emb AW687872 AW687872 NF014D07RT1F1061 Developing root Medicago ...	46	2e-09
	emb AW687276 AW687276 NF007H04RT1F1043 Developing root Medicago ...	46	7e-09
	emb AW621314 AW621314 EST312112 tomato root during/after fruit s...	44	1e-08
	emb AW922142 AW922142 LG1_323_G10.b1_A002 Light Grown 1 (LG1) So...	58	1e-07
5	emb AW164470 AW164470 se73a09.y1 Gm-c1023 Glycine max cDNA clone...	58	2e-07
	emb AW201360 AW201360 sf02b11.y1 Gm-c1027 Glycine max cDNA clone...	47	2e-07
	emb AW757161 AW757161 sl29h09.y1 Gm-c1027 Glycine max cDNA clone...	46	3e-07
	emb AW689694 AW689694 NF023C12ST1F1000 Developing stem Medicago ...	44	3e-07
	emb AW686342 AW686342 NF040F06NR1F1000 Nodulated root Medicago t...	46	3e-07
10	emb AW622151 AW622151 EST312949 tomato root during/after fruit s...	47	6e-07
	emb AW623994 AW623994 EST321939 tomato flower buds 3-8 mm, Corne...	48	6e-07
	emb AW621737 AW621737 EST312535 tomato root during/after fruit s...	47	6e-07
	emb AI482693 AI482693 EST242016 tomato shoot, Cornell Lycopersic...	48	7e-07
	emb AW622612 AW622612 EST313412 tomato root during/after fruit s...	46	1e-06
15	emb AW596685 AW596685 sj15e02.y1 Gm-c1032 Glycine max cDNA clone...	49	2e-06
	emb AW328890 AW328890 N200082e rootphos(-) Medicago truncatula c...	41	2e-06
	emb AW621604 AW621604 EST312402 tomato root during/after fruit s...	45	2e-06
	emb AI725483 AI725483 BNLGHi12267 Six-day Cotton fiber Gossypium...	40	4e-06
	emb AI726639 AI726639 BNLGHi6294 Six-day Cotton fiber Gossypium ...	51	4e-06
20	emb AI488194 AI488194 EST246516 tomato ovary, TAMU Lycopersicon ...	40	4e-06
	emb AW616223 AW616223 EST307262 L. hirsutum trichome, Cornell Un...	53	5e-06
	emb AW650481 AW650481 EST328935 tomato germinating seedlings, TA...	53	5e-06
	emb AI731912 AI731912 BNLGHi11257 Six-day Cotton fiber Gossypium...	51	6e-06
	emb AW981891 AW981891 PC19H06 Pine TriplEx pollen cone library P...	51	6e-06
25	emb AI726794 AI726794 BNLGHi6582 Six-day Cotton fiber Gossypium ...	50	7e-06
	gb BE057806 BE057806 sn07e03.y1 Gm-c1016 Glycine max cDNA clone ...	48	1e-05
	emb AI731726 AI731726 BNLGHi10587 Six-day Cotton fiber Gossypium...	37	1e-05
	emb AI959774 AI959774 sc94a03.y1 Gm-c1019 Glycine max cDNA clone...	36	2e-05
	emb AW509227 AW509227 sh92h02.y1 Gm-c1016 Glycine max cDNA clone...	42	2e-05
30	emb AI054484 AI054484 coau0001C01 Cotton Boll Abscission Zone cD...	42	3e-05
	emb AW127684 AW127684 M110431 DSLC Medicago truncatula cDNA clon...	38	3e-05
	emb AW564505 AW564505 LG1_295_D11.b1_A002 Light Grown 1 (LG1) So...	49	9e-05
	emb AI487871 AI487871 EST246193 tomato ovary, TAMU Lycopersicon ...	39	1e-04
	emb AJ276421 CAR276421 Cicer arietinum partial mRNA for putative...	48	1e-04
35	emb AW277884 AW277884 sf88f10.y1 Gm-c1019 Glycine max cDNA clone...	42	2e-04
	emb AW459066 AW459066 sh18h02.y1 Gm-c1016 Glycine max cDNA clone...	40	2e-04
	emb AW926586 AW926586 HVSMEg0007J20 Hordeum vulgare pre-anthesis...	47	2e-04
	emb AI731989 AI731989 BNLGHi11154 Six-day Cotton fiber Gossypium...	45	3e-04
	emb AW011080 AW011080 ST16D12 Pine TriplEx shoot tip library Pin...	43	3e-04
40	gb BE124032 BE124032 EST394157 DSIL Medicago truncatula cDNA clo...	47	3e-04
	emb AI730716 AI730716 BNLGHi7722 Six-day Cotton fiber Gossypium ...	47	3e-04
	emb AW929104 AW929104 EST337808 tomato flower buds 8 mm to pre-a...	33	5e-04
	emb AW624906 AW624906 EST313735 tomato radicle, 5 d post-imbibit...	35	5e-04
	emb AW706408 AW706408 sj56h10.y1 Gm-c1033 Glycine max cDNA clone...	46	6e-04
45	gb BE054438 BE054438 GA_Ea0004H20f Gossypium arboreum 7-10 dpa ...	45	7e-04
	emb AW109570 AW109570 gate0004H20f Gossypium arboreum 7-10 dpa f...	45	7e-04
	emb AW279386 AW279386 sf66f11.y1 Gm-c1013 Glycine max cDNA clone...	37	7e-04
	emb AW720472 AW720472 LjNEST19f4r Lotus japonicus nodule library...	35	7e-04
	emb AW458524 AW458524 sh10c06.y1 Gm-c1016 Glycine max cDNA clone...	37	8e-04
50	emb AI731645 AI731645 BNLGHi10354 Six-day Cotton fiber Gossypium...	46	8e-04
	emb AI729137 AI729137 BNLGHi12747 Six-day Cotton fiber Gossypium...	46	8e-04
	emb AW574285 AW574285 EST316876 GVN Medicago truncatula cDNA clo...	33	0.001
	emb AI728284 AI728284 BNLGHi10336 Six-day Cotton fiber Gossypium...	45	0.001
	emb AW160215 AW160215 EST290073 L. pennellii trichome, Cornell U...	45	0.002
55	emb AI729089 AI729089 BNLGHi12599 Six-day Cotton fiber Gossypium...	45	0.002
	gb H74345 H74345 249 Deletion-treated Brassica napus cDNA clone ...	37	0.002
	emb AW733443 AW733443 sk73f03.y1 Gm-c1016 Glycine max cDNA clone...	37	0.002
	emb AW509209 AW509209 sh92f05.y1 Gm-c1016 Glycine max cDNA clone...	38	0.002
	emb AW459862 AW459862 sh96c02.y1 Gm-c1016 Glycine max cDNA clone...	37	0.002
60	emb AW459861 AW459861 sh96c01.y1 Gm-c1016 Glycine max cDNA clone...	37	0.002
	emb AJ011567 DLA011567 Digitalis lanata mRNA for lanatoside 15'-...	38	0.002

emb|AW616728|AW616728 EST323139 L. hirsutum trichome, Cornell Un... 33 0.003
 emb|AW733540|AW733540 sk74h07.y1 Gm-c1016 Glycine max cDNA clone... 37 0.003
 emb|AW733459|AW733459 sk73h02.y1 Gm-c1016 Glycine max cDNA clone... 37 0.003
 emb|AW396681|AW396681 sh29d09.y1 Gm-c1017 Glycine max cDNA clone... 44 0.003
 5 gb|BE023812|BE023812 sm92g03.y1 Gm-c1015 Glycine max cDNA clone ... 44 0.003
 gb|BE023398|BE023398 sm81c12.y1 Gm-c1015 Glycine max cDNA clone ... 44 0.003
 emb|AW984927|AW984927 NXNV_131_B12_F Nsf Xylem Normal wood Verti... 38 0.003
 emb|AW127455|AW127455 M110643 DSIL Medicago truncatula cDNA clon... 36 0.003
 gb|L37975|L37975 BNAF0021E Mustard flower buds Brassica rapa cDN... 35 0.004
 10 emb|AW099099|AW099099 sd34d08.y1 Gm-c1012 Glycine max cDNA clone... 43 0.004
 gb|BE057305|BE057305 sn01c10.y1 Gm-c1015 Glycine max cDNA clone ... 43 0.004
 emb|AW458657|AW458657 sh12a06.y1 Gm-c1016 Glycine max cDNA clone... 43 0.004
 emb|AW923224|AW923224 DG1_50_A07.b1_A002 Dark Grown 1 (DG1) Sorg... 43 0.004
 emb|AW648494|AW648494 EST326948 tomato germinating seedlings, TA... 43 0.005
 15 emb|AI965889|AI965889 sc79c08.y1 Gm-c1018 Glycine max cDNA clone... 43 0.005
 emb|AI487258|AI487258 EST245580 tomato ovary, TAMU Lycopersicon ... 43 0.005
 emb|AW218200|AW218200 EST303381 tomato radicle, 5 d post-imbibit... 43 0.005
 emb|AI486112|AI486112 EST244433 tomato ovary, TAMU Lycopersicon ... 43 0.005
 gb|BE033445|BE033445 ME02B01 ME Mesembryanthemum crystallinum cD... 38 0.006
 20 emb|AW348454|AW348454 GM210002A22E12R Gm-r1021 Glycine max cDNA ... 39 0.006
 emb|AI900221|AI900221 sc02f01.y1 Gm-c1012 Glycine max cDNA clone... 32 0.006
 emb|AW666820|AW666820 GA_Ea0006B14 Gossypium arboreum 7-10 dpa ... 35 0.006
 emb|AW624162|AW624162 EST322107 tomato flower buds 3-8 mm, Corne... 34 0.006
 emb|AW667892|AW667892 GA_Ea0011E24 Gossypium arboreum 7-10 dpa ... 42 0.007
 25 emb|AW667522|AW667522 GA_Ea0009J12 Gossypium arboreum 7-10 dpa ... 42 0.007
 emb|AW730008|AW730008 GA_Ea0027E20 Gossypium arboreum 7-10 dpa ... 36 0.008
 emb|AT000294|AT000294 AT000294 Apple young fruit cDNA library Ma... 42 0.010
 emb|AW100112|AW100112 sd20e02.y2 Gm-c1012 Glycine max cDNA clone... 30 0.012
 emb|AW394864|AW394864 sh36e01.y1 Gm-c1017 Glycine max cDNA clone... 41 0.014
 30

Query= AC006577.16_r_at 12778_r_at /id_source genbank /description
 "gb|aad25772.1|ac006577_8 (ac006577) belongs to the pf|00657
 lipase/acylhydrolase with gds1-motif family. ests gb|t44453,
 gb|t04815, gb|t45993, gb|r30138, gb|ai099570 and gb|t22281 come from
 35 this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family
 /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006577|/ncgi
 http://www.ncgr.org/cgi-bin/ff?ac006577
 40 (1194 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

45 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

50 emb|Y10156|BNMYAP12 B.napus for myrosinase-associated protein, c... 224 e-163
 emb|Y10155|BNMYAP9 B.napus for myrosinase-associated protein, cl... 224 e-160
 gb|U39289|BNU39289 Brassica napus myrosinase-associated protein ... 227 e-156
 gb|U39319|BNU39319 Brassica napus myrosinase-associated protein ... 176 e-127
 emb|AJ223307|BNAJ3307 Brassica napus gene encoding induced myros... 176 6e-99
 55 emb|AW568594|AW568594 si78g03.y1 Gm-c1031 Glycine max cDNA clone... 47 1e-13
 emb|AW288014|AW288014 N100858e rootphos(-) Medicago truncatula c... 67 3e-13
 emb|AW774945|AW774945 EST334096 KV3 Medicago truncatula cDNA clo... 46 5e-13
 emb|AW685185|AW685185 NF025E06NR1F1000 Nodulated root Medicago t... 62 1e-10
 emb|AW922141|AW922141 LG1_323_G11.b1_A002 Light Grown 1 (LG1) So... 65 5e-10
 60 emb|AW687872|AW687872 NF014D07RT1F1061 Developing root Medicago ... 46 2e-09
 emb|AW687276|AW687276 NF007H04RT1F1043 Developing root Medicago ... 46 7e-09

	emb AW621314 AW621314 EST312112 tomato root during/after fruit s...	44	1e-08
	emb AW922142 AW922142 LG1_323_G10.b1_A002 Light Grown 1 (LG1) So...	58	1e-07
	emb AW164470 AW164470 se73a09.y1 Gm-c1023 Glycine max cDNA clone...	58	2e-07
	emb AW201360 AW201360 sf02b11.y1 Gm-c1027 Glycine max cDNA clone...	47	2e-07
5	emb AW757161 AW757161 sl29h09.y1 Gm-c1027 Glycine max cDNA clone...	46	3e-07
	emb AW689694 AW689694 NF023C12ST1F1000 Developing stem Medicago ...	44	3e-07
	emb AW686342 AW686342 NF040F06NR1F1000 Nodulated root Medicago t...	46	3e-07
	emb AW622151 AW622151 EST312949 tomato root during/after fruit s...	47	6e-07
	emb AW623994 AW623994 EST321939 tomato flower buds 3-8 mm, Corne...	48	6e-07
10	emb AW621737 AW621737 EST312535 tomato root during/after fruit s...	47	6e-07
	emb AI482693 AI482693 EST242016 tomato shoot, Cornell Lycopersic...	48	7e-07
	emb AW622612 AW622612 EST313412 tomato root during/after fruit s...	46	1e-06
	emb AW596685 AW596685 sj15e02.y1 Gm-c1032 Glycine max cDNA clone...	49	2e-06
	emb AW328890 AW328890 N200082e rootphos(-) Medicago truncatula c...	41	2e-06
15	emb AW621604 AW621604 EST312402 tomato root during/after fruit s...	45	2e-06
	emb AI725483 AI725483 BNLGHi12267 Six-day Cotton fiber Gossypium...	40	4e-06
	emb AI726639 AI726639 BNLGHi6294 Six-day Cotton fiber Gossypium ...	51	4e-06
	emb AI488194 AI488194 EST246516 tomato ovary, TAMU Lycopersicon ...	40	4e-06
	emb AW616223 AW616223 EST307262 L. hirsutum trichome, Cornell Un...	53	5e-06
20	emb AW650481 AW650481 EST328935 tomato germinating seedlings, TA...	53	5e-06
	emb AI731912 AI731912 BNLGHi11257 Six-day Cotton fiber Gossypium...	51	6e-06
	emb AW981891 AW981891 PC19H06 Pine TriplEx pollen cone library P...	51	6e-06
	emb AI726794 AI726794 BNLGHi6582 Six-day Cotton fiber Gossypium ...	50	7e-06
	gb BE057806 BE057806 sn07e03.y1 Gm-c1016 Glycine max cDNA clone ...	48	1e-05
25	emb AI731726 AI731726 BNLGHi10587 Six-day Cotton fiber Gossypium...	37	1e-05
	emb AI959774 AI959774 sc94a03.y1 Gm-c1019 Glycine max cDNA clone...	36	2e-05
	emb AW509227 AW509227 sh92h02.y1 Gm-c1016 Glycine max cDNA clone...	42	2e-05
	emb AI054484 AI054484 coau0001C01 Cotton Boll Abscission Zone cD...	42	3e-05
	emb AW127684 AW127684 M110431 DSLC Medicago truncatula cDNA clon...	38	3e-05
30	emb AW564505 AW564505 LG1_295_D11.b1_A002 Light Grown 1 (LG1) So...	49	9e-05
	emb AI487871 AI487871 EST246193 tomato ovary, TAMU Lycopersicon ...	39	1e-04
	emb AJ276421 CAR276421 Cicer arietinum partial mRNA for putative...	48	1e-04
	emb AW277884 AW277884 sf88f10.y1 Gm-c1019 Glycine max cDNA clone...	42	2e-04
	emb AW459066 AW459066 sh18h02.y1 Gm-c1016 Glycine max cDNA clone...	40	2e-04
35	emb AW926586 AW926586 HVSMEg0007J20 Hordeum vulgare pre-anthesis...	47	2e-04
	emb AI731989 AI731989 BNLGHi11154 Six-day Cotton fiber Gossypium...	45	3e-04
	emb AW011080 AW011080 ST16D12 Pine TriplEx shoot tip library Pin...	43	3e-04
	gb BE124032 BE124032 EST394157 DSIL Medicago truncatula cDNA clo...	47	3e-04
	emb AI730716 AI730716 BNLGHi7722 Six-day Cotton fiber Gossypium ...	47	3e-04
40	emb AW929104 AW929104 EST337808 tomato flower buds 8 mm to pre-a...	33	5e-04
	emb AW624906 AW624906 EST313735 tomato radicle, 5 d post-imbibit...	35	5e-04
	emb AW706408 AW706408 sj56h10.y1 Gm-c1033 Glycine max cDNA clone...	46	6e-04
	gb BE054438 BE054438 GA_Ea0004H20f Gossypium arboreum 7-10 dpa ...	45	7e-04
	emb AW109570 AW109570 gate0004H20f Gossypium arboreum 7-10 dpa f...	45	7e-04
45	emb AW279386 AW279386 sf66f11.y1 Gm-c1013 Glycine max cDNA clone...	37	7e-04
	emb AW720472 AW720472 LjNEST19f4r Lotus japonicus nodule library...	35	7e-04
	emb AW458524 AW458524 sh10c06.y1 Gm-c1016 Glycine max cDNA clone...	37	8e-04
	emb AI731645 AI731645 BNLGHi10354 Six-day Cotton fiber Gossypium...	46	8e-04
	emb AI729137 AI729137 BNLGHi12747 Six-day Cotton fiber Gossypium...	46	8e-04
50	emb AW574285 AW574285 EST316876 GVN Medicago truncatula cDNA clo...	33	0.001
	emb AI728284 AI728284 BNLGHi10336 Six-day Cotton fiber Gossypium...	45	0.001
	emb AW160215 AW160215 EST290073 L. pennellii trichome, Cornell U...	45	0.002
	emb AI729089 AI729089 BNLGHi12599 Six-day Cotton fiber Gossypium...	45	0.002
	gb H74345 H74345 249 Deletion-treated Brassica napus cDNA clone ...	37	0.002
55	emb AW733443 AW733443 sk73f03.y1 Gm-c1016 Glycine max cDNA clone...	37	0.002
	emb AW509209 AW509209 sh92f05.y1 Gm-c1016 Glycine max cDNA clone...	38	0.002
	emb AW459862 AW459862 sh96c02.y1 Gm-c1016 Glycine max cDNA clone...	37	0.002
	emb AW459861 AW459861 sh96c01.y1 Gm-c1016 Glycine max cDNA clone...	37	0.002
	emb AJ011567 DLA011567 Digitalis lanata mRNA for lanatoside 15'...	38	0.002
60	emb AW616728 AW616728 EST323139 L. hirsutum trichome, Cornell Un...	33	0.003
	emb AW733540 AW733540 sk74h07.y1 Gm-c1016 Glycine max cDNA clone...	37	0.003

emb|AW733459|AW733459 sk73h02.y1 Gm-c1016 Glycine max cDNA clone... 37 0.003
 emb|AW396681|AW396681 sh29d09.y1 Gm-c1017 Glycine max cDNA clone... 44 0.003
 gb|BE023812|BE023812 sm92g03.y1 Gm-c1015 Glycine max cDNA clone ... 44 0.003
 gb|BE023398|BE023398 sm81c12.y1 Gm-c1015 Glycine max cDNA clone ... 44 0.003
 5 emb|AW984927|AW984927 NXNV_131_B12_F Nsf Xylem Normal wood Verti... 38 0.003
 emb|AW127455|AW127455 M110643 DSIL Medicago truncatula cDNA clon... 36 0.003
 gb|L37975|L37975 BNAF0021E Mustard flower buds Brassica rapa cDN... 35 0.004
 emb|AW099099|AW099099 sd34d08.y1 Gm-c1012 Glycine max cDNA clone... 43 0.004
 gb|BE057305|BE057305 sn01c10.y1 Gm-c1015 Glycine max cDNA clone ... 43 0.004
 10 emb|AW458657|AW458657 sh12a06.y1 Gm-c1016 Glycine max cDNA clone... 43 0.004
 emb|AW923224|AW923224 DG1_50_A07.b1_A002 Dark Grown 1 (DG1) Sorg... 43 0.004
 emb|AW648494|AW648494 EST326948 tomato germinating seedlings, TA... 43 0.005
 emb|AI965889|AI965889 sc79c08.y1 Gm-c1018 Glycine max cDNA clone... 43 0.005
 emb|AI487258|AI487258 EST245580 tomato ovary, TAMU Lycopersicon ... 43 0.005
 15 emb|AW218200|AW218200 EST303381 tomato radicle, 5 d post-imbibit... 43 0.005
 emb|AI486112|AI486112 EST244433 tomato ovary, TAMU Lycopersicon ... 43 0.005
 gb|BE033445|BE033445 ME02B01 ME Mesembryanthemum crystallinum cD... 38 0.006
 emb|AW348454|AW348454 GM210002A22E12R Gm-r1021 Glycine max cDNA ... 39 0.006
 emb|AI900221|AI900221 sc02f01.y1 Gm-c1012 Glycine max cDNA clone... 32 0.006
 20 emb|AW666820|AW666820 GA_Ea0006B14 Gossypium arboreum 7-10 dpa ... 35 0.006
 emb|AW624162|AW624162 EST322107 tomato flower buds 3-8 mm, Corne... 34 0.006
 emb|AW667892|AW667892 GA_Ea0011E24 Gossypium arboreum 7-10 dpa ... 42 0.007
 emb|AW667522|AW667522 GA_Ea0009J12 Gossypium arboreum 7-10 dpa ... 42 0.007
 emb|AW730008|AW730008 GA_Ea0027E20 Gossypium arboreum 7-10 dpa ... 36 0.008
 25 emb|AT000294|AT000294 AT000294 Apple young fruit cDNA library Ma... 42 0.010
 emb|AW100112|AW100112 sd20e02.y2 Gm-c1012 Glycine max cDNA clone... 30 0.012
 emb|AW394864|AW394864 sh36e01.y1 Gm-c1017 Glycine max cDNA clone... 41 0.014

30 Query= AC006577.16_f_at 12779_f_at /id_source genbank /description
 "gb|aad25772.1|ac006577_8 (ac006577) belongs to the pf|00657
 lipase/acylhydrolase with gds1-motif family. ests gb|t44453,
 gb|t04815, gb|t45993, gb|r30138, gb|ai099570 and gb|t22281 come from
 this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family
 35 /chip nova /gb_link /ncgi
 (1194 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

	Score	E	(bits)	Value
45	Sequences producing significant alignments:			
	emb Y10156 BNMYAP12	B.napus for myrosinase-associated protein, c...	224	e-163
	emb Y10155 BNMYAP9	B.napus for myrosinase-associated protein, cl...	224	e-160
	gb U39289 BNU39289	Brassica napus myrosinase-associated protein ...	227	e-156
	gb U39319 BNU39319	Brassica napus myrosinase-associated protein ...	176	e-127
50	emb AJ223307 BNAJ3307	Brassica napus gene encoding induced myros...	176	6e-99
	emb AW568594 AW568594	si78g03.y1 Gm-c1031 Glycine max cDNA clone...	47	1e-13
	emb AW288014 AW288014	N100858e rootphos(-) Medicago truncatula c...	67	3e-13
	emb AW774945 AW774945	EST334096 KV3 Medicago truncatula cDNA clo...	46	5e-13
	emb AW685185 AW685185	NF025E06NR1F1000 Nodulated root Medicago t...	62	1e-10
55	emb AW922141 AW922141	LG1_323_G11.b1_A002 Light Grown 1 (LG1) So...	65	5e-10
	emb AW687872 AW687872	NF014D07RT1F1061 Developing root Medicago ...	46	2e-09
	emb AW687276 AW687276	NF007H04RT1F1043 Developing root Medicago ...	46	7e-09
	emb AW621314 AW621314	EST312112 tomato root during/after fruit s...	44	1e-08
	emb AW922142 AW922142	LG1_323_G10.b1_A002 Light Grown 1 (LG1) So...	58	1e-07
60	emb AW164470 AW164470	se73a09.y1 Gm-c1023 Glycine max cDNA clone...	58	2e-07
	emb AW201360 AW201360	sf02b11.y1 Gm-c1027 Glycine max cDNA clone...	47	2e-07

	emb AW757161 AW757161 sl29h09.y1 Gm-c1027 Glycine max cDNA clone...	46 3e-07
	emb AW689694 AW689694 NF023C12ST1F1000 Developing stem Medicago ...	44 3e-07
	emb AW686342 AW686342 NF040F06NR1F1000 Nodulated root Medicago t...	46 3e-07
	emb AW622151 AW622151 EST312949 tomato root during/after fruit s...	47 6e-07
5	emb AW623994 AW623994 EST321939 tomato flower buds 3-8 mm, Corne...	48 6e-07
	emb AW621737 AW621737 EST312535 tomato root during/after fruit s...	47 6e-07
	emb AI482693 AI482693 EST242016 tomato shoot, Cornell Lycopersic...	48 7e-07
	emb AW622612 AW622612 EST313412 tomato root during/after fruit s...	46 1e-06
	emb AW596685 AW596685 sj15e02.y1 Gm-c1032 Glycine max cDNA clone...	49 2e-06
10	emb AW328890 AW328890 N200082e rootphos(-) Medicago truncatula c...	41 2e-06
	emb AW621604 AW621604 EST312402 tomato root during/after fruit s...	45 2e-06
	emb AI725483 AI725483 BNLGHi12267 Six-day Cotton fiber Gossypium...	40 4e-06
	emb AI726639 AI726639 BNLGHi6294 Six-day Cotton fiber Gossypium ...	51 4e-06
	emb AI488194 AI488194 EST246516 tomato ovary, TAMU Lycopersicon ...	40 4e-06
15	emb AW616223 AW616223 EST307262 L. hirsutum trichome, Cornell Un...	53 5e-06
	emb AW650481 AW650481 EST328935 tomato germinating seedlings, TA...	53 5e-06
	emb AI731912 AI731912 BNLGHi11257 Six-day Cotton fiber Gossypium...	51 6e-06
	emb AW981891 AW981891 PC19H06 Pine TriplEx pollen cone library P...	51 6e-06
	emb AI726794 AI726794 BNLGHi6582 Six-day Cotton fiber Gossypium ...	50 7e-06
20	gb BE057806 BE057806 sn07e03.y1 Gm-c1016 Glycine max cDNA clone ...	48 1e-05
	emb AI731726 AI731726 BNLGHi10587 Six-day Cotton fiber Gossypium...	37 1e-05
	emb AI959774 AI959774 sc94a03.y1 Gm-c1019 Glycine max cDNA clone...	36 2e-05
	emb AW509227 AW509227 sh92h02.y1 Gm-c1016 Glycine max cDNA clone...	42 2e-05
	emb AI054484 AI054484 coau0001C01 Cotton Boll Abscission Zone cD...	42 3e-05
25	emb AW127684 AW127684 M110431 DSLC Medicago truncatula cDNA clon...	38 3e-05
	emb AW564505 AW564505 LG1_295_D11.b1_A002 Light Grown 1 (LG1) So...	49 9e-05
	emb AI487871 AI487871 EST246193 tomato ovary, TAMU Lycopersicon ...	39 1e-04
	emb AJ276421 CAR276421 Cicer arietinum partial mRNA for putative...	48 1e-04
	emb AW277884 AW277884 sf88f10.y1 Gm-c1019 Glycine max cDNA clone...	42 2e-04
30	emb AW459066 AW459066 sh18h02.y1 Gm-c1016 Glycine max cDNA clone...	40 2e-04
	emb AW926586 AW926586 HVSMEg0007J20 Hordeum vulgare pre-anthesis...	47 2e-04
	emb AI731989 AI731989 BNLGHi11154 Six-day Cotton fiber Gossypium...	45 3e-04
	emb AW011080 AW011080 ST16D12 Pine TriplEx shoot tip library Pin...	43 3e-04
	gb BE124032 BE124032 EST394157 DSIL Medicago truncatula cDNA clo...	47 3e-04
35	emb AI730716 AI730716 BNLGHi7722 Six-day Cotton fiber Gossypium ...	47 3e-04
	emb AW929104 AW929104 EST337808 tomato flower buds 8 mm to pre-a...	33 5e-04
	emb AW624906 AW624906 EST313735 tomato radicle, 5 d post-imbibit...	35 5e-04
	emb AW706408 AW706408 sj56h10.y1 Gm-c1033 Glycine max cDNA clone...	46 6e-04
	gb BE054438 BE054438 GA__Ea0004H20f Gossypium arboreum 7-10 dpa ...	45 7e-04
40	emb AW109570 AW109570 gate0004H20f Gossypium arboreum 7-10 dpa f...	45 7e-04
	emb AW279386 AW279386 sf66f11.y1 Gm-c1013 Glycine max cDNA clone...	37 7e-04
	emb AW720472 AW720472 LjNEST19f4r Lotus japonicus nodule library...	35 7e-04
	emb AW458524 AW458524 sh10c06.y1 Gm-c1016 Glycine max cDNA clone...	37 8e-04
	emb AI731645 AI731645 BNLGHi10354 Six-day Cotton fiber Gossypium...	46 8e-04
45	emb AI729137 AI729137 BNLGHi12747 Six-day Cotton fiber Gossypium...	46 8e-04
	emb AW574285 AW574285 EST316876 GVN Medicago truncatula cDNA clo...	33 0.001
	emb AI728284 AI728284 BNLGHi10336 Six-day Cotton fiber Gossypium...	45 0.001
	emb AW160215 AW160215 EST290073 L. pennellii trichome, Cornell U...	45 0.002
	emb AI729089 AI729089 BNLGHi12599 Six-day Cotton fiber Gossypium...	45 0.002
50	gb H74345 H74345 249 Deletion-treated Brassica napus cDNA clone ...	37 0.002
	emb AW733443 AW733443 sk73f03.y1 Gm-c1016 Glycine max cDNA clone...	37 0.002
	emb AW509209 AW509209 sh92f05.y1 Gm-c1016 Glycine max cDNA clone...	38 0.002
	emb AW459862 AW459862 sh96c02.y1 Gm-c1016 Glycine max cDNA clone...	37 0.002
	emb AW459861 AW459861 sh96c01.y1 Gm-c1016 Glycine max cDNA clone...	37 0.002
55	emb AJ011567 DLA011567 Digitalis lanata mRNA for lanatoside 15'...	38 0.002
	emb AW616728 AW616728 EST323139 L. hirsutum trichome, Cornell Un...	33 0.003
	emb AW733540 AW733540 sk74h07.y1 Gm-c1016 Glycine max cDNA clone...	37 0.003
	emb AW733459 AW733459 sk73h02.y1 Gm-c1016 Glycine max cDNA clone...	37 0.003
	emb AW396681 AW396681 sh29d09.y1 Gm-c1017 Glycine max cDNA clone...	44 0.003
60	gb BE023812 BE023812 sm92g03.y1 Gm-c1015 Glycine max cDNA clone ...	44 0.003
	gb BE023398 BE023398 sm81c12.y1 Gm-c1015 Glycine max cDNA clone ...	44 0.003

emb|AW984927|AW984927 NXNV_131_B12_F Nsf Xylem Normal wood Verti... 38 0.003
 emb|AW127455|AW127455 M110643 DSIL Medicago truncatula cDNA clon... 36 0.003
 gb|L37975|L37975 BNAF0021E Mustard flower buds Brassica rapa cDN... 35 0.004
 emb|AW099099|AW099099 sd34d08.y1 Gm-c1012 Glycine max cDNA clone... 43 0.004
 5 gb|BE057305|BE057305 sn01c10.y1 Gm-c1015 Glycine max cDNA clone ... 43 0.004
 emb|AW458657|AW458657 sh12a06.y1 Gm-c1016 Glycine max cDNA clone... 43 0.004
 emb|AW923224|AW923224 DG1_50_A07.b1_A002 Dark Grown 1 (DG1) Sorg... 43 0.004
 emb|AW648494|AW648494 EST326948 tomato germinating seedlings, TA... 43 0.005
 emb|AI965889|AI965889 sc79c08.y1 Gm-c1018 Glycine max cDNA clone... 43 0.005
 10 emb|AI487258|AI487258 EST245580 tomato ovary, TAMU Lycopersicon ... 43 0.005
 emb|AW218200|AW218200 EST303381 tomato radicle, 5 d post-imbibit... 43 0.005
 emb|AI486112|AI486112 EST244433 tomato ovary, TAMU Lycopersicon ... 43 0.005
 gb|BE033445|BE033445 ME02B01 ME Mesembryanthemum crystallinum cD... 38 0.006
 emb|AW348454|AW348454 GM210002A22E12R Gm-r1021 Glycine max cDNA ... 39 0.006
 15 emb|AI900221|AI900221 sc02f01.y1 Gm-c1012 Glycine max cDNA clone... 32 0.006
 emb|AW666820|AW666820 GA_Ea0006B14 Gossypium arboreum 7-10 dpa ... 35 0.006
 emb|AW624162|AW624162 EST322107 tomato flower buds 3-8 mm, Corne... 34 0.006
 emb|AW667892|AW667892 GA_Ea0011E24 Gossypium arboreum 7-10 dpa ... 42 0.007
 emb|AW667522|AW667522 GA_Ea0009J12 Gossypium arboreum 7-10 dpa ... 42 0.007
 20 emb|AW730008|AW730008 GA_Ea0027E20 Gossypium arboreum 7-10 dpa ... 36 0.008
 emb|AT000294|AT000294 AT000294 Apple young fruit cDNA library Ma... 42 0.010
 emb|AW100112|AW100112 sd20e02.y2 Gm-c1012 Glycine max cDNA clone... 30 0.012
 emb|AW394864|AW394864 sh36e01.y1 Gm-c1017 Glycine max cDNA clone... 41 0.014

25

Query= AC003114.16_s_at 13067_s_at /id_source genbank /description
 "gb|aac24083.1| (ac003114) match to calreticulin (atcrt1) mrna
 gb|u27698 and dna gb|u66344. ests gb|t45719, gb|t22451, gb|h36323 and
 gb|aa042519 come from this gene. [arabidopsis thaliana]" /blast_score
 30 0 /ec_number /family /chip nova /gb_link /ncgi
 (1335 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

35

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

40

emb|AF019376|AF019376 Brassica napus calreticulin mRNA, complete... 619 0.0

gb|U74630|RCU74630 Ricinus communis calreticulin mRNA, complete ... 747 0.0

emb|Z71395|NPCAL1MNR N.plumbaginifolia mRNA for calreticulin. 742 0.0

emb|AF134733|AF134733 Prunus armeniaca calcium-binding protein c... 741 0.0

45

emb|AJ002057|BVMRNAC Beta vulgaris mRNA for calreticulin. 730 0.0

emb|X85382|NTRNATCAL N.tabacum mRNA for calreticulin. 726 0.0

emb|AF052040|AF052040 Berberis stolonifera calreticulin mRNA, co... 722 0.0

emb|X80756|CAPCRTC C.annuum PCRTC mRNA. 471 0.0

gb|L27348|BLYCRH1A Hordeum vulgare calreticulin (CRH1) mRNA, par... 670 0.0

50

gb|L27349|BLYCRH2A Hordeum vulgare calreticulin (CRH2) mRNA, par... 669 0.0

gb|U74631|RCU74631 Ricinus communis calreticulin gene, complete ... 201 e-172

emb|AW039860|AW039860 EST282333 tomato mixed elicitor, BTI Lycop... 517 e-145

emb|AB018243|AB018243 Solanum melongena EEF22 mRNA for calreticu... 510 e-143

emb|AI782264|AI782264 EST263143 tomato susceptible, Cornell Lyco... 497 e-140

55

emb|AW441195|AW441195 EST310591 tomato fruit red ripe, TAMU Lyco... 487 e-136

emb|AJ000765|CRAJ765 Chlamydomonas reinhardtii mRNA for calretic... 393 e-135

emb|AW930392|AW930392 EST340945 tomato fruit mature green, TAMU ... 478 e-134

emb|AW667951|AW667951 GA_Ea0012A11 Gossypium arboreum 7-10 dpa ... 472 e-132

emb|AW944954|AW944954 EST337004 tomato flower buds 3-8 mm, Corne... 469 e-131

60

emb|AW773947|AW773947 EST332933 KV3 Medicago truncatula cDNA clo... 469 e-131

emb|AW650947|AW650947 EST329401 tomato germinating seedlings, TA... 468 e-131

- emb|AW622049|AW622049 EST312847 tomato root during/after fruit s... 467 e-131
emb|AW216727|AW216727 EST295441 tomato callus, TAMU Lycopersicon... 460 e-128
emb|AW731454|AW731454 GA_Ea0030H17 Gossypium arboreum 7-10 dpa ... 456 e-127
emb|AI735991|AI735991 sb21e08.y1 Gm-cl007 Glycine max cDNA clone... 450 e-125
5 emb|Y09078|DBCALLKPR D.bioculata mRNA for calreticulin-like prot... 228 e-124
emb|AA660877|AA660877 00772 MtRHE Medicago truncatula cDNA 5' si... 310 e-123
emb|AW668560|AW668560 GA_Ea0014K06 Gossypium arboreum 7-10 dpa ... 441 e-123
emb|AW509432|AW509432 si37b03.y1 Gm-r1030 Glycine max cDNA clone... 321 e-122
emb|AW773889|AW773889 EST332875 KV3 Medicago truncatula cDNA clo... 437 e-122
10 gb|BE059929|BE059929 sn38b08.y1 Gm-cl016 Glycine max cDNA clone ... 431 e-120
emb|AW219282|AW219282 EST301764 tomato root during/after fruit s... 426 e-118
emb|AW695765|AW695765 NF098D02ST1F1016 Developing stem Medicago ... 421 e-118
emb|AW626316|AW626316 EST320223 tomato radicle, 5 d post-imbibit... 422 e-117
emb|AA660477|AA660477 00363 MtRHE Medicago truncatula cDNA 5' si... 421 e-117
15 emb|AW727433|AW727433 GA_Ea0012B12 Gossypium arboreum 7-10 dpa ... 421 e-117
emb|AW650460|AW650460 EST328914 tomato germinating seedlings, TA... 419 e-116
emb|AW621571|AW621571 EST312369 tomato root during/after fruit s... 419 e-116
emb|AW309216|AW309216 sg05g07.y1 Gm-cl019 Glycine max cDNA clone... 414 e-115
emb|AW184893|AW184893 se82a03.y1 Gm-cl023 Glycine max cDNA clone... 413 e-114
20 emb|AW738476|AW738476 EST339903 tomato flower buds, anthesis, Co... 412 e-114
emb|AW685878|AW685878 NF031C11NR1F1000 Nodulated root Medicago t... 411 e-114
emb|AW933869|AW933869 EST359712 tomato fruit mature green, TAMU ... 407 e-113
emb|AW220942|AW220942 EST297411 tomato fruit mature green, TAMU ... 406 e-112
emb|AW277466|AW277466 sf82d10.y1 Gm-cl019 Glycine max cDNA clone... 406 e-112
25 emb|AW568477|AW568477 si59c07.y1 Gm-r1030 Glycine max cDNA clone... 403 e-111
emb|AW649817|AW649817 EST328271 tomato germinating seedlings, TA... 402 e-111
emb|AW773817|AW773817 EST332803 KV3 Medicago truncatula cDNA clo... 399 e-110
emb|AI495184|AI495184 sa89b11.y1 Gm-cl004 Glycine max cDNA clone... 398 e-110
emb|AI973534|AI973534 sc88a04.y1 Gm-cl019 Glycine max cDNA clone... 397 e-110
30 emb|AW035959|AW035959 EST282818 tomato callus, TAMU Lycopersicon... 396 e-109
emb|AW932476|AW932476 EST358319 tomato fruit mature green, TAMU ... 395 e-109
emb|AW979917|AW979917 EST341567 tomato root deficiency, Cornell ... 395 e-109
emb|AW649196|AW649196 EST327650 tomato germinating seedlings, TA... 391 e-108
emb|AI960982|AI960982 sc93e09.y1 Gm-cl019 Glycine max cDNA clone... 386 e-106
35 emb|AW033083|AW033083 EST276642 tomato callus, TAMU Lycopersicon... 385 e-106
emb|AW596414|AW596414 sj12b07.y1 Gm-cl032 Glycine max cDNA clone... 384 e-106
emb|AW648010|AW648010 EST326464 tomato germinating seedlings, TA... 382 e-105
emb|AW725587|AW725587 GA_Ea0018N14 Gossypium arboreum 7-10 dpa ... 379 e-104
emb|AW725609|AW725609 GA_Ea0018P14 Gossypium arboreum 7-10 dpa ... 379 e-104
40 emb|AW727696|AW727696 GA_Ea0015K01 Gossypium arboreum 7-10 dpa ... 303 e-103
emb|AW705880|AW705880 sk52a09.y1 Gm-cl019 Glycine max cDNA clone... 372 e-102
emb|AW306403|AW306403 se50b10.y1 Gm-cl017 Glycine max cDNA clone... 369 e-101
emb|AW720057|AW720057 LjNEST13b1r Lotus japonicus nodule library... 367 e-101
emb|AW033447|AW033447 EST277018 tomato callus, TAMU Lycopersicon... 367 e-101
45 emb|AW933031|AW933031 EST358874 tomato fruit mature green, TAMU ... 366 e-100
emb|AW649360|AW649360 EST327814 tomato germinating seedlings, TA... 366 e-100
emb|AW035234|AW035234 EST280496 tomato callus, TAMU Lycopersicon... 364 1e-99
emb|AW907386|AW907386 EST343509 potato stolon, Cornell Universit... 361 9e-99
emb|AW756722|AW756722 sl26d08.y1 Gm-cl027 Glycine max cDNA clone... 359 3e-98
50 emb|AW760501|AW760501 sl51b04.y1 Gm-cl027 Glycine max cDNA clone... 358 6e-98
emb|AI726591|AI726591 BNLGHi6198 Six-day Cotton fiber Gossypium ... 354 8e-97
emb|AW201052|AW201052 se97c10.y1 Gm-cl027 Glycine max cDNA clone... 347 1e-94
emb|Y09816|EGCALRPR E.gracilis mRNA for calreticulin precursor. 255 1e-93
emb|AI728389|AI728389 BNLGHi10665 Six-day Cotton fiber Gossypium... 329 4e-89
55 emb|AI437497|AI437497 sa34a12.y1 Gm-cl004 Glycine max cDNA clone... 329 4e-89
emb|AW509028|AW509028 si39c02.y1 Gm-r1030 Glycine max cDNA clone... 325 4e-88
emb|AI896365|AI896365 EST265808 tomato callus, TAMU Lycopersicon... 325 6e-88
emb|AW043340|AW043340 ST32B12 Pine TriplEx shoot tip library Pin... 324 1e-87
emb|AI812952|AI812952 22G9 Pine Lambda Zap Xylem library Pinus t... 255 1e-86
60 emb|AW648456|AW648456 EST326910 tomato germinating seedlings, TA... 316 3e-85
emb|AI899646|AI899646 EST269089 tomato susceptible, Cornell Lyco... 316 3e-85

- emb|AW624478|AW624478 EST322423 tomato flower buds 3-8 mm, Corne... 312 3e-84
 emb|AV407468|AV407468 AV407468 Lotus japonicus young plants (two... 310 1e-83
 emb|AI895452|AI895452 EST264895 tomato callus, TAMU Lycopersicon... 310 2e-83
 emb|AW649764|AW649764 EST328218 tomato germinating seedlings, TA... 308 5e-83
 5 emb|AW132963|AW132963 se12f08.y1 Gm-cl013 Glycine max cDNA clone... 307 1e-82
 emb|AI726703|AI726703 BNLGHi6370 Six-day Cotton fiber Gossypium ... 301 8e-81
 emb|AW727636|AW727636 GA_Ea0015E17 Gossypium arboreum 7-10 dpa ... 300 1e-80
 emb|AW216358|AW216358 EST295102 tomato callus, TAMU Lycopersicon... 295 7e-79
 emb|AW731131|AW731131 GA_Ea0008P21 Gossypium arboreum 7-10 dpa ... 291 8e-78
 10 emb|AW728940|AW728940 GA_Ea0018J21 Gossypium arboreum 7-10 dpa ... 291 1e-77
 emb|AI771812|AI771812 EST252912 tomato ovary, TAMU Lycopersicon ... 290 2e-77
 emb|AI489195|AI489195 EST247534 tomato ovary, TAMU Lycopersicon ... 290 2e-77
 emb|AW266258|AW266258 L30-2972T3 Ice plant Lambda Uni-Zap XR exp... 283 2e-75
 emb|AV413324|AV413324 AV413324 Lotus japonicus young plants (two... 283 2e-75
 15 emb|AW560421|AW560421 EST315469 DSIR Medicago truncatula cDNA cl... 270 1e-74
 emb|AW754529|AW754529 PC03C03 Pine TriplEx pollen cone library P... 280 2e-74
 emb|AW042889|AW042889 ST26F06 Pine TriplEx shoot tip library Pin... 279 3e-74
 emb|AW043146|AW043146 ST29H08 Pine TriplEx shoot tip library Pin... 273 2e-73
- 20
 Query= AC003680.50_at 13100_at /id_source genbank /description
 gb|aac06158.1| (ac003680) putative cytochrome p450 [arabidopsis
 thaliana] /blast_score 0 /ec_number /family monooxygenase /chip nova
 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
 25 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac003680|/ncgi
 http://www.ncgr.org/cgi-bin/ff?ac003680
 (1647 letters)
- Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters
- Searching.....done
- Score E
 35 Sequences producing significant alignments: (bits) Value
- emb|AJ249799|CAR249799 Cicer arietinum partial mRNA for cytochro... 308 e-114
 emb|AB032833|AB032833 Cicer arietinum CYP76D1 mRNA for cytochrom... 289 5e-87
 emb|AJ011862|CRO011862 Catharanthus roseus mRNA for flavonoid 3'... 191 5e-86
 40 gb|U72654|EGU72654 Eustoma grandiflorum flavonoid 3'5'-hydroxyla... 179 8e-85
 emb|AI897763|AI897763 EST267206 tomato ovary, TAMU Lycopersicon ... 305 7e-82
 emb|X71658|SMCYPEG8 S.melongena CYP76A1 mRNA. 278 3e-81
 emb|X71657|SMCYPEG7 S.melongena CYP76A2 mRNA for hydroxylase. 269 6e-81
 emb|Y09920|HT7EC0DET Helianthus tuberosus mRNA for 7-ethoxycouma... 300 2e-80
 45 emb|Y10098|HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... 300 2e-80
 dbj|D85184|D85184 Gentiana triflora mRNA for flavonoid 3',5'-hyd... 121 9e-79
 emb|X70824|SMPEG1 S.melongena pEG1 mRNA for hydroxylase P450. 171 1e-77
 dbj|E05111|E05111 cDNA encoding solanum flavonoid 3',5'-hydroxyg... 171 1e-77
 gb|M32885|AVOCYP Avocado cytochrome P-450LXXIA1 (cyp71A1) mRNA, ... 283 3e-75
 50 emb|AF134590|AF134590 Papaver somniferum (S)-N-methylcoclaurine ... 223 6e-75
 emb|AF191772|AF191772 Papaver somniferum (S)-N-methylcoclaurine ... 221 1e-74
 emb|AF022459|AF022459 Glycine max cytochrome P450 monooxygenase ... 280 3e-74
 emb|AI484957|AI484957 EST243220 tomato ovary, TAMU Lycopersicon ... 280 3e-74
 emb|AF155332|AF155332 Petunia x hybrida flavonoid 3'-hydroxylase... 186 2e-70
 55 emb|AF014800|AF014800 Eschscholzia californica (S)-N-methylcocla... 212 9e-70
 gb|U09610|U09610 Berberis stolonifera cytochrome P-450 CYP80 mRN... 264 1e-69
 emb|AF014801|AF014801 Eschscholzia californica (S)-N-methylcocla... 211 3e-69
 emb|AI488646|AI488646 EST246985 tomato ovary, TAMU Lycopersicon ... 260 2e-68
 emb|Y09424|NRCYP71A6 N.racemosa mRNA for cytochrome P450, CYP71A... 260 2e-68
 60 emb|AF022458|AF022458 Glycine max cytochrome P450 monooxygenase ... 259 3e-68
 emb|AI938505|AI938505 sb46e03.y1 Gm-cl015 Glycine max cDNA clone... 259 4e-68

- emb|Y10490|GMC450CP3 G.max mRNA for putative cytochrome P450, cl... 259 4e-68
emb|AF029856|AF029856 Sorghum bicolor cytochrome P450 CYP98A1 (C... 258 8e-68
emb|Y09423|NRCYP71A5 Nepeta racemosa mRNA for cytochrome P450, C... 256 3e-67
5 emb|AW726065|AW726065 GA_Ea0020I21 Gossypium arboreum 7-10 dpa ... 186 4e-67
emb|AI897760|AI897760 EST267203 tomato ovary, TAMU Lycopersicon ... 138 2e-66
emb|Y10489|GMC450CP1 G.max mRNA for putative cytochrome P450, cl... 248 1e-64
emb|X96784|NTP450GEN N.tabacum cytochrome P-450 gene. 247 2e-64
gb|U48435|SCU48435 Solanum chacoense putative cytochrome P450 ge... 247 2e-64
emb|AW730128|AW730128 GA_Ea0027P19 Gossypium arboreum 7-10 dpa ... 184 6e-63
10 emb|AI777331|AI777331 EST263739 tomato seed, TAMU Lycopersicon e... 240 3e-62
emb|AF029858|AF029858 Sorghum bicolor cytochrome P450 CYP71E1 (C... 208 3e-62
emb|AW728802|AW728802 GA_Ea0028I12 Gossypium arboreum 7-10 dpa ... 166 5e-62
emb|AW668189|AW668189 GA_Ea0013B20 Gossypium arboreum 7-10 dpa ... 184 5e-62
emb|AW666599|AW666599 GA_Ea0005B16 Gossypium arboreum 7-10 dpa ... 175 5e-62
15 emb|Y10493|GMC450CP7 G.max mRNA for putative cytochrome P450, cl... 160 2e-61
emb|AW394470|AW394470 sh05e04.y1 Gm-c1016 Glycine max cDNA clone... 237 3e-61
emb|AW234222|AW234222 sf22f08.y1 Gm-c1028 Glycine max cDNA clone... 237 3e-61
emb|AF124815|AF124815 Mentha spicata cytochrome p450 mRNA, compl... 162 3e-61
gb|U48434|SCU48434 Solanum chacoense cytochrome P450 mRNA, compl... 236 3e-61
20 dbj|D14589|D14589 Eustoma russellianum mRNA for flavonoid 3',5'-... 179 5e-61
gb|BE023051|BE023051 sm78h02.y1 Gm-c1015 Glycine max cDNA clone ... 235 7e-61
gb|L24438|THLCYP450A Thlaspi arvense germline cytochrome P450 mR... 235 7e-61
emb|AJ249802|CAR249802 Cicer arietinum partial mRNA for cytochro... 235 9e-61
emb|AF166332|AF166332 Nicotiana tabacum cytochrome P450 gene, co... 235 9e-61
25 gb|BE054146|BE054146 GA_Ea0034H12f Gossypium arboreum 7-10 dpa ... 234 2e-60
emb|AW569699|AW569699 si79c08.y1 Gm-c1031 Glycine max cDNA clone... 233 2e-60
emb|Z22545|PHFLAHYDB P.hybrida flavonoid 3',5'-hydroxylase mRNA. 182 3e-60
dbj|D14588|PETHF1 Petunia hybrida Hfl mRNA for flavonoid-3',5'-h... 182 3e-60
emb|AI730111|AI730111 BNLGHi6162 Six-day Cotton fiber Gossypium ... 226 5e-60
30 emb|AF122821|AF122821 Capsicum annuum cytochrome P450 (PepCYP) m... 231 8e-60
emb|AJ238612|CRO238612 Catharanthus roseus mRNA for cytochrome P... 230 2e-59
emb|Z22544|PHFLAHYDA P.hybrida flavonoid 3',5'-hydroxylase mRNA. 179 2e-59
dbj|D14590|D14590 Campanula medium mRNA for flavonoid 3',5'-hydr... 178 5e-59
emb|Z33875|CYMPCP450 M.piperita gene for cytochrome P-450 oxidase. 228 8e-59
35 emb|AI726383|AI726383 BNLGHi5702 Six-day Cotton fiber Gossypium ... 227 2e-58
emb|AI779370|AI779370 EST260249 tomato susceptible, Cornell Lyco... 225 7e-58
emb|AW728587|AW728587 GA_Ea0017C12 Gossypium arboreum 7-10 dpa ... 225 1e-57
emb|AB006790|AB006790 Petunia x hybrida IMT-2 mRNA for cytochrom... 150 1e-57
emb|AI728431|AI728431 BNLGHi10763 Six-day Cotton fiber Gossypium... 154 2e-57
40 emb|AF124816|AF124816 Mentha x piperita cytochrome p450 isoform ... 146 2e-57
emb|AF081575|AF081575 Petunia x hybrida flavonoid 3',5'-hydroxyl... 172 4e-57
emb|X70981|SMCYPEG2 S.melongena CYP71A1 mRNA for P450 hydroxylase. 140 4e-57
emb|X95342|NTHSR515 N.tabacum mRNA for HSR515 protein. 100 5e-57
emb|AB028151|AB028151 Antirrhinum majus AFNS2 mRNA for cytochrom... 115 9e-57
45 emb|AW459662|AW459662 sh90c05.y1 Gm-c1016 Glycine max cDNA clone... 221 9e-57
emb|Y10492|GMC450CP5 G.max mRNA for putative cytochrome P450, cl... 124 4e-56
emb|AW053855|AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp... 168 5e-56
emb|AW255799|AW255799 ML868 peppermint glandular trichome Mentha... 217 2e-55
emb|AF124817|AF124817 Mentha x piperita cytochrome p450 isoform ... 141 2e-55
50 emb|AW832652|AW832652 sm15g02.y1 Gm-c1027 Glycine max cDNA clone... 121 3e-55
emb|X71654|SMCYP71B3 S.melongena CYP71A2 mRNA for hydroxylase. 144 4e-55
dbj|D14990|POTCPEG4 Eggplant mRNA for cytochrome P-450EG4, compl... 144 4e-55
emb|AW255096|AW255096 ML139 peppermint glandular trichome Mentha... 182 2e-54
emb|AW930824|AW930824 EST356667 tomato fruit mature green, TAMU ... 214 2e-54
55 emb|AW395730|AW395730 sg74f08.y1 Gm-c1007 Glycine max cDNA clone... 213 3e-54
emb|AW726043|AW726043 GA_Ea0020H22 Gossypium arboreum 7-10 dpa ... 143 4e-54
emb|AI895030|AI895030 EST264473 tomato callus, TAMU Lycopersicon... 211 1e-53
emb|AB028152|AB028152 Torenia hybrida TFNS5 mRNA for cytochrome ... 114 1e-53
emb|AW832405|AW832405 sm09e01.y1 Gm-c1027 Glycine max cDNA clone... 210 2e-53
60 emb|AB022733|AB022733 Glycyrrhiza echinata CYP Ge-51 mRNA for cy... 109 3e-53
emb|AW308831|AW308831 sf72g04.y1 Gm-c1013 Glycine max cDNA clone... 203 5e-53

emb|AF022157|AF022157 Glycine max cytochrome P450 monooxygenase ... 158 7e-53
 emb|AW774664|AW774664 EST333815 KV3 Medicago truncatula cDNA clo... 208 9e-53
 emb|AF029857|AF029857 Sorghum bicolor cytochrome P450 CYP99A1 (C... 98 1e-52
 emb|AB001380|AB001380 Glycyrrhiza echinata CYP93B1 mRNA for cyto... 109 1e-52
 5 emb|AW616345|AW616345 EST322756 L. hirsutum trichome, Cornell Un... 208 1e-52
 emb|AW690420|AW690420 NF033B04ST1F1000 Developing stem Medicago ... 129 1e-52
 emb|AF000403|AF000403 Lotus japonicus putative cytochrome P450 ... 145 2e-52
 emb|AW922446|AW922446 DG1_19_F10.g1_A002 Dark Grown 1 (DG1) Sorg... 204 2e-51
 emb|AI729430|AI729430 BNLGHi13332 Six-day Cotton fiber Gossypium... 171 2e-51
 10 emb|AJ010324|PAJ10324 Populus trichocarpa cv trichobel mRNA for ... 93 4e-51
 emb|AF156976|AF156976 Gerbera hybrida flavone synthase II (CYP93... 110 4e-51
 emb|AB025016|AB025016 Lotus japonicus mRNA for cytochrome P450, ... 152 6e-51
 emb|AI779369|AI779369 EST260248 tomato susceptible, Cornell Lyco... 202 8e-51
 emb|AI727414|AI727414 BNLGHi7936 Six-day Cotton fiber Gossypium ... 181 1e-50
 15

Query= AC000375.44_at 13115_at /id_source genbank /description
 "gb|aab60774.1| (ac000375) ests gb|u75592.gb|t13956.gb|t43869 come
 from from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number
 20 /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000375| /ncgi
 http://www.ncgr.org/cgi-bin/ff?ac000375
 (1533 letters)
 25

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done
 30

	Score	E	
			(bits) Value
	Sequences producing significant alignments:		
35	gb BE020282 BE020282 sm42g12.y1 Gm-c1028 Glycine max cDNA clone ...	91	2e-39
	emb AW831934 AW831934 sm18a01.y1 Gm-c1027 Glycine max cDNA clone...	91	3e-38
	emb AI895084 AI895084 EST264527 tomato callus, TAMU Lycopersicon...	88	2e-37
	emb AW731252 AW731252 GA_Ea0030E03 Gossypium arboreum 7-10 dpa ...	93	2e-31
	emb AW650703 AW650703 EST329157 tomato germinating seedlings, TA...	88	2e-28
	emb AW648696 AW648696 EST327066 tomato germinating seedlings, TA...	85	7e-25
40	emb AT000481 AT000481 AT000481 Brassica rapa guard cell Brassica...	62	3e-23
	emb AI895460 AI895460 EST264903 tomato callus, TAMU Lycopersicon...	77	2e-22
	emb AW776692 AW776692 EST335757 DSIL Medicago truncatula cDNA cl...	68	7e-21
	emb AI774644 AI774644 EST255744 tomato resistant, Cornell Lycope...	65	4e-19
	emb AW560992 AW560992 EST316040 DSIR Medicago truncatula cDNA cl...	68	2e-18
45	emb AW034968 AW034968 EST279197 tomato callus, TAMU Lycopersicon...	61	2e-15
	emb AW034372 AW034372 EST277943 tomato callus, TAMU Lycopersicon...	62	1e-13
	gb BE021411 BE021411 sm48g02.y1 Gm-c1028 Glycine max cDNA clone ...	60	6e-13
	emb AW032312 AW032312 EST275766 tomato callus, TAMU Lycopersicon...	69	9e-12
	emb AW399297 AW399297 EST309797 L. pennellii trichome, Cornell U...	46	2e-11
50	emb AW032231 AW032231 EST275685 tomato callus, TAMU Lycopersicon...	62	6e-11
	emb AW032133 AW032133 EST275587 tomato callus, TAMU Lycopersicon...	62	6e-11
	emb AW030333 AW030333 EST273588 tomato callus, TAMU Lycopersicon...	55	8e-11
	gb BE020267 BE020267 sm42f07.y1 Gm-c1028 Glycine max cDNA clone ...	69	1e-10
	emb AW773655 AW773655 EST332641 KV3 Medicago truncatula cDNA clo...	55	1e-10
55	emb AI896893 AI896893 EST266336 tomato callus, TAMU Lycopersicon...	62	1e-10
	emb AW278353 AW278353 sf43a06.y1 Gm-c1009 Glycine max cDNA clone...	49	2e-09
	emb AW687210 AW687210 NF007B09RT1F1076 Developing root Medicago ...	55	1e-08
	emb AT000955 AT000955 AT000955 Brassica rapa guard cell Brassica...	60	3e-08
	emb AW029692 AW029692 EST272947 tomato callus, TAMU Lycopersicon...	48	4e-08
60	emb AT000818 AT000818 AT000818 Brassica rapa guard cell Brassica...	59	7e-08
	emb AW774597 AW774597 EST333748 KV3 Medicago truncatula cDNA clo...	47	2e-07

	emb AW127319 AW127319 M110490 DSIL Medicago truncatula cDNA clon...	48 2e-05
	emb AW279607 AW279607 sf67d05.y1 Gm-cl013 Glycine max cDNA clone...	49 1e-04
	emb AI966004 AI966004 sc25c10.y1 Gm-cl013 Glycine max cDNA clone...	49 1e-04
	emb Z48431 AFABF2 A.fatua mRNA for DNA-binding protein (clone AB...	48 2e-04
5	emb AB024510 AB024510 Nicotiana tabacum mRNA for TMV response-re...	48 2e-04
	emb AI485065 AI485065 EST243369 tomato ovary, TAMU Lycopersicon ...	47 3e-04
	gb BE058097 BE058097 sn11c07.y1 Gm-cl016 Glycine max cDNA clone ...	47 3e-04
	emb AF211645 AF211645 AF211645 34.1B Nicotiana tabacum cDNA clon...	45 0.001
	emb AV419361 AV419361 AV419361 Lotus japonicus young plants (two...	45 0.001
10	emb AI488776 AI488776 EST247115 tomato ovary, TAMU Lycopersicon ...	45 0.001
	emb AB028022 AB028022 Nicotiana tabacum wizz mRNA, complete cds.	45 0.001
	emb AI930972 AI930972 sb45e05.y1 Gm-cl015 Glycine max cDNA clone...	45 0.002
	emb AW693799 AW693799 NF069C11ST1F1085 Developing stem Medicago ...	44 0.003
	emb AW696711 AW696711 NF110A11ST1F1084 Developing stem Medicago ...	44 0.003
15	emb AW222373 AW222373 EST299184 tomato fruit red ripe, TAMU Lyco...	44 0.004
	emb AW164824 AW164824 se78d01.y1 Gm-cl023 Glycine max cDNA clone...	43 0.005
	emb AI900530 AI900530 sc07d02.y1 Gm-cl012 Glycine max cDNA clone...	43 0.005
	gb BE022598 BE022598 sm75a10.y1 Gm-cl015 Glycine max cDNA clone ...	43 0.007
	emb AW459004 AW459004 sh18a06.y1 Gm-cl016 Glycine max cDNA clone...	43 0.007
20	emb AW186261 AW186261 se65e10.y1 Gm-cl019 Glycine max cDNA clone...	43 0.007
	emb AI966537 AI966537 sc51e10.y1 Gm-cl015 Glycine max cDNA clone...	43 0.007
	emb AW569748 AW569748 si79h08.y1 Gm-cl031 Glycine max cDNA clone...	43 0.007
	emb AW568563 AW568563 si78d04.y1 Gm-cl031 Glycine max cDNA clone...	43 0.007
	emb AW219364 AW219364 EST301846 tomato root during/after fruit s...	43 0.007
25	gb BE059498 BE059498 sn32h03.y1 Gm-cl016 Glycine max cDNA clone ...	42 0.013
	emb AW432526 AW432526 sh75d09.y1 Gm-cl015 Glycine max cDNA clone...	42 0.013
	emb AW930573 AW930573 EST341030 tomato fruit mature green, TAMU ...	42 0.013
	emb AW310205 AW310205 sf32g08.x1 Gm-cl028 Glycine max cDNA clone...	42 0.013
	gb L35779 L35779 BNAESTG Mustard flower buds Brassica rapa cDNA ...	42 0.013
30	emb AW233985 AW233985 sf32g08.y1 Gm-cl028 Glycine max cDNA clone...	42 0.013
	emb AI899266 AI899266 EST268709 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AI486062 AI486062 EST244383 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AI487230 AI487230 EST245552 tomato ovary, TAMU Lycopersicon ...	41 0.017
	gb BE021550 BE021550 sm59h03.y1 Gm-cl028 Glycine max cDNA clone ...	41 0.017
35	emb AI483704 AI483704 EST249575 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AW032373 AW032373 EST275827 tomato callus, TAMU Lycopersicon...	41 0.017
	emb AI490542 AI490542 EST249096 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AI490377 AI490377 EST248703 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AI488666 AI488666 EST247005 tomato ovary, TAMU Lycopersicon ...	41 0.017
40	emb AI771634 AI771634 EST252734 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AI771930 AI771930 EST253030 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AW030227 AW030227 EST273482 tomato callus, TAMU Lycopersicon...	41 0.017
	emb AI488453 AI488453 EST246792 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AI489221 AI489221 EST247560 tomato ovary, TAMU Lycopersicon ...	41 0.017
45	emb AI485880 AI485880 EST244201 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AI484959 AI484959 EST243222 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AI485716 AI485716 EST244037 tomato ovary, TAMU Lycopersicon...	41 0.017
	emb AI489915 AI489915 EST248254 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AI486696 AI486696 EST245018 tomato ovary, TAMU Lycopersicon ...	41 0.017
50	emb AW035780 AW035780 EST281934 tomato callus, TAMU Lycopersicon...	41 0.017
	emb AI895108 AI895108 EST264551 tomato callus, TAMU Lycopersicon...	41 0.017
	emb AI486874 AI486874 EST245196 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AI489796 AI489796 EST248135 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AI771686 AI771686 EST252786 tomato ovary, TAMU Lycopersicon ...	41 0.017
55	emb AW254736 AW254736 ML1023 peppermint glandular trichome Menth...	41 0.017
	emb AW031802 AW031802 EST275256 tomato callus, TAMU Lycopersicon...	41 0.017
	emb AI489016 AI489016 EST247355 tomato ovary, TAMU Lycopersicon ...	41 0.017
	emb AI054839 AI054839 coau0002E21 Cotton Boll Abscission Zone cD...	32 0.018
	emb AW568786 AW568786 si61a10.y1 Gm-r1030 Glycine max cDNA clone...	41 0.024
60	emb AI938647 AI938647 sb56f08.y1 Gm-cl018 Glycine max cDNA clone...	41 0.024
	emb AI938638 AI938638 sb56e08.y1 Gm-cl018 Glycine max cDNA clone...	41 0.024

emb|AW775215|AW775215 EST331937 GVN Medicago truncatula cDNA clo... 40 0.044
 emb|AW685095|AW685095 NF025C08NR1F1000 Nodulated root Medicago t... 40 0.044
 emb|AW686657|AW686657 NF043G05NR1F1000 Nodulated root Medicago t... 40 0.044
 gb|BE020052|BE020052 sm38d10.y1 Gm-cl028 Glycine max cDNA clone ... 40 0.060
 5 emb|AW733406|AW733406 sk73b02.y1 Gm-cl016 Glycine max cDNA clone... 40 0.060
 emb|AW597599|AW597599 sj96c04.y1 Gm-cl023 Glycine max cDNA clone... 40 0.060
 emb|AI774675|AI774675 EST255775 tomato resistant, Cornell Lycopersicon... 39 0.083
 emb|AW685473|AW685473 NF030C03NR1F1000 Nodulated root Medicago t... 39 0.083
 emb|AI774760|AI774760 EST255860 tomato resistant, Cornell Lycopersicon... 39 0.083
 10 emb|AW559645|AW559645 EST314757 DSIR Medicago truncatula cDNA cl... 39 0.083
 emb|AW458207|AW458207 sh79g06.y1 Gm-cl016 Glycine max cDNA clone... 39 0.083

Query= AC002333.210_s_at 13154_s_at /id_source genbank /description
 15 gb|aab64047.1| (ac002333) putative endochitinase [arabidopsis
 thaliana] /blast_score 1.00e-148 /ec_number /family /chip nova
 /gb_link /ncgi
 (1062 letters)

20 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

25 Score E
 Sequences producing significant alignments: (bits) Value

emb|X61488|BNCHITIN B.napus mRNA for chitinase. 453 e-166
 gb|U97521|VVU97521 Vitis vinifera class IV endochitinase (VvChi4... 212 1e-95
 30 gb|U97522|VVU97522 Vitis vinifera class IV endochitinase (VvChi4... 211 4e-95
 emb|X57187|PVCHITIN P.vulgaris mRNA for chitinase. 135 8e-86
 dbj|D45183|D45183 Chenopodium amaranticolor mRNA for chitinase, ... 136 5e-82
 emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 185 5e-81
 emb|Z46948|SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re... 182 8e-80
 35 emb|X75945|BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. 156 4e-79
 emb|A23392|A23392 B.vulgaris mRNA for chitinase 4 (B15). 156 4e-79
 dbj|D45182|D45182 Chenopodium amaranticolor mRNA for chitinase, ... 119 4e-78
 dbj|D45181|D45181 Chenopodium amaranticolor mRNA for chitinase, ... 119 7e-78
 dbj|D45184|D45184 Chenopodium amaranticolor mRNA for chitinase, ... 119 1e-77
 40 emb|X88803|VURNACHI4 V.unguiculata mRNA for chitinase clase 4 (p... 103 6e-77
 gb|L42467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 105 1e-75
 gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 84 7e-73
 gb|BE034166|BE034166 MG05H02 MG Mesembryanthemum crystallinum cD... 140 1e-72
 gb|BE034428|BE034428 MH04G02 MH Mesembryanthemum crystallinum cD... 139 3e-72
 45 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 133 2e-70
 gb|BE034976|BE034976 ML07H11 ML Mesembryanthemum crystallinum cD... 131 1e-69
 emb|AF112963|AF112963 Triticum aestivum chitinase II precursor (... 239 1e-66
 gb|L25826|BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. 130 2e-66
 emb|AI897733|AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... 177 5e-66
 50 gb|U52845|DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... 167 9e-65
 emb|AI897843|AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... 172 2e-64
 gb|U52846|DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP... 165 4e-64
 gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 111 7e-64
 gb|U52847|DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP... 162 2e-63
 55 gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 93 4e-63
 gb|U52848|DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3... 161 1e-62
 emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem Medicago ... 144 2e-62
 gb|BE035287|BE035287 MM04H04 MM Mesembryanthemum crystallinum cD... 141 1e-59
 emb|AW680953|AW680953 WS1_9_A06.b1_A002 Water-stressed 1 (WS1) S... 139 4e-58
 60 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 147 3e-57
 emb|AI897217|AI897217 EST266756 tomato ovary, TAMU Lycopersicon ... 177 4e-57

- emb|AI776153|AI776153 EST257241 tomato resistant, Cornell Lycopse... 177 5e-56
emb|AI898279|AI898279 EST267722 tomato ovary, TAMU Lycopersicon ... 141 2e-55
gb|BE033502|BE033502 ME03F10 ME Mesembryanthemum crystallinum cD... 86 3e-55
emb|AW030814|AW030814 EST274069 tomato callus, TAMU Lycopersicon... 140 6e-55
5 emb|AI485982|AI485982 EST244303 tomato ovary, TAMU Lycopersicon ... 138 3e-54
emb|AW035013|AW035013 EST279284 tomato callus, TAMU Lycopersicon... 137 4e-54
emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root Medicago t... 98 1e-53
emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 134 2e-53
emb|AW924422|AW924422 WS1_69_C06.b1_A002 Water-stressed 1 (WS1) ... 139 4e-53
10 emb|Z46950|SNCHJET19 S.nigra mRNA chitinase class II, pathogenes... 130 7e-53
gb|BE034447|BE034447 MH05A08 MH Mesembryanthemum crystallinum cD... 86 8e-53
emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 116 2e-52
gb|U83592|MSU83592 Medicago sativa class I chitinase mRNA, compl... 116 1e-51
gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 116 1e-51
15 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 117 9e-51
emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 124 2e-50
gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 141 6e-50
emb|AF090336|AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA... 149 1e-49
emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 165 4e-49
20 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 120 4e-49
emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 115 9e-49
emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 112 1e-48
gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 112 1e-48
emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 115 1e-48
25 emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed 1 (WS1) ... 140 2e-48
gb|BE034450|BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 83 3e-48
gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 112 5e-48
emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 112 5e-48
emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 139 9e-48
30 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 139 9e-48
emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 118 3e-47
emb|AF061806|AF061806 Elaeagnus umbellata basic chitinase mRNA, ... 118 4e-47
gb|M94105|ALCCHITIN Allium sativum chitinase mRNA, 3' end. 116 7e-47
emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 120 2e-46
35 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 116 3e-46
emb|AW922596|AW922596 DG1_46_C01.b1_A002 Dark Grown 1 (DG1) Sorg... 79 3e-46
emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 116 3e-46
gb|BE034267|BE034267 MH02D06 MH Mesembryanthemum crystallinum cD... 74 3e-46
gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 122 4e-46
40 emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 116 4e-46
emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 112 7e-46
emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 121 9e-46
emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 109 1e-45
emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 112 2e-45
45 emb|X74919|PVGEC9 P.vulgaris gene for endochitinase. 135 2e-45
gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 116 2e-45
gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 109 2e-45
gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 116 3e-45
gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 109 6e-45
50 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 108 8e-45
emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 147 2e-44
gb|BE033398|BE033398 ME01A01 ME Mesembryanthemum crystallinum cD... 141 4e-44
emb|AA739579|AA739579 344 PtIFG2 Pinus taeda cDNA clone 8562M 3'... 107 1e-43
emb|AW560048|AW560048 EST315096 DSIR Medicago truncatula cDNA cl... 116 1e-43
55 emb|A23396|A23396 B.vulgaris gene for chitinase 76. 105 3e-43
emb|AW267781|AW267781 EST305909 DSIR Medicago truncatula cDNA cl... 115 4e-43
emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 108 8e-43
emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 125 1e-42
emb|AI352718|AI352718 MB46-29 PZ204.BNlib Brassica napus cDNA cl... 144 4e-42
60 gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 80 5e-42
emb|AI729668|AI729668 BNLGHi13889 Six-day Cotton fiber Gossypium... 111 2e-41

emb|AF061805|AF061805 Elaeagnus umbellata acidic chitinase mRNA,... 116 3e-41
 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 117 4e-41
 emb|Z15138|LECHI14 L.esculentum mRNA for chitinase (partial). 114 1e-40
 gb|U30465|LEU30465 Lycopersicon esculentum class II chitinase (C... 114 2e-40
 5 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 100 1e-39

Query= AL031394.56_at 13176_at /id_source genbank /description
 10 emb|caa20567.1| (al031394) putative protein [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031394| /ncgi
 http://www.ncgr.org/cgi-bin/ff?al031394
 (1116 letters)

15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

20 Searching.....done

		Score	E	
	Sequences producing significant alignments:		(bits)	Value
25	emb AW671006 AW671006 LG1_278_H12.b1_A002 Light Grown 1 (LG1) So...	81	6e-28	
	emb AA520813 AA520813 TgESTzz64d07.r1 TgME49 invivo Bradyzoite c...	38	0.16	
	gb U43491 SCU43491 Saccharomyces cerevisiae cosmid clone pEOA156...	37	0.31	
	emb Z74916 SCYOR008C S.cerevisiae chromosome XV reading frame OR...	37	0.31	
	gb U39481 SCU39481 Saccharomyces cerevisiae Slglp (SLG1) gene, c...	37	0.31	
30	emb AA680906 AA680906 LmFrAm0494 Leishmania major Amastigote ful...	33	1.0	
	emb AF193903 AF193903 Cafeteria roenbergensis mitochondrial DNA,...	35	1.1	
	emb AF229795 AF229795 Vigna radiata beta galactosidase mRNA, com...	35	1.5	
	emb AW683786 AW683786 NF001A06NR1F1038 Nodulated root Medicago t...	35	1.5	
	emb AC005802 AC005802 Leishmania major chromosome 3 clone L6202 ...	34	2.1	
	emb AC005893 AC005893 Leishmania major chromosome 3 clone L822 s...	34	2.1	
35	emb AA520166 AA520166 TgESTzz39b08.s1 TgME49 invivo Bradyzoite c...	34	2.9	
	emb AW618793 AW618793 EST320779 L. pennellii trichome, Cornell U...	34	2.9	
	emb AW306460 AW306460 se51a02.y1 Gm-cl017 Glycine max cDNA clone...	34	2.9	
	emb AQ502036 AQ502036 V10E12 mTn-3xHA/lacZ Insertion Library Sac...	33	3.9	
	gb U87148 HVU87148 Hordeum vulgare nucellin mRNA, complete cds.	33	3.9	
40	emb AF017430 AF017430 Hordeum vulgare EEA1 mRNA, complete cds.	33	3.9	
	emb AQ500344 AQ500344 V41B12 mTn-3xHA/lacZ Insertion Library Sac...	33	3.9	
	emb Z71686 SCYNR071C S.cerevisiae chromosome XIV reading frame O...	33	3.9	
	emb AQ501720 AQ501720 V15F6 mTn-3xHA/lacZ Insertion Library Sacc...	33	3.9	
	emb AQ872965 AQ872965 V56D9 mTn-3xHA/lacZ Insertion Library, str...	33	3.9	
45	emb AW126050 AW126050 N100246e rootphos(-) Medicago truncatula c...	33	5.4	
	emb AW127669 AW127669 M110413 DSLC Medicago truncatula cDNA clon...	33	5.4	
	emb AW126177 AW126177 N100022e rootphos(-) Medicago truncatula c...	33	5.4	
	emb AW126137 AW126137 N100334e rootphos(-) Medicago truncatula c...	33	5.4	
	emb AW509583 AW509583 ga61f07.y1 Moss EST library PPU Physcomitr...	33	5.4	
50	emb AQ503147 AQ503147 V44D10 mTn-3xHA/lacZ Insertion Library Sac...	33	5.4	
	emb AQ501343 AQ501343 V23B5 mTn-3xHA/lacZ Insertion Library Sacc...	33	5.4	
	emb Z98559 SPAC23C11 S.pombe chromosome I cosmid c23C11.	33	5.4	
	emb AW672219 AW672219 LG1_358_B09.b1_A002 Light Grown 1 (LG1) So...	33	5.4	
	emb AW925272 AW925272 HVSMEg0001G19 Hordeum vulgare pre-anthesis...	33	5.4	
55	emb AA783066 AA783066 alh02c9.r1 Aspergillus nidulans 24hr asexu...	26	5.7	
	emb AC013353 AC013353 Trypanosoma brucei chromosome VI clone RPC...	32	7.4	
	emb AV409938 AV409938 AV409938 Lotus japonicus young plants (two...	32	7.4	
	emb AW780906 AW780906 sl86c03.y1 Gm-cl037 Glycine max cDNA clone...	32	7.4	
	emb AI443278 AI443278 sa46f11.y1 Gm-cl004 Glycine max cDNA clone...	32	7.4	
60	emb AW156670 AW156670 se29c01.y1 Gm-cl015 Glycine max cDNA clone...	32	7.4	
	emb AW277786 AW277786 sf86e12.y1 Gm-cl019 Glycine max cDNA clone...	32	7.4	

emb|AE001432|AE001432 Plasmodium falciparum chromosome 2, sectio... 32 7.4
emb|AW734710|AW734710 sk98e12.y1 Gm-c1035 Glycine max cDNA clone... 32 7.4
emb|AW099005|AW099005 sd33a02.y1 Gm-c1012 Glycine max cDNA clone... 32 7.4
emb|AW704821|AW704821 sk40a01.y1 Gm-c1019 Glycine max cDNA clone... 32 7.4
5 emb|AW277436|AW277436 sf82a10.y1 Gm-c1019 Glycine max cDNA clone... 32 7.4
emb|AW459299|AW459299 sh23c01.y1 Gm-c1016 Glycine max cDNA clone... 32 7.4
emb|AV407743|AV407743 AV407743 Lotus japonicus young plants (two... 32 7.4
emb|AW757240|AW757240 sl30h11.y1 Gm-c1027 Glycine max cDNA clone... 32 7.4

10
Query= AL021961.24_at 13588_at /id_source genbank /description
emb|caal7552.1| (al021961) phosphoglycerate dehydrogenase - like
protein [arabidopsis thaliana] /blast_score 0 /ec_number /family
dehydrogenase /chip nova /gb_link
15 http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021961|/ncgi
http://www.ncgr.org/cgi-bin/ff?al021961
(1812 letters)

20 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

25 Score E
Sequences producing significant alignments: (bits) Value

emb|AW930291|AW930291 EST340748 tomato fruit mature green, TAMU ... 415 e-115
emb|AW625643|AW625643 EST319550 tomato radicle, 5 d post-imbibit... 398 e-110
30 emb|AW666282|AW666282 sk34f11.y1 Gm-c1028 Glycine max cDNA clone... 393 e-108
emb|AW650696|AW650696 EST329150 tomato germinating seedlings, TA... 226 e-103
emb|AW691093|AW691093 NF041B09ST1F1000 Developing stem Medicago ... 355 e-102
emb|AW926942|AW926942 HVSMEg0009B01 Hordeum vulgare pre-anthesis... 339 e-102
gb|BE055044|BE055044 GA_Ea0031H08f Gossypium arboreum 7-10 dpa ... 341 2e-99
35 emb|AW696933|AW696933 NF112E03ST1F1021 Developing stem Medicago ... 357 4e-98
emb|AW731385|AW731385 GA_Ea0030K22 Gossypium arboreum 7-10 dpa ... 344 2e-95
emb|AW688234|AW688234 NF005A05ST1F1000 Developing stem Medicago ... 348 6e-95
gb|BE036418|BE036418 MO24D12 MO Mesembryanthemum crystallinum cD... 279 1e-94
gb|BE052354|BE052354 GA_Ea0034P16f Gossypium arboreum 7-10 dpa ... 346 3e-94
40 emb|AW423801|AW423801 sh52b02.y1 Gm-c1017 Glycine max cDNA clone... 339 4e-92
emb|AI813214|AI813214 3C4 Pine Lambda Zap Xylem library Pinus ta... 336 4e-92
emb|AW692700|AW692700 NF054C07ST1F1000 Developing stem Medicago ... 304 7e-87
emb|AW737130|AW737130 EST338557 tomato flower buds, anthesis, Co... 318 1e-85
emb|AW727978|AW727978 GA_Ea0029C18 Gossypium arboreum 7-10 dpa ... 285 3e-80
45 gb|BE020170|BE020170 sm39e05.y1 Gm-c1028 Glycine max cDNA clone ... 291 1e-77
emb|AW944677|AW944677 00152 leafy spurge Lambda HybriZAP 2.1 two... 291 1e-77
emb|AW926887|AW926887 HVSMEg0008N09 Hordeum vulgare pre-anthesis... 280 3e-74
emb|AW689358|AW689358 NF018C09ST1F1000 Developing stem Medicago ... 253 3e-73
emb|AW755716|AW755716 sl08b12.y1 Gm-c1036 Glycine max cDNA clone... 267 2e-70
50 emb|AW625020|AW625020 EST313849 tomato radicle, 5 d post-imbibit... 253 4e-66
gb|BE060782|BE060782 HVSMEg0013F14f Hordeum vulgare pre-anthesis... 234 1e-60
emb|AW687344|AW687344 NF008F03RT1F1029 Developing root Medicago ... 215 1e-54
emb|AV395160|AV395160 AV395160 Chlamydomonas reinhardtii C9 Chla... 208 1e-52
emb|AW907004|AW907004 EST343231 potato stolon, Cornell Universit... 205 7e-52
55 emb|AW398821|AW398821 EST309321 L. pennellii trichome, Cornell U... 201 2e-50
emb|AW203801|AW203801 sf38d05.y1 Gm-c1028 Glycine max cDNA clone... 196 5e-49
emb|AW923236|AW923236 DG1_50_A11.g1_A002 Dark Grown 1 (DG1) Sorg... 191 1e-47
emb|AW428657|AW428657 Ljirnp22-731-a5 Ljirnp Lambda HybriZap ... 185 8e-46
emb|AW650818|AW650818 EST329272 tomato germinating seedlings, TA... 155 2e-44
60 emb|AW736943|AW736943 NXNV_081_H10_F Nsf Xylem Normal wood Verti... 180 3e-44
emb|AW697347|AW697347 NF115F08ST1F1074 Developing stem Medicago ... 175 9e-43

- emb|AW695961|AW695961 NF101A09ST1F1068 Developing stem Medicago ... 172 6e-42
 gb|BE055879|BE055879 GA__Ea0026P04f Gossypium arboreum 7-10 dpa ... 172 8e-42
 gb|L47851|L47851 BNAF1389 Mustard flower buds Brassica rapa cDNA... 166 8e-41
 emb|AW688606|AW688606 NF009E07ST1F1000 Developing stem Medicago ... 112 2e-39
 5 gb|BE123645|BE123645 NXNV_150_D07_F Nsf Xylem Normal wood Vertic... 164 2e-39
 emb|AA660997|AA660997 00894 MtRHE Medicago truncatula cDNA 5' si... 73 3e-39
 emb|AV428639|AV428639 AV428639 Lotus japonicus young plants (two... 160 3e-38
 emb|AV408249|AV408249 AV408249 Lotus japonicus young plants (two... 160 3e-38
 emb|AL031180|SPUNK4 S.pombe chromosome I cosmid c2E11. 103 1e-36
 10 dbj|D89185|D89185 Schizosaccharomyces pombe mRNA, partial cds, c... 103 1e-36
 emb|AW317181|AW317181 sf38d05.x1 Gm-c1028 Glycine max cDNA clone... 148 1e-34
 dbj|E12500|E12500 Nucleotide sequence of eta gene of cephalospor... 89 2e-34
 emb|Z97052|SPCC4G3 S.pombe chromosome III cosmid c4G3. 83 2e-33
 emb|AA840711|AA840711 CAN22 Anther cDNA library of Hot pepper Ca... 101 5e-33
 15 emb|AL157811|SPAC186 S.pombe chromosome I cosmid c186. 98 1e-32
 emb|AJ273311|AJ273311 AJ273311 Metarhizium anisopliae ARSEF 2575... 91 1e-32
 gb|BE058285|BE058285 sn14b01.y1 Gm-c1016 Glycine max cDNA clone ... 138 1e-31
 gb|BE060772|BE060772 HVSMEg0013F04f Hordeum vulgare pre-anthesis... 95 2e-31
 gb|U18839|SCE9747 Saccharomyces cerevisiae chromosome V cosmids ... 84 6e-31
 20 emb|AC005761|AC005761 Leishmania major chromosome 3 clone L952 s... 78 7e-31
 emb|AW693956|AW693956 NF071B03ST1F1027 Developing stem Medicago ... 89 5e-30
 emb|AI165568|AI165568 A086P59U Hybrid aspen plasmid library Popu... 132 5e-30
 emb|Z37997|SC9877 S.cerevisiae chromosome IX cosmid 9877. 84 5e-30
 emb|AW599036|AW599036 gb01c10.y1 Moss EST library PPN Physcomitr... 116 5e-25
 25 emb|AF079881|AF079881 Entodinium caudatum D-3-phosphoglycerate d... 56 1e-24
 emb|AL033389|SPBC1773 S.pombe chromosome II cosmid c1773. 105 3e-22
 emb|Z71550|SCYNL274C S.cerevisiae chromosome XIV reading frame O... 89 8e-22
 emb|AT000538|AT000538 AT000538 Brassica rapa guard cell Brassica... 105 1e-21
 gb|BE054038|BE054038 GA__Ea0008F24f Gossypium arboreum 7-10 dpa ... 102 7e-21
 30 emb|AT000607|AT000607 AT000607 Brassica rapa guard cell Brassica... 100 9e-21
 gb|U43503|SCU43503 Saccharomyces cerevisiae chromosome XVI cosmi... 89 1e-16
 emb|AW283359|AW283359 LG1_223_C04.g1_A002 Light Grown 1 (LG1) So... 89 1e-16
 emb|AW736063|AW736063 EST332049 KV3 Medicago truncatula cDNA clo... 88 2e-16
 emb|AW689996|AW689996 NF026G01ST1F1000 Developing stem Medicago ... 86 7e-16
 35 emb|AQ874261|AQ874261 V105E9 mTn-3xHA/lacZ Insertion Library, st... 84 2e-15
 gb|H74366|H74366 270 Deletion-treated Brassica napus cDNA clone ... 82 2e-14
 emb|AI822999|AI822999 L30-850T3 Ice plant Lambda Uni-Zap XR expr... 78 3e-13
 emb|Z21493|MISTFDHD S.tuberosum mRNA for formate dehydrogenase. 78 3e-13
 gb|BE055276|BE055276 GA__Ea0034L16f Gossypium arboreum 7-10 dpa ... 57 4e-13
 40 emb|AW442114|AW442114 EST311510 tomato fruit red ripe, TAMU Lyco... 77 4e-13
 emb|AW625680|AW625680 EST319587 tomato radicle, 5 d post-imbibit... 77 4e-13
 emb|AW651324|AW651324 EST329778 tomato germinating seedlings, TA... 77 4e-13
 emb|AI486949|AI486949 EST245271 tomato ovary, TAMU Lycopersicon ... 77 4e-13
 emb|AW030822|AW030822 EST274077 tomato callus, TAMU Lycopersicon... 77 4e-13
 45 emb|AI484846|AI484846 EST243107 tomato ovary, TAMU Lycopersicon ... 77 4e-13
 emb|AW647711|AW647711 EST307192 tomato germinating seedlings, TA... 77 4e-13
 emb|AW442123|AW442123 EST311519 tomato fruit red ripe, TAMU Lyco... 77 4e-13
 emb|AI490350|AI490350 EST248676 tomato ovary, TAMU Lycopersicon ... 77 5e-13
 emb|AW981354|AW981354 EST392507 DSIL Medicago truncatula cDNA cl... 75 1e-12
 50 dbj|D88272|D88272 Hordeum vulgare mRNA for formate dehydrogenase... 75 2e-12
 emb|AI488120|AI488120 EST246442 tomato ovary, TAMU Lycopersicon ... 74 3e-12
 emb|AW780701|AW780701 sl75g02.y1 Gm-c1027 Glycine max cDNA clone... 55 3e-12
 emb|AW266848|AW266848 L48-192T3 Ice plant Lambda Uni-Zap XR expr... 74 4e-12
 emb|AW693443|AW693443 NF065D03ST1F1000 Developing stem Medicago ... 66 4e-12
 55 dbj|D49433|D49433 Pumpkin colne HPR2 hydroxypyruvate reductases ... 72 1e-11
 dbj|D49432|D49432 Pumpkin clone HPR1 hydroxypyruvate reductases ... 72 1e-11
 emb|AW278707|AW278707 sf96b06.y1 Gm-c1019 Glycine max cDNA clone... 72 1e-11
 gb|U01067|PUMHPR Cucurbita pepo Halloween NADH-dependent hydroxy... 72 2e-11
 emb|AI490396|AI490396 EST248734 tomato ovary, TAMU Lycopersicon ... 71 3e-11
 60 emb|X14609|CSNDHR Cucumis sativus mRNA for NAPH-dependent hydrox... 70 5e-11
 emb|AJ001429|RGDMANDER Rhodotorula graminis mRNA for D-mandelate... 70 6e-11

emb|AW040337|AW040337 EST283201 tomato mixed elicitor, BTI Lycop... 70 6e-11
emb|AW037837|AW037837 EST279466 tomato mixed elicitor, BTI Lycop... 70 6e-11
emb|AL033497|CAC49C10 C.albicans cosmid Ca49C10. 70 6e-11
5 emb|AI897727|AI897727 EST267170 tomato ovary, TAMU Lycopersicon ... 69 9e-11
emb|AI898454|AI898454 EST267897 tomato ovary, TAMU Lycopersicon ... 69 9e-11

Query= AL035394.196_at 13627_at /id_source genbank /description
emb|caa23036.1| (al035394) putative na⁺/h⁺-exchanging protein
10 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
/gb_link http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035394| /ncgi
http://www.ncgr.org/cgi-bin/ff?al035394
(2463 letters)

15 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

20

Score E
Sequences producing significant alignments: (bits) Value

25 emb|AW736388|AW736388 EST332307 KV3 Medicago truncatula cDNA clo... 243 5e-63
emb|AW622441|AW622441 EST313229 tomato root during/after fruit s... 204 2e-51
emb|AL157994|SPAC105 S.pombe chromosome I cosmid c105. 192 1e-47
emb|AQ841817|AQ841817 T134068 Soybean RFLP probe Glycine max gen... 186 8e-46
emb|X77087|SJ100567 S.cerevisiae (S288C) J0909, J0911, J0914 and... 150 5e-35
emb|Z49369|SCYJL094C S.cerevisiae chromosome X reading frame ORF... 150 5e-35
30 emb|AW774205|AW774205 EST333356 KV3 Medicago truncatula cDNA clo... 120 8e-28
emb|AW559356|AW559356 EST314404 DSIR Medicago truncatula cDNA cl... 104 2e-23
emb|AQ361449|AQ361449 mgxb0004G06r CUGI Rice Blast BAC Library P... 59 4e-16
emb|AT000678|AT000678 AT000678 Brassica rapa guard cell Brassica... 79 2e-13
emb|AV409975|AV409975 AV409975 Lotus japonicus young plants (two... 59 5e-11
35 emb|AT000552|AT000552 AT000552 Brassica rapa guard cell Brassica... 57 6e-07
emb|AW980088|AW980088 EST341613 tomato root deficiency, Cornell ... 45 8e-07
emb|AW307241|AW307241 sf54e09.y1 Gm-c1009 Glycine max cDNA clone... 48 1e-06
emb|AW334422|AW334422 S34F3 AGS-1 Pneumocystis carinii f. sp. ca... 52 2e-05
emb|AQ842018|AQ842018 T134304 Soybean RFLP probe Glycine max gen... 47 1e-04
40 emb|AV410314|AV410314 AV410314 Lotus japonicus young plants (two... 40 0.010
emb|AW163886|AW163886 Ljirnpes17-312-a12 Ljirnp Lambda HybriZap... 34 0.019
emb|AQ849208|AQ849208 LMAJFV1_lm43f12.y1 Leishmania major FV1 ra... 41 0.042
emb|AW690188|AW690188 NF029E07ST1F1000 Developing stem Medicago ... 35 0.044
emb|Y15086|CFHEPABC Cylindrotheca fusiformis hepA, hepB, hepC ge... 39 0.21
45 emb|AL112906|CNS01AGI Botrytis cinerea strain T4 cDNA library un... 38 0.28
emb|AW725682|AW725682 GA__Ea0019E05 Gossypium arboreum 7-10 dpa ... 37 0.54
emb|AW727060|AW727060 GA__Ea0011B07 Gossypium arboreum 7-10 dpa ... 36 1.0
emb|AL034559|PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq... 36 1.4
emb|AF127331|AF127331 Euplotes crassus histone H1-1 (H1-1) gene,... 36 1.4
50 emb|AW729298|AW729298 GA__Ea0024K04 Gossypium arboreum 7-10 dpa ... 28 1.6
emb|AL139794|LMFP1105 Leishmania major Friedlin chromosome 4 PAC... 35 1.9
emb|AB028188|AB028188 Penicillium digitatum DNA fragment contain... 35 2.6
emb|Z48093|GVEITS133 G.verna DNA for internal transcribed spacer... 28 3.2
emb|AL353012|SPBC1711 S.pombe chromosome II cosmid c1711. 35 3.6
55 gb|BE036059|BE036059 MO19C02 MO Mesembryanthemum crystallinum cD... 35 3.6
gb|BE036176|BE036176 MO20A07 MO Mesembryanthemum crystallinum cD... 35 3.6
emb|AW693672|AW693672 NF067B05ST1F1044 Developing stem Medicago ... 35 3.6
emb|AJ274013|AJ274013 AJ274013 Metarhizium anisopliae ARSEF 2575... 35 3.6
gb|U80041|AFU80041 Avena fatua Af10-protein mRNA, complete cds. 34 5.0
60 emb|AI612607|AI612607 TENG0370 T. Cruzi epimastigote normalised ... 34 5.0
emb|X04693|SOPCG Spinach gene for plastocyanin. 34 5.0

- emb|AW010989|AW010989 ST15D02 Pine TriplEx shoot tip library Pin... 34 5.0
 emb|AB013876|AB013876 Chlorella vulgaris gene, a unique region o... 34 5.0
 emb|AZ215593|AZ215593 Sheared DNA-74E9.TR Sheared DNA Trypanosom... 34 6.8
 emb|AQ845769|AQ845769 LMAJFV1_lm25g04.x1 Leishmania major FV1 ra... 34 6.8
 5 gb|M33825|TRBMVAT5A T.brucei MVAT5-like variant surface glycopro... 34 6.8
 emb|AC005802|AC005802 Leishmania major chromosome 3 clone L6202 ... 34 6.8
 emb|AQ640120|AQ640120 927P1-18A3.TP 927P1 Trypanosoma brucei gen... 34 6.8
 emb|AW299087|AW299087 EST305761 KV2 Medicago truncatula cDNA clo... 34 6.8
 emb|AQ163144|AQ163144 mgxb0023A11r CUGI Rice Blast BAC Library P... 34 6.8
 10 emb|AF183445|CLITSYDK1 Codonopsis lanceolata internal transcribe... 34 6.8
 emb|AC005893|AC005893 Leishmania major chromosome 3 clone L822 s... 34 6.8
 gb|L06030|TRBVSGH Trypanosoma brucei MVAT5-RX2 variant surface g... 34 6.8
 gb|L04971|TRBVSGM Trypanosoma brucei variant surface glycoprotei... 34 6.8
 emb|AW564995|AW564995 LG1_313_B04.b1_A002 Light Grown 1 (LG1) So... 34 6.8
 15 emb|AI050199|AI050199 TENU1447 T. cruzi epimastigote normalized ... 34 6.8
 emb|AW597619|AW597619 sj96f04.y1 Gm-c1023 Glycine max cDNA clone... 34 6.8
 emb|AF224499|AF224499 Triticum aestivum KNOTTED-1-like homeobox ... 34 6.8
 gb|N60227|N60227 TgESTzy10g08.r1 TgRH Tachyzoite cDNA Toxoplasma... 33 9.4
 emb|X68032|MTENOD12 M.truncatula ENOD12 gene. 33 9.4
 20 emb|AW126974|AW126974 ga16h04.y1 Moss EST library PPU Physcomitr... 33 9.4
 emb|AA274329|AA274329 TgESTzz24g03.s1 TgME49 invivo Bradyzoite c... 33 9.4
 gb|BE054344|BE054344 GA_Ea0035E03f Gossypium arboreum 7-10 dpa ... 33 9.4
 emb|AA009393|AA009393 TgESTzz08e11.r1 TgME49 Tachyzoite cDNA Tox... 33 9.4
 emb|Y16262|DCY16262 Daucus carota mRNA for neutral invertase. 33 9.4
 25 gb|BE035627|BE035627 MO12F02 MO Mesembryanthemum crystallinum cD... 33 9.4
 emb|AA274264|AA274264 TgESTzz25f05.s1 TgME49 invivo Bradyzoite c... 33 9.4

- Query= AC002387.185_at 13631_at /id_source genbank /description
 30 gb|aab82634.1| (ac002387) putative transketolase precursor
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002387|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002387|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002387|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac002387>
 35 (2371 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

- 40 Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

- 45 emb|Z50099|STTKETMR S.tuberosum mRNA for transketolase. 1372 0.0
 gb|L76554|SPITRAN Spinacia oleracea transketolase mRNA, chloropl... 1350 0.0
 emb|Y15781|CAY15781 Capsicum annuum mRNA for plastid transketola... 1344 0.0
 emb|A52295|A52295 Sequence 1 from Patent EP0723017. 1283 0.0
 emb|Z46648|CPTKT7 C.plantagineum tkt7 gene for transketolase. 1063 0.0
 50 emb|Z46647|CPTKT10 C.plantagineum tkt10 gene for transketolase. 1038 0.0
 emb|Z46646|CPTKT3 C.plantagineum tkt3 gene for transketolase. 1014 0.0
 emb|AJ249787|CPA249787 Cyanophora paradoxa mRNA for putative tra... 557 0.0
 emb|AL033501|CAC41C10 C.albicans cosmid Ca41C10. 253 e-175
 emb|AC007872|AC007872 The sequence of an Aspergillus parasiticus... 167 e-158
 55 gb|H55032|H55032 HHU58a Sorghum bicolor cv. TX430 Sorghum bicolo... 233 e-151
 emb|AC005299|AC005299 emericella nidulans chromosome viii cosmid... 166 e-147
 emb|AC004395|AC004395 Emericella nidulans Chromosome VIII Cosmid... 166 e-147
 emb|AW443928|AW443928 EST308858 tomato mixed elicitor, BTI Lycop... 468 e-131
 emb|AW667519|AW667519 GA_Ea0009J09 Gossypium arboreum 7-10 dpa ... 463 e-129
 60 emb|AI778813|AI778813 EST259692 tomato susceptible, Cornell Lyco... 453 e-126
 emb|AW776720|AW776720 EST335785 DSIL Medicago truncatula cDNA cl... 450 e-125

- emb|AW695194|AW695194 NF092E10ST1F1082 Developing stem Medicago ... 370 e-124
emb|AI774685|AI774685 EST255785 tomato resistant, Cornell Lycopersicon ... 444 e-123
emb|AW618386|AW618386 EST320372 *L. pennellii* trichome, Cornell U... 434 e-120
5 gb|BE052708|BE052708 GA__Ea0031N21f *Gossypium arboreum* 7-10 dpa ... 431 e-119
emb|AW737315|AW737315 EST338838 tomato flower buds, anthesis, Co... 409 e-113
emb|AW694020|AW694020 NF071G12ST1F1099 Developing stem Medicago ... 406 e-112
gb|BE060293|BE060293 HVSMEg0011O04f *Hordeum vulgare* pre-anthesis... 405 e-112
emb|AW649769|AW649769 EST328223 tomato germinating seedlings, TA... 377 e-111
emb|AW234850|AW234850 sf19h07.y1 Gm-c1028 Glycine max cDNA clone... 399 e-110
10 emb|AW760220|AW760220 sl59e08.y1 Gm-c1027 Glycine max cDNA clone... 388 e-106
emb|AW929526|AW929526 EST338314 tomato flower buds 8 mm to pre-a... 386 e-106
emb|AW596420|AW596420 sj12c01.y1 Gm-c1032 Glycine max cDNA clone... 380 e-104
emb|AI730390|AI730390 BNLGHi6849 Six-day Cotton fiber *Gossypium* ... 302 e-102
emb|AI778812|AI778812 EST259691 tomato susceptible, Cornell Lyco... 372 e-102
15 emb|AW720123|AW720123 LjNEST14e4r *Lotus japonicus* nodule library... 369 e-101
emb|AW697121|AW697121 NF115C09ST1F1069 Developing stem Medicago ... 334 e-101
emb|AW726320|AW726320 GA__Ea0021F03 *Gossypium arboreum* 7-10 dpa ... 354 1e-99
emb|AQ841855|AQ841855 T134114 Soybean RFLP probe Glycine max gen... 358 4e-98
emb|AW564025|AW564025 LG1_281_F10.b1_A002 Light Grown 1 (LG1) So... 359 4e-98
20 emb|AW979915|AW979915 EST341564 tomato root deficiency, Cornell ... 349 6e-95
emb|AI781665|AI781665 EST262544 tomato susceptible, Cornell Lyco... 348 1e-94
emb|Z26486|PSTKTG *P. stipitis* TKT gene for transketolase. 261 8e-93
emb|AW039152|AW039152 EST281387 tomato mixed elicitor, BTI Lycopersicon ... 339 7e-92
gb|BE053034|BE053034 GA__Ea0031O21f *Gossypium arboreum* 7-10 dpa ... 338 9e-92
25 emb|AW691000|AW691000 NF040C09ST1F1000 Developing stem Medicago ... 338 9e-92
emb|AW290149|AW290149 NXNV012F12F Nsf Xylem Normal wood Vertical... 337 2e-91
emb|AW203636|AW203636 sf36e03.y1 Gm-c1028 Glycine max cDNA clone... 332 6e-90
emb|AI966148|AI966148 sc34c04.y1 Gm-c1014 Glycine max cDNA clone... 330 4e-89
emb|Z71255|SCCHR XVI *S. cerevisiae* chromosome XVI 165536 bp sequen... 225 2e-88
30 gb|U51033|YSCP9513 *Saccharomyces cerevisiae* chromosome XVI cosmi... 225 2e-88
emb|Z49219|SC9499X *S. cerevisiae* chromosome XVI cosmid 9499. 225 2e-88
emb|X73224|SCTKL1 *S. cerevisiae* TKL1 gene for transketolase. 225 2e-88
emb|AL033385|SPBC2G5 *S. pombe* chromosome II cosmid c2G5. 198 2e-87
emb|AV388967|AV388967 AV388967 *Chlamydomonas reinhardtii* C9 Chla... 322 8e-87
35 emb|AV391940|AV391940 AV391940 *Chlamydomonas reinhardtii* C9 Chla... 321 1e-86
emb|AW587453|AW587453 IPPGHZ0039 Cotton fiber and embryo Lambda ... 276 3e-86
gb|U65983|KLU65983 *Kluyveromyces lactis* transketolase (TKL1) gen... 211 1e-85
emb|AW035937|AW035937 EST282796 tomato callus, TAMU Lycopersicon... 316 5e-85
emb|AW156809|AW156809 se31b02.y1 Gm-c1015 Glycine max cDNA clone... 315 1e-84
40 emb|AA660853|AA660853 00748 MTRHE Medicago truncatula cDNA 5' si... 282 1e-83
emb|AV393839|AV393839 AV393839 *Chlamydomonas reinhardtii* C9 Chla... 230 1e-83
emb|AA556878|AA556878 720 Loblolly pine C Pinus taeda cDNA clone... 289 2e-83
emb|AW689533|AW689533 NF021G12ST1F1000 Developing stem Medicago ... 308 8e-83
emb|AW776795|AW776795 EST335860 DSIL Medicago truncatula cDNA cl... 307 2e-82
45 emb|AW694632|AW694632 NF078D05ST1F1045 Developing stem Medicago ... 285 4e-82
emb|AV391577|AV391577 AV391577 *Chlamydomonas reinhardtii* C9 Chla... 304 1e-81
emb|AV388182|AV388182 AV388182 *Chlamydomonas reinhardtii* C9 Chla... 304 2e-81
emb|AW688641|AW688641 NF009H10ST1F1000 Developing stem Medicago ... 282 8e-80
emb|AW508848|AW508848 si41b02.y1 Gm-r1030 Glycine max cDNA clone... 298 9e-80
50 emb|AW695046|AW695046 NF082H06ST1F1059 Developing stem Medicago ... 297 3e-79
emb|X78993|SCRACII *S. cerevisiae* genomic DNA 70kb region of the r... 200 3e-79
emb|X73532|SCTKL2 *S. cerevisiae* gene for transketolase. 200 3e-79
emb|Z35985|SCYBR116C *S. cerevisiae* chromosome II reading frame OR... 200 3e-79
emb|AW564318|AW564318 LG1_290_F06.b1_A002 Light Grown 1 (LG1) So... 293 4e-78
55 emb|AW201472|AW201472 sf03e09.y1 Gm-c1027 Glycine max cDNA clone... 292 6e-78
emb|AB025004|AB025004 *Cicer arietinum* mRNA for transketolase, pa... 292 8e-78
emb|AW746874|AW746874 WS1_56_C06.b1_A002 Water-stressed 1 (WS1) ... 291 2e-77
emb|AW776336|AW776336 EST335401 DSIL Medicago truncatula cDNA cl... 290 4e-77
emb|AW696241|AW696241 NF104D02ST1F1016 Developing stem Medicago ... 288 1e-76
60 emb|AV395290|AV395290 AV395290 *Chlamydomonas reinhardtii* C9 Chla... 288 1e-76
emb|AW287516|AW287516 LG1_242_A07.b1_A002 Light Grown 1 (LG1) So... 283 4e-75

emb|AW907301|AW907301 EST343424 potato stolon, Cornell Universit... 281 1e-74
 dbj|D89172|D89172 Schizosaccharomyces pombe mRNA, partial cds, c... 171 3e-73
 emb|AV394221|AV394221 AV394221 Chlamydomonas reinhardtii C9 Chla... 275 4e-73
 emb|AV387871|AV387871 AV387871 Chlamydomonas reinhardtii C9 Chla... 275 1e-72
 5 emb|AI162975|AI162975 A028P14U Hybrid aspen plasmid library Popu... 273 1e-72
 emb|AJ234429|HVU234429 Hordeum vulgare partial mRNA; clone cMWG0... 271 1e-71
 emb|AW398784|AW398784 EST309284 L. pennellii trichome, Cornell U... 271 2e-71
 gb|BE056580|BE056580 894010C09.y1 C. reinhardtii CC-1690, normal... 267 2e-70
 emb|AW694944|AW694944 NF081G03ST1F1023 Developing stem Medicago ... 258 4e-70
 10 emb|AW041543|AW041543 EST284407 tomato mixed elicitor, BTI Lycop... 265 8e-70
 emb|AW980590|AW980590 EST391743 GVN Medicago truncatula cDNA clo... 265 1e-69
 emb|AF173677|AF173677 Beta vulgaris clone TK109UNI transketolase... 132 2e-69
 emb|AQ842082|AQ842082 T134371 Soybean RFLP probe Glycine max gen... 263 4e-69
 emb|AQ842006|AQ842006 T134292 Soybean RFLP probe Glycine max gen... 263 4e-69
 15 emb|AI726103|AI726103 BNLGHi5028 Six-day Cotton fiber Gossypium ... 260 3e-68
 emb|AW695133|AW695133 NF091E12ST1F1098 Developing stem Medicago ... 258 6e-68
 emb|AA819992|AA819992 L0-171M13R Ice plant Lambda Uni-Zap XR exp... 258 1e-67
 emb|AW180358|AW180358 MgA0465f MgA Library Mycosphaerella gramin... 144 1e-66
 emb|AI563214|AI563214 EST00338 watermelon lambda zap library Cit... 249 1e-65
 20 emb|AF086822|AF086822 Candida boidinii dihydroxyacetone synthase... 163 7e-65
 emb|AW696579|AW696579 NF106E10ST1F1082 Developing stem Medicago ... 249 7e-65
 gb|M63302|YSCTRANSK S.cerevisiae transketolase gene, complete cds. 168 5e-64

25 Query= AL022347.46_at 13659_at /id_source genbank /description
 emb|caa18462.1| (al022347) serine/threonine kinase-like protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022347| /ncgi
 30 http://www.ncgr.org/cgi-bin/ff?al022347
 (2037 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

35 Searching.....done

	Score	E	(bits)	Value
Sequences producing significant alignments:				
40	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k...	385	e-125	
	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2.	343	e-111	
	emb AB008191 AB008191 Brassica rapa mRNA for SRK29, complete cds.	348	e-109	
	emb Y18260 BOY18260 Brassica oleracea mRNA for SRK15 protein, pa...	346	e-109	
45	emb AB024416 AB024416 Brassica oleracea SRK2-b mRNA, complete cds.	347	e-109	
	emb Y14285 BOY14285 Brassica oleracea mRNA for SFR1 protein.	333	e-108	
	emb Y18259 BOY18259 Brassica oleracea mRNA for SRK5 protein, par...	342	e-107	
	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	328	e-106	
	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	334	e-105	
50	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	329	e-104	
	emb Y14286 BOY14286 Brassica oleracea SFR3 gene, partial.	205	e-104	
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	326	e-103	
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	330	e-103	
	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	336	e-102	
55	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti...	325	e-101	
	dbj D30049 BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti...	290	e-100	
	emb Y12530 BOARLKGGEN B.oleraceae gene encoding serine/threonine ...	131	1e-95	
	emb AB032474 AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc...	282	3e-94	
	dbj D38564 BOLRPKB Brassica campestris mRNA for receptor protein...	281	3e-93	
60	dbj D38563 BOLRPKA Brassica campestris mRNA for receptor protein...	276	4e-93	
	emb AB000970 AB000970 Brassica campestris gene for receptor kina...	129	1e-91	

- emb|AW620957|AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone... 275 9e-91
 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 254 1e-90
 emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 115 8e-90
 emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 292 1e-89
 5 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 127 2e-88
 gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 219 9e-88
 gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 284 8e-86
 emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 118 3e-85
 emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 313 4e-84
 10 emb|X79432|BOSRK3 B.oleracea SRK3 gene. 118 6e-84
 emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 112 8e-84
 emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 113 7e-83
 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 113 1e-82
 emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 122 9e-82
 15 gb|BE057261|BE057261 sm99f12.y1 Gm-c1015 Glycine max cDNA clone ... 296 4e-79
 emb|AW831390|AW831390 sm22a06.y1 Gm-c1028 Glycine max cDNA clone... 216 1e-75
 emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 126 2e-75
 emb|AW760240|AW760240 sl59g07.y1 Gm-c1027 Glycine max cDNA clone... 283 4e-75
 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 122 5e-75
 20 emb|AW442344|AW442344 EST311740 tomato fruit red ripe, TAMU Lyco... 221 3e-72
 gb|BE034949|BE034949 ML07F03 ML Mesembryanthemum crystallinum cD... 269 7e-71
 dbj|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 125 8e-71
 emb|AI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 268 1e-70
 emb|AI486193|AI486193 EST244514 tomato ovary, TAMU Lycopersicon ... 188 7e-68
 25 emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 242 2e-66
 emb|AI896155|AI896155 EST265598 tomato callus, TAMU Lycopersicon... 172 3e-65
 emb|AW203661|AW203661 sf36g06.y1 Gm-c1028 Glycine max cDNA clone... 205 5e-64
 emb|AW666141|AW666141 sk32f11.y1 Gm-c1028 Glycine max cDNA clone... 197 5e-64
 emb|AW220677|AW220677 EST297146 tomato fruit mature green, TAMU ... 237 1e-62
 30 emb|AI897876|AI897876 EST267319 tomato ovary, TAMU Lycopersicon ... 166 1e-61
 emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 236 6e-61
 emb|AI486584|AI486584 EST244905 tomato ovary, TAMU Lycopersicon ... 166 1e-60
 emb|Y16999|TCA16999 Theobroma cacao microsatellite DNA, clone mT... 132 2e-58
 emb|AW309544|AW309544 sf20h08.x1 Gm-c1028 Glycine max cDNA clone... 177 4e-58
 35 emb|AI822907|AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr... 126 3e-57
 emb|AI967314|AI967314 Ljirmp00-017 Ljirmp Lambda HybriZap two... 138 4e-57
 emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 223 4e-57
 emb|AI822355|AI822355 L0-804T3 Ice plant Lambda Uni-Zap XR expre... 126 7e-57
 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 131 2e-56
 40 emb|AW033458|AW033458 EST277029 tomato callus, TAMU Lycopersicon... 219 8e-56
 emb|AI899009|AI899009 EST268452 tomato ovary, TAMU Lycopersicon ... 172 6e-55
 emb|AI901283|AI901283 sc31d08.y1 Gm-c1014 Glycine max cDNA clone... 171 3e-54
 emb|AI771857|AI771857 EST252957 tomato ovary, TAMU Lycopersicon ... 169 7e-54
 emb|AI488101|AI488101 EST246423 tomato ovary, TAMU Lycopersicon ... 169 7e-54
 45 emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 109 1e-53
 emb|AI898581|AI898581 EST268024 tomato ovary, TAMU Lycopersicon ... 172 3e-53
 emb|AW054349|AW054349 L30-1774T3 Ice plant Lambda Uni-Zap XR exp... 126 5e-53
 emb|AI899156|AI899156 EST268599 tomato ovary, TAMU Lycopersicon ... 172 1e-52
 emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 137 2e-52
 50 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 136 1e-51
 emb|AI822347|AI822347 L0-796T3 Ice plant Lambda Uni-Zap XR expre... 118 5e-51
 emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 172 7e-51
 emb|AW667985|AW667985 GA__Ea0012C15 Gossypium arboreum 7-10 dpa ... 106 1e-50
 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 72 2e-50
 55 emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago L... 135 2e-50
 emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 108 3e-49
 emb|AI896953|AI896953 EST266396 tomato callus, TAMU Lycopersicon... 179 3e-49
 emb|Z18884|BOSRKRPC B.oleracea encoding S-receptor kinase relate... 121 1e-48
 emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 134 7e-48
 60 emb|AW034624|AW034624 EST278308 tomato callus, TAMU Lycopersicon... 192 1e-47
 emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 96 1e-47

emb|AW394449|AW394449 sh05d09.y1 Gm-c1016 Glycine max cDNA clone... 121 1e-47
emb|AW687052|AW687052 NF005E02RT1F1017 Developing root Medicago ... 190 3e-47
emb|AF220602|AF220602 Lycopersicon pimpinellifolium Rio Grande 7... 111 3e-47
gb|U59317|LPU59317 Lycopersicon pimpinellifolium serine/threonin... 107 3e-47
5 gb|U13923|LEU13923 Lycopersicon pimpinellifolium serine/threonin... 107 3e-47
emb|AW034993|AW034993 EST279222 tomato callus, TAMU Lycopersicon... 178 4e-47
emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 131 8e-47
emb|AW053331|AW053331 L30-1528T3 Ice plant Lambda Uni-Zap XR exp... 126 1e-46
emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 188 1e-46
10 emb|Z18861|BOSRK RPA B.oleracea encoding S-receptor kinase relate... 118 2e-46
emb|AI729170|AI729170 BNLGHI12834 Six-day Cotton fiber Gossypium... 128 3e-46
emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 108 7e-46
emb|AF220603|AF220603 Lycopersicon esculentum VFNT Cherry Pto lo... 109 1e-45
emb|AI775997|AI775997 EST257097 tomato resistant, Cornell Lycope... 185 1e-45
15 gb|U59318|LEU59318 Lycopersicon esculentum serine/threonine prot... 105 1e-45
emb|AW775756|AW775756 EST334821 DSIL Medicago truncatula cDNA cl... 135 2e-45
emb|Z73295|CRPK1 C.roseus mRNA for receptor-like protein kinase. 68 3e-45
gb|U59316|LEU59316 Lycopersicon esculentum serine/threonine prot... 103 1e-44
20
Query= AC005662.56_at 14083_at /id_source genbank /description
gb|aac78535.1| (ac005662) putative embryo-abundant protein
[arabidopsis thaliana] /blast_score 1.00e-155 /ec_number /family
/chip nova /gb_link
25 http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005662|/ncgi
http://www.ncgr.org/cgi-bin/ff?ac005662
(966 letters)
30 Database: plantfungal
661,018 sequences; 426,114,510 total letters
Searching.....done
35 Score E
Sequences producing significant alignments: (bits) Value
emb|AW685935|AW685935 NF031H09NR1F1000 Nodulated root Medicago t... 299 1e-83
emb|AW032722|AW032722 EST276281 tomato callus, TAMU Lycopersicon... 310 1e-83
40 emb|AI489127|AI489127 EST247466 tomato ovary, TAMU Lycopersicon ... 310 1e-83
emb|AI489097|AI489097 EST247436 tomato ovary, TAMU Lycopersicon ... 310 1e-83
emb|AI781847|AI781847 EST262726 tomato susceptible, Cornell Lyco... 309 2e-83
emb|AW442260|AW442260 EST311656 tomato fruit red ripe, TAMU Lyco... 308 4e-83
emb|AI781496|AI781496 EST262375 tomato susceptible, Cornell Lyco... 308 4e-83
45 emb|AI898923|AI898923 EST268366 tomato ovary, TAMU Lycopersicon ... 307 8e-83
emb|AI894834|AI894834 EST264277 tomato callus, TAMU Lycopersicon... 306 2e-82
emb|AW033760|AW033760 EST277331 tomato callus, TAMU Lycopersicon... 306 2e-82
emb|AI490417|AI490417 EST248743 tomato ovary, TAMU Lycopersicon ... 304 7e-82
emb|AW686492|AW686492 NF042A07NR1F1000 Nodulated root Medicago t... 299 8e-82
50 emb|AI898538|AI898538 EST267981 tomato ovary, TAMU Lycopersicon ... 303 1e-81
emb|AI488586|AI488586 EST246925 tomato ovary, TAMU Lycopersicon ... 303 2e-81
emb|AI775239|AI775239 EST256339 tomato resistant, Cornell Lycope... 302 4e-81
emb|AI771731|AI771731 EST252831 tomato ovary, TAMU Lycopersicon ... 301 5e-81
emb|AI780639|AI780639 EST261614 tomato susceptible, Cornell Lyco... 299 2e-80
55 emb|AW029697|AW029697 EST272952 tomato callus, TAMU Lycopersicon... 299 2e-80
emb|AI485286|AI485286 EST243590 tomato ovary, TAMU Lycopersicon ... 298 5e-80
emb|AI897802|AI897802 EST267245 tomato ovary, TAMU Lycopersicon ... 297 6e-80
emb|AW223714|AW223714 EST300525 tomato fruit red ripe, TAMU Lyco... 297 9e-80
emb|AW220845|AW220845 EST297314 tomato fruit mature green, TAMU ... 292 3e-78
60 emb|AW684608|AW684608 NF018H07NR1F1000 Nodulated root Medicago t... 292 3e-78
emb|AI489777|AI489777 EST248116 tomato ovary, TAMU Lycopersicon ... 292 4e-78

	emb AW132650 AW132650 se08b10.y1 Gm-c1013 Glycine max cDNA clone...	291 7e-78
	emb AI483572 AI483572 EST249422 tomato ovary, TAMU Lycopersicon ...	288 4e-77
	emb AI778435 AI778435 EST259314 tomato susceptible, Cornell Lyco...	286 1e-76
	emb AI897140 AI897140 EST266583 tomato ovary, TAMU Lycopersicon ...	286 1e-76
5	emb AI488011 AI488011 EST246333 tomato ovary, TAMU Lycopersicon ...	286 2e-76
	emb AI771230 AI771230 EST252246 tomato ovary, TAMU Lycopersicon ...	281 4e-75
	emb AW218445 AW218445 EST303628 tomato radicle, 5 d post-imbibit...	281 6e-75
	emb AI897359 AI897359 EST266802 tomato ovary, TAMU Lycopersicon ...	279 2e-74
	emb AW931636 AW931636 EST357479 tomato fruit mature green, TAMU ...	277 7e-74
10	emb AI898026 AI898026 EST267469 tomato ovary, TAMU Lycopersicon ...	276 2e-73
	emb AI897018 AI897018 EST266461 tomato ovary, TAMU Lycopersicon ...	270 9e-72
	emb AI487404 AI487404 EST245726 tomato ovary, TAMU Lycopersicon ...	270 2e-71
	emb AI485049 AI485049 EST243353 tomato ovary, TAMU Lycopersicon ...	269 3e-71
	emb AI484072 AI484072 EST249943 tomato ovary, TAMU Lycopersicon ...	267 8e-71
15	emb AI485145 AI485145 EST243449 tomato ovary, TAMU Lycopersicon ...	266 2e-70
	emb AW708004 AW708004 EST0051 Grape berries Lambda Zap II Librar...	266 2e-70
	emb AW038382 AW038382 EST280065 tomato mixed elicitor, BTI Lycop...	264 5e-70
	emb AI898224 AI898224 EST267667 tomato ovary, TAMU Lycopersicon ...	245 1e-69
	emb AI483780 AI483780 EST249651 tomato ovary, TAMU Lycopersicon ...	259 2e-68
20	gb L47672 PIAEMB34R Picea glauca embryo-abundant protein (EMB34)...	199 3e-66
	emb AW684859 AW684859 NF022D03NR1F1000 Nodulated root Medicago t...	189 1e-64
	emb AW222134 AW222134 EST298945 tomato fruit red ripe, TAMU Lyco...	243 2e-63
	emb AW625379 AW625379 EST319202 tomato radicle, 5 d post-imbibit...	242 4e-63
	emb AI485781 AI485781 EST244102 tomato ovary, TAMU Lycopersicon ...	240 1e-62
25	emb AW728861 AW728861 GA__Ea0028O02 Gossypium arboreum 7-10 dpa ...	189 2e-59
	emb AI489435 AI489435 EST247774 tomato ovary, TAMU Lycopersicon ...	224 7e-58
	emb AI485480 AI485480 EST243801 tomato ovary, TAMU Lycopersicon ...	221 5e-57
	emb AW030923 AW030923 EST274230 tomato callus, TAMU Lycopersicon...	219 3e-56
	emb AI771831 AI771831 EST252931 tomato ovary, TAMU Lycopersicon ...	219 3e-56
30	emb AI488694 AI488694 EST247033 tomato ovary, TAMU Lycopersicon ...	216 2e-55
	emb AI897044 AI897044 EST266487 tomato ovary, TAMU Lycopersicon ...	216 2e-55
	emb AW127616 AW127616 M110351 DSLC Medicago truncatula cDNA clon...	207 1e-52
	emb AW221131 AW221131 EST297600 tomato fruit mature green, TAMU ...	203 2e-51
	gb BE036025 BE036025 MO18F06 MO Mesembryanthemum crystallinum cD...	197 1e-49
35	emb AW310620 AW310620 sg22b10.x1 Gm-c1024 Glycine max cDNA clone...	138 4e-49
	emb AA660966 AA660966 00863 MtrHE Medicago truncatula cDNA 5' si...	193 2e-48
	emb AI488052 AI488052 EST246374 tomato ovary, TAMU Lycopersicon ...	191 6e-48
	emb AI483934 AI483934 EST249805 tomato ovary, TAMU Lycopersicon ...	190 2e-47
	emb AW687553 AW687553 NF010H04RT1F1043 Developing root Medicago ...	189 2e-47
40	emb AI488394 AI488394 EST246716 tomato ovary, TAMU Lycopersicon ...	189 3e-47
	emb AW687876 AW687876 NF014D11RT1F1093 Developing root Medicago ...	179 2e-44
	emb AW031053 AW031053 EST274360 tomato callus, TAMU Lycopersicon...	175 6e-43
	emb AI771906 AI771906 EST253006 tomato ovary, TAMU Lycopersicon ...	174 1e-42
	emb AI771730 AI771730 EST252830 tomato ovary, TAMU Lycopersicon ...	171 5e-42
45	emb AI895638 AI895638 EST265081 tomato callus, TAMU Lycopersicon...	164 9e-40
	emb AW441823 AW441823 EST311219 tomato fruit red ripe, TAMU Lyco...	164 9e-40
	emb AW981333 AW981333 EST392486 DSIL Medicago truncatula cDNA cl...	156 3e-37
	emb AI486213 AI486213 EST244534 tomato ovary, TAMU Lycopersicon ...	153 2e-36
	emb AV425590 AV425590 AV425590 Lotus japonicus young plants (two...	148 6e-35
50	emb AW563884 AW563884 LG1_272_D05.b1_A002 Light Grown 1 (LG1) So...	136 3e-31
	emb AI489302 AI489302 EST247641 tomato ovary, TAMU Lycopersicon ...	129 4e-29
	emb AI967559 AI967559 Ljirmp05-409-e8 Ljirnp Lambda HybriZap ...	120 2e-26
	emb AI898395 AI898395 EST267838 tomato ovary, TAMU Lycopersicon ...	115 7e-25
	emb AI782642 AI782642 EST263521 tomato susceptible, Cornell Lyco...	105 7e-22
55	emb AI725304 AI725304 1170 PtIFG2 Pinus taeda cDNA clone 9256r, ...	78 2e-18
	emb AW096566 AW096566 EST289746 tomato mixed elicitor, BTI Lycop...	90 3e-17
	emb AI899609 AI899609 EST269052 tomato susceptible, Cornell Lyco...	90 3e-17
	emb AI899596 AI899596 EST269039 tomato susceptible, Cornell Lyco...	90 3e-17
	emb AW443878 AW443878 EST308808 tomato mixed elicitor, BTI Lycop...	90 3e-17
60	emb AI486045 AI486045 EST244366 tomato ovary, TAMU Lycopersicon ...	90 3e-17
	emb AW222135 AW222135 EST298946 tomato fruit red ripe, TAMU Lyco...	89 4e-17

emb|AW032431|AW032431 EST275970 tomato callus, TAMU Lycopersicon... 87 2e-16
 emb|AI778055|AI778055 EST258934 tomato susceptible, Cornell Lyco... 87 2e-16
 emb|AW185076|AW185076 se86d10.y1 Gm-c1023 Glycine max cDNA clone... 69 4e-14
 emb|AA740029|AA740029 794 PtIFG2 Pinus taeda cDNA clone 9256M 3'... 77 3e-13
 5 emb|Z92685|Z92685 223/4 Norway spruce mRNA Picea abies cDNA clon... 76 5e-13
 emb|AW564832|AW564832 LG1_305_G04.b1_A002 Light Grown 1 (LG1) So... 51 2e-05
 gb|U00029|YSCH9177 Saccharomyces cerevisiae chromosome VIII cosm... 35 2e-05
 emb|AW670960|AW670960 LG1_278_A08.b1_A002 Light Grown 1 (LG1) So... 50 3e-05
 emb|AW713879|AW713879 h3g02ne.fl Neurospora crassa evening cDNA ... 40 1e-04
 10 emb|AW443870|AW443870 EST308800 tomato mixed elicitor, BTI Lycop... 41 0.011
 emb|AW678240|AW678240 WS1_14_G12.b1_A002 Water-stressed 1 (WS1) ... 37 0.26
 emb|AL034559|PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq... 36 0.50
 gb|U10549|ANU10549 Aspergillus niger protein kinase C (pkcA) gen... 35 0.94
 gb|U74447|ZAU74447 Zinnia angustifolia internal transcribed spac... 33 0.95
 15 emb|AZ217616|AZ217616 Sheared DNA-90G1.TF Sheared DNA Trypanosom... 31 2.1

20 Query= AC002291.12_at 14096_at /id_source genbank /description no hits
 found. /blast_score /ec_number /family /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002291|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002291|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002291|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac002291>
 (159 letters)

25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

30 Searching.....done

		Score	E	
				(bits) Value
	Sequences producing significant alignments:			
	emb AQ161515 AQ161515 mgxb0008C06r CUGI Rice Blast BAC Library P...	32	0.026	
35	emb AQ324421 AQ324421 mgxb0018F21r CUGI Rice Blast BAC Library P...	32	0.026	
	emb AL116063 CNS01CW7 Botrytis cinerea strain T4 cDNA library un...	29	0.24	
	emb AQ940444 AQ940444 Sheared DNA-35C4.TF Sheared DNA Trypanosom...	24	0.40	
	emb AQ362000 AQ362000 mgxb0004E15r CUGI Rice Blast BAC Library P...	28	0.62	
	emb AQ945662 AQ945662 Sheared DNA-49E8.TR Sheared DNA Trypanosom...	25	1.5	
40	emb AW266254 AW266254 L30-2966T3 Ice plant Lambda Uni-Zap XR exp...	27	1.6	
	emb AL355929 NCB21J21 Neurospora crassa DNA linkage group II BAC...	27	1.6	
	emb AW726145 AW726145 GA__Ea0020M12 Gossypium arboreum 7-10 dpa ...	26	2.2	
	emb AW661015 AW661015 832009D11.y1 C. reinhardtii CC-125 nutrien...	23	2.7	
	emb AV391625 AV391625 AV391625 Chlamydomonas reinhardtii C9 Chla...	23	2.7	
45	emb AI055219 AI055219 coau0003G03 Cotton Boll Abscission Zone cD...	23	2.7	
	emb AL354533 LMFL6294 Leishmania major Friedlin chromosome 21 co...	26	4.1	
	gb N98018 N98018 2045C3 czapPFDd2.1, Debopam Chakrabarti Plasmod...	26	4.1	
	emb AA519693 AA519693 TgESTzz27f07.r1 TgME49 invivo Bradyzoite c...	26	4.1	
	emb AA519224 AA519224 TgESTzz39g08.s1 TgME49 invivo Bradyzoite c...	26	4.1	
50	emb AW650822 AW650822 EST329276 tomato germinating seedlings, TA...	26	4.1	
	emb AA531994 AA531994 TgESTzz46c10.r1 TgME49 invivo Bradyzoite c...	26	4.1	
	emb AA520816 AA520816 TgESTzz64d11.r1 TgME49 invivo Bradyzoite c...	26	4.1	
	gb U15615 TCU15615 Trypanosoma cruzi reverse transcriptase-like ...	26	4.1	
	emb AQ848398 AQ848398 LMAJFV1_lm61f01.x1 Leishmania major FV1 ra...	26	4.1	
55	emb AL136536 SPBC1703 S.pombe chromosome II cosmid c1703.	26	4.1	
	emb AA520593 AA520593 TgESTzz62e12.r1 TgME49 invivo Bradyzoite c...	26	4.1	
	emb Z81402 CAZ81402 C.aeruginosa 28S rRNA gene.	26	4.1	
	emb AW979496 AW979496 EST310517 tomato root deficiency, Cornell ...	26	4.1	
	emb AW671199 AW671199 LG1_330_F04.b1_A002 Light Grown 1 (LG1) So...	25	5.7	
60	emb Z74775 SCYOL033W S.cerevisiae chromosome XV reading frame OR...	25	5.7	
	emb AA897901 AA897901 NCP4C5T3 Perithecial Neurospora crassa cDN...	25	5.7	

emb|AW694603|AW694603 NF078B02ST1F1015 Developing stem Medicago ... 25 5.7
 emb|Z74776|SCYOL034W S.cerevisiae chromosome XV reading frame OR... 25 5.7
 emb|AQ904542|AQ904542 GSSTc04164 Trypanosome cruzi random genomi... 25 5.7
 gb|L39015|YSCMSE1G Saccharomyces cerevisiae nuclear-encoded mito... 25 5.7
 5 gb|BE054352|BE054352 GA_Ea0035E11f Gossypium arboreum 7-10 dpa ... 25 5.7
 emb|AI707320|AI707320 T7446 MVAT4 bloodstream form of serodeme W... 25 5.7
 emb|AW730403|AW730403 GA_Ea0023O04 Gossypium arboreum 7-10 dpa ... 25 5.7
 emb|X87148|VPPPCGEN V.planifolia mRNA for phosphoenolpyruvate ca... 25 5.7
 emb|AW031408|AW031408 EST274862 tomato callus, TAMU Lycopersicon... 25 5.7
 10 emb|AI730886|AI730886 BNLGHi8147 Six-day Cotton fiber Gossypium ... 25 5.7
 emb|AW695893|AW695893 NF100D11ST1F1093 Developing stem Medicago ... 25 5.7
 emb|AW310777|AW310777 sg25a11.x1 Gm-c1024 Glycine max cDNA clone... 22 6.0
 emb|AV410755|AV410755 AV410755 Lotus japonicus young plants (two... 25 7.8
 emb|AQ445006|AQ445006 GSSTc0636 Trypanosoma cruzi random genomic... 25 7.8
 15 emb|Z49821|SCPDR10 S.cerevisiae PDR10, MYO2, PDR10, SCD5, MIP1, ... 25 7.8
 emb|AC008152|AC008152 Leishmania major chromosome 35 clone L7936... 25 7.8
 emb|AQ399859|AQ399859 mgxb0012H02f CUGI Rice Blast BAC Library P... 25 7.8
 emb|AF175710|AF175710 Pleurotus eryngii peroxidase PS1 precursor... 25 7.8
 emb|AW186653|AW186653 BNLGHi12240 Six-day Cotton fiber Gossypium... 25 7.8
 20 emb|AJ131048|CAR131048 Cicer arietinum mRNA for protein kinase, ... 25 7.8
 emb|AW775371|AW775371 EST334436 DSIL Medicago truncatula cDNA cl... 25 7.8
 emb|AC021894|AC021894 Leishmania major chromosome 35 clone L8650... 25 7.8
 emb|Z75236|SCYOR328W S.cerevisiae chromosome XV reading frame OR... 25 7.8
 emb|AI069165|AI069165 mgae0005dC01f Magnaporthe grisea Appressor... 25 7.8
 25 emb|AI068528|AI068528 mgae0002dE03f Magnaporthe grisea Appressor... 25 7.8
 emb|AI068407|AI068407 mgae0002aH09f Magnaporthe grisea Appressor... 25 7.8
 emb|AL109846|SPBC17G9 S.pombe chromosome II cosmid c17G9. 23 9.1
 emb|Z72244|CNIGRITS1 C.nigricans DNA for internal transcribed sp... 21 9.5

30 Query= AL035528.279_i_at 14110_i_at /id_source genbank /description
 emb|cab36854.1| (al035528) putative disease resistance protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family disease
 /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 35 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035528| /ncgi
 http://www.ncgr.org/cgi-bin/ff?al035528
 (2508 letters)

Database: plantfungal
 40 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	(bits)	Value
45	Sequences producing significant alignments:			
	emb AF119041 AF119041 Lycopersicon esculentum haplotype Southern...	105	4e-61	
	emb AF119040 AF119040 Lycopersicon esculentum haplotype Northern...	112	1e-59	
	emb AJ002235 LHJ002235 Lycopersicon hirsutum Cf-4 resistance gen...	103	1e-59	
50	emb AJ002236 LPJ002236 Lycopersicon pimpinellifolium Cf-9 resist...	103	2e-57	
	gb U42444 U42444 Lycopersicon pimpinellifolium leucine rich repe...	122	4e-57	
	emb A57130 A57130 Sequence 1 from Patent WO9531564.	122	4e-57	
	gb U42445 U42445 Lycopersicon pimpinellifolium leucine rich repe...	122	4e-57	
	emb A57133 A57133 Sequence 4 from Patent WO9531564.	122	4e-57	
55	emb AF053995 AF053995 Lycopersicon esculentum Hcr2-0B (Hcr2-0B) ...	121	2e-56	
	emb AF053997 AF053997 Lycopersicon esculentum Hcr2-5B (Hcr2-5B) ...	109	1e-52	
	emb A67432 A67432 Sequence 5 from Patent WO9743429.	109	1e-52	
	emb AF053996 AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr...	101	5e-49	
	emb AF053998 AF053998 Lycopersicon esculentum Hcr2-5D (Hcr2-5D) ...	127	7e-49	
60	emb A67434 A67434 Sequence 7 from Patent WO9743429.	127	7e-49	
	emb AF053993 AF053993 Lycopersicon esculentum disease resistance...	127	7e-49	

	emb A67429 A67429 Sequence 2 from Patent WO9743429.	127 7e-49
	emb A67428 A67428 Sequence 1 from Patent WO9743429.	127 7e-49
	emb AB029327 AB029327 Nicotiana tabacum mRNA for elicitor-induci...	102 3e-48
	emb AF053994 AF053994 Lycopersicon esculentum Hcr2-0A (Hcr2-0A) ...	103 2e-42
5	emb Y12640 LECF4A L.esculentum Cf-4A gene.	100 1e-40
	emb AJ002237 LEJ002237 Lycopersicon esculentum haplotype of the ...	100 8e-39
	emb A58270 A58270 Sequence 1 from Patent WO9635790.	93 6e-37
	gb U15936 LPU15936 Lycopersicon pimpinellifolium Cf-9 precursor ...	93 3e-36
	gb U77888 INU77888 Ipomoea nil receptor-like protein kinase (inr...	99 4e-29
10	emb AI778581 AI778581 EST259460 tomato susceptible, Cornell Lyco...	99 3e-26
	emb AI486572 AI486572 EST244893 tomato ovary, TAMU Lycopersicon ...	88 5e-26
	emb AI898269 AI898269 EST267712 tomato ovary, TAMU Lycopersicon ...	88 5e-26
	emb AW267955 AW267955 EST306297 DSIR Medicago truncatula cDNA cl...	81 3e-25
	emb AF053127 AF053127 Malus domestica leucine-rich receptor-like...	84 1e-24
15	emb AQ367638 AQ367638 tox0002D20f CUGI Tomato BAC Library Lycop...	81 8e-24
	emb AW306675 AW306675 se53h08.y1 Gm-c1017 Glycine max cDNA clone...	90 6e-23
	emb AW299082 AW299082 EST305756 KV2 Medicago truncatula cDNA clo...	83 1e-22
	emb AW980804 AW980804 EST391957 GVN Medicago truncatula cDNA clo...	86 3e-22
	emb AW616452 AW616452 EST322863 L. hirsutum trichome, Cornell Un...	86 8e-22
20	emb AZ044600 AZ044600 Gm_UMb001_116_G01.R UMN Soybean BAC Librar...	106 8e-22
	emb AF197946 AF197946 Glycine max receptor protein kinase-like p...	85 1e-21
	emb AF197947 AF197947 Glycine max receptor protein kinase-like p...	82 1e-21
	emb AW775087 AW775087 EST334238 KV3 Medicago truncatula cDNA clo...	85 2e-21
	emb AW033129 AW033129 EST276688 tomato callus, TAMU Lycopersicon...	86 5e-21
25	emb X81367 TAAWJL172 T.aestivum (subclone pAWJL172) AWJL172 gene.	71 9e-21
	emb AW398661 AW398661 EST309161 L. pennellii trichome, Cornell U...	85 2e-20
	emb AW398651 AW398651 EST309151 L. pennellii trichome, Cornell U...	85 2e-20
	emb AW217935 AW217935 EST296649 tomato flower buds, anthesis, Co...	79 4e-20
	emb AI726155 AI726155 BNLGHi5095 Six-day Cotton fiber Gossypium ...	78 5e-20
30	emb AF159296 AF159296 Lycopersicon esculentum pollen extensin-li...	70 1e-19
	emb AW267958 AW267958 EST306300 DSIR Medicago truncatula cDNA cl...	97 6e-19
	emb Y10816 LIY10816 L.infantum psa gene.	70 7e-19
	gb U77041 MDU77041 Malus domestica polygalacturonase-inhibiting ...	76 7e-19
	emb AI898226 AI898226 EST267669 tomato ovary, TAMU Lycopersicon ...	95 2e-18
35	emb AW030004 AW030004 EST273259 tomato callus, TAMU Lycopersicon...	95 2e-18
	emb AF159171 AF159171 Eucalyptus nitens polygalacturonase-inhibi...	74 3e-18
	emb AF159170 AF159170 Eucalyptus saligna polygalacturonase-inhib...	74 3e-18
	emb AF159167 AF159167 Eucalyptus grandis polygalacturonase-inhib...	74 3e-18
	emb AI352869 AI352869 MB70-4A PZ204.BNlib Brassica napus cDNA cl...	89 3e-18
40	emb X81370 TAAWJL236 T.aestivum (subclone pAWJL236) AWJL236 gene.	78 4e-18
	emb Z49063 ADPGIP A.deliciosa pgip mRNA for polygalacturonase in...	74 5e-18
	emb AF159169 AF159169 Eucalyptus urophylla polygalacturonase-inh...	74 7e-18
	gb U62279 SBU62279 Sorghum bicolor leucine-rich repeat-contains...	93 8e-18
	emb AW738046 AW738046 EST339473 tomato flower buds, anthesis, Co...	93 1e-17
45	emb AW307311 AW307311 sf55d03.y1 Gm-c1009 Glycine max cDNA clone...	80 1e-17
	gb L09264 PYPPGI Pyrus communis polygalacturonase inhibitor mRNA...	71 2e-17
	emb AF159168 AF159168 Eucalyptus camaldulensis polygalacturonase...	74 2e-17
	emb AW689207 AW689207 NF016F04ST1F1000 Developing stem Medicago ...	78 2e-17
	emb AA738549 AA738549 SbRLK7 Sorghum bicolor cv. TX430 leaf Sorg...	90 5e-17
50	emb AI897228 AI897228 EST266767 tomato ovary, TAMU Lycopersicon ...	90 5e-17
	emb AW688235 AW688235 NF005A07ST1F1000 Developing stem Medicago ...	89 1e-16
	emb AW694992 AW694992 NF082D01ST1F1012 Developing stem Medicago ...	83 2e-16
	emb AW432582 AW432582 sh76d03.y1 Gm-c1015 Glycine max cDNA clone...	89 2e-16
	emb AW399097 AW399097 EST309597 L. pennellii trichome, Cornell U...	69 2e-16
55	emb AI443128 AI443128 sa84f10.y1 Gm-c1004 Glycine max cDNA clone...	81 2e-16
	emb AI899284 AI899284 EST268727 tomato ovary, TAMU Lycopersicon ...	88 3e-16
	emb Y14600 SBRLK1 Sorghum bicolor mRNA for protein serine/threon...	88 4e-16
	emb AA738545 AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg...	87 5e-16
	emb AW033367 AW033367 EST276938 tomato callus, TAMU Lycopersicon...	87 5e-16
60	emb AV419297 AV419297 AV419297 Lotus japonicus young plants (two...	63 7e-16
	emb AW689888 AW689888 NF025H09ST1F1000 Developing stem Medicago ...	86 1e-15

emb|AA557055|AA557055 897 Loblolly pine N Pinus taeda cDNA clone... 86 1e-15
 emb|AI779817|AI779817 EST260696 tomato susceptible, Cornell Lyco... 80 1e-15
 emb|AW399471|AW399471 EST309971 L. pennellii trichome, Cornell U... 55 1e-15
 gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor... 85 2e-15
 5 emb|AW164782|AW164782 se77g01.y1 Gm-c1023 Glycine max cDNA clone... 85 2e-15
 emb|A67797|A67797 Sequence 2 from Patent WO9743427. 85 2e-15
 emb|AW929780|AW929780 EST354050 tomato flower buds 8 mm to pre-a... 80 2e-15
 emb|AI730245|AI730245 BNLGHi6465 Six-day Cotton fiber Gossypium ... 64 2e-15
 emb|AW929854|AW929854 EST354124 tomato flower buds 8 mm to pre-a... 80 3e-15
 10 emb|AV408986|AV408986 AV408986 Lotus japonicus young plants (two... 84 5e-15
 emb|AW671867|AW671867 LG1_352_F06.b1_A002 Light Grown 1 (LG1) So... 84 5e-15
 emb|AI488023|AI488023 EST246345 tomato ovary, TAMU Lycopersicon ... 84 5e-15
 emb|AI782076|AI782076 EST262955 tomato susceptible, Cornell Lyco... 84 6e-15
 emb|AV428126|AV428126 AV428126 Lotus japonicus young plants (two... 84 6e-15
 15 emb|AW695797|AW695797 NF098F06ST1F1058 Developing stem Medicago ... 84 6e-15
 emb|AW869870|AW869870 NXNV_122_E02_F Nsf Xylem Normal wood Verti... 66 9e-15
 emb|AI856215|AI856215 sb39c10.x1 Gm-c1014 Glycine max cDNA clone... 83 9e-15
 emb|AW929189|AW929189 EST337977 tomato flower buds 8 mm to pre-a... 83 9e-15
 emb|AW616567|AW616567 EST322978 L. hirsutum trichome, Cornell Un... 83 9e-15
 20 emb|AW697060|AW697060 NF111H11ST1F1095 Developing stem Medicago ... 77 1e-14
 emb|X81369|TAAWJL218 T.aestivumn (subclone pAWJL218) AWJL218 gene. 83 1e-14
 emb|AI776963|AI776963 EST251989 tomato callus, TAMU Lycopersicon... 83 1e-14
 emb|AW443205|AW443205 EST308135 tomato mixed elicitor, BTI Lycop... 83 1e-14
 emb|AW696757|AW696757 NF110F02ST1F1025 Developing stem Medicago ... 83 1e-14
 25

Query= AL035528.279_s_at 14111_s_at /id_source genbank /description
 emb|cab36854.1| (al035528) putative disease resistance protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 30 /gb_link /ncgi
 (2508 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters
 35

Searching.....done

	Score	E	(bits)	Value
Sequences producing significant alignments:				
40	emb AF119041 AF119041	Lycopersicon esculentum haplotype Southern...	105	4e-61
	emb AF119040 AF119040	Lycopersicon esculentum haplotype Northern...	112	1e-59
	emb AJ002235 LHJ002235	Lycopersicon hirsutum Cf-4 resistance gen...	103	1e-59
	emb AJ002236 LPJ002236	Lycopersicon pimpinellifolium Cf-9 resist...	103	2e-57
45	gb U42444 U42444	Lycopersicon pimpinellifolium leucine rich repe...	122	4e-57
	emb A57130 A57130	Sequence 1 from Patent WO9531564.	122	4e-57
	gb U42445 U42445	Lycopersicon pimpinellifolium leucine rich repe...	122	4e-57
	emb A57133 A57133	Sequence 4 from Patent WO9531564.	122	4e-57
	emb AF053995 AF053995	Lycopersicon esculentum Hcr2-0B (Hcr2-0B) ...	121	2e-56
50	emb AF053997 AF053997	Lycopersicon esculentum Hcr2-5B (Hcr2-5B) ...	109	1e-52
	emb A67432 A67432	Sequence 5 from Patent WO9743429.	109	1e-52
	emb AF053996 AF053996	Lycopersicon pimpinellifolium Hcr2-2A (Hcr...	101	5e-49
	emb AF053998 AF053998	Lycopersicon esculentum Hcr2-5D (Hcr2-5D) ...	127	7e-49
	emb A67434 A67434	Sequence 7 from Patent WO9743429.	127	7e-49
55	emb AF053993 AF053993	Lycopersicon esculentum disease resistance...	127	7e-49
	emb A67429 A67429	Sequence 2 from Patent WO9743429.	127	7e-49
	emb A67428 A67428	Sequence 1 from Patent WO9743429.	127	7e-49
	emb AB029327 AB029327	Nicotiana tabacum mRNA for elicitor-induci...	102	3e-48
	emb AF053994 AF053994	Lycopersicon esculentum Hcr2-0A (Hcr2-0A) ...	103	2e-42
60	emb Y12640 LECF4A	L.esculentum Cf-4A gene.	100	1e-40
	emb AJ002237 LEJ002237	Lycopersicon esculentum haplotype of the ...	100	8e-39

- emb|A58270|A58270 Sequence 1 from Patent WO9635790. 93 6e-37
gb|U15936|LPU15936 Lycopersicon pimpinellifolium Cf-9 precursor ... 93 3e-36
gb|U77888|INU77888 Ipomoea nil receptor-like protein kinase (inr... 99 4e-29
emb|AI778581|AI778581 EST259460 tomato susceptible, Cornell Lyco... 99 3e-26
5 emb|AI486572|AI486572 EST244893 tomato ovary, TAMU Lycopersicon ... 88 5e-26
emb|AI898269|AI898269 EST267712 tomato ovary, TAMU Lycopersicon ... 88 5e-26
emb|AW267955|AW267955 EST306297 DSIR Medicago truncatula cDNA cl... 81 3e-25
emb|AF053127|AF053127 Malus domestica leucine-rich receptor-like... 84 1e-24
emb|AQ367638|AQ367638 tox0002D20f CUGI Tomato BAC Library Lycop... 81 8e-24
10 emb|AW306675|AW306675 se53h08.y1 Gm-c1017 Glycine max cDNA clone... 90 6e-23
emb|AW299082|AW299082 EST305756 KV2 Medicago truncatula cDNA clo... 83 1e-22
emb|AW980804|AW980804 EST391957 GVN Medicago truncatula cDNA clo... 86 3e-22
emb|AW616452|AW616452 EST322863 L. hirsutum trichome, Cornell Un... 86 8e-22
emb|AZ044600|AZ044600 Gm_UMb001_116_G01.R UMN Soybean BAC Librar... 106 8e-22
15 emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 85 1e-21
emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 82 1e-21
emb|AW775087|AW775087 EST334238 KV3 Medicago truncatula cDNA clo... 85 2e-21
emb|AW033129|AW033129 EST276688 tomato callus, TAMU Lycopersicon... 86 5e-21
emb|X81367|TAAWJL172 T.aestivumn (subclone pAWJL172) AWJL172 gene. 71 9e-21
20 emb|AW398661|AW398661 EST309161 L. pennellii trichome, Cornell U... 85 2e-20
emb|AW398651|AW398651 EST309151 L. pennellii trichome, Cornell U... 85 2e-20
emb|AW217935|AW217935 EST296649 tomato flower buds, anthesis, Co... 79 4e-20
emb|AI726155|AI726155 BNLGHi5095 Six-day Cotton fiber Gossypium ... 78 5e-20
emb|AF159296|AF159296 Lycopersicon esculentum pollen extensin-li... 70 1e-19
25 emb|AW267958|AW267958 EST306300 DSIR Medicago truncatula cDNA cl... 97 6e-19
emb|Y10816|LIY10816 L.infantum psa gene. 70 7e-19
gb|U77041|MDU77041 Malus domestica polygalacturonase-inhibiting ... 76 7e-19
emb|AI898226|AI898226 EST267669 tomato ovary, TAMU Lycopersicon ... 95 2e-18
emb|AW030004|AW030004 EST273259 tomato callus, TAMU Lycopersicon... 95 2e-18
30 emb|AF159171|AF159171 Eucalyptus nitens polygalacturonase-inhibi... 74 3e-18
emb|AF159170|AF159170 Eucalyptus saligna polygalacturonase-inhib... 74 3e-18
emb|AF159167|AF159167 Eucalyptus grandis polygalacturonase-inhib... 74 3e-18
emb|AI352869|AI352869 MB70-4A PZ204.BNlib Brassica napus cDNA cl... 89 3e-18
emb|X81370|TAAWJL236 T.aestivumn (subclone pAWJL236) AWJL236 gene. 78 4e-18
35 emb|Z49063|ADPGIP A.deliciosa pgip mRNA for polygalacturonase in... 74 5e-18
emb|AF159169|AF159169 Eucalyptus urophylla polygalacturonase-inh... 74 7e-18
gb|U62279|SBU62279 Sorghum bicolor leucine-rich repeat-containin... 93 8e-18
emb|AW738046|AW738046 EST339473 tomato flower buds, anthesis, Co... 93 1e-17
emb|AW307311|AW307311 sf55d03.y1 Gm-c1009 Glycine max cDNA clone... 80 1e-17
40 gb|L09264|PYPPGI Pyrus communis polygalacturonase inhibitor mRNA... 71 2e-17
emb|AF159168|AF159168 Eucalyptus camaldulensis polygalacturonase... 74 2e-17
emb|AW689207|AW689207 NF016F04ST1F1000 Developing stem Medicago ... 78 2e-17
emb|AA738549|AA738549 SbRLK7 Sorghum bicolor cv. TX430 leaf Sorg... 90 5e-17
emb|AI897228|AI897228 EST266767 tomato ovary, TAMU Lycopersicon ... 90 5e-17
45 emb|AW688235|AW688235 NF005A07ST1F1000 Developing stem Medicago ... 89 1e-16
emb|AW694992|AW694992 NF082D01ST1F1012 Developing stem Medicago ... 83 2e-16
emb|AW432582|AW432582 sh76d03.y1 Gm-c1015 Glycine max cDNA clone... 89 2e-16
emb|AW399097|AW399097 EST309597 L. pennellii trichome, Cornell U... 69 2e-16
emb|AI443128|AI443128 sa84f10.y1 Gm-c1004 Glycine max cDNA clone... 81 2e-16
50 emb|AI899284|AI899284 EST268727 tomato ovary, TAMU Lycopersicon ... 88 3e-16
emb|Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 88 4e-16
emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 87 5e-16
emb|AW033367|AW033367 EST276938 tomato callus, TAMU Lycopersicon... 87 5e-16
emb|AV419297|AV419297 AV419297 Lotus japonicus young plants (two... 63 7e-16
55 emb|AW689888|AW689888 NF025H09ST1F1000 Developing stem Medicago ... 86 1e-15
emb|AA557055|AA557055 897 Loblolly pine N Pinus taeda cDNA clone... 86 1e-15
emb|AI779817|AI779817 EST260696 tomato susceptible, Cornell Lyco... 80 1e-15
emb|AW399471|AW399471 EST309971 L. pennellii trichome, Cornell U... 55 1e-15
gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor-... 85 2e-15
60 emb|AW164782|AW164782 se77g01.y1 Gm-c1023 Glycine max cDNA clone... 85 2e-15
emb|A67797|A67797 Sequence 2 from Patent WO9743427. 85 2e-15

emb|AW929780|AW929780 EST354050 tomato flower buds 8 mm to pre-a... 80 2e-15
emb|AI730245|AI730245 BNLGHi6465 Six-day Cotton fiber Gossypium ... 64 2e-15
emb|AW929854|AW929854 EST354124 tomato flower buds 8 mm to pre-a... 80 3e-15
emb|AV408986|AV408986 AV408986 Lotus japonicus young plants (two... 84 5e-15
5 emb|AW671867|AW671867 LG1_352_F06.b1_A002 Light Grown 1 (LG1) So... 84 5e-15
emb|AI488023|AI488023 EST246345 tomato ovary, TAMU Lycopersicon ... 84 5e-15
emb|AI782076|AI782076 EST262955 tomato susceptible, Cornell Lyco... 84 6e-15
emb|AV428126|AV428126 AV428126 Lotus japonicus young plants (two... 84 6e-15
emb|AW695797|AW695797 NF098F06ST1F1058 Developing stem Medicago ... 84 6e-15
10 emb|AW869870|AW869870 NXNV_122_E02_F Nsf Xylem Normal wood Verti... 66 9e-15
emb|AI856215|AI856215 sb39c10.x1 Gm-cl014 Glycine max cDNA clone... 83 9e-15
emb|AW929189|AW929189 EST337977 tomato flower buds 8 mm to pre-a... 83 9e-15
emb|AW616567|AW616567 EST322978 L. hirsutum trichome, Cornell Un... 83 9e-15
emb|AW697060|AW697060 NF111H11ST1F1095 Developing stem Medicago ... 77 1e-14
15 emb|X81369|TAAWJL218 T.aestivum (subclone pAWJL218) AWJL218 gene. 83 1e-14
emb|AI776963|AI776963 EST251989 tomato callus, TAMU Lycopersicon... 83 1e-14
emb|AW443205|AW443205 EST308135 tomato mixed elicitor, BTI Lycop... 83 1e-14
emb|AW696757|AW696757 NF110F02ST1F1025 Developing stem Medicago ... 83 1e-14
20
Query= AF077407.30_at 14116_at /id_source genbank /description
"gb|aac26243.1| (af077407) contains similarity to sugar transporters
(pfam: sugar_tr.hmm, score: 395.39) [arabidopsis thaliana]"
/blast_score 0 /ec_number /family /chip nova /gb_link
25 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|af077407|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|af077407|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|af077407|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?af077407>
(1581 letters)
30 Database: plantfungal
661,018 sequences; 426,114,510 total letters
Searching.....done
35 Score E
Sequences producing significant alignments: (bits) Value
emb|AJ132224|LES132224 Lycopersicon esculentum mRNA for hexose t... 819 0.0
emb|AJ010942|LES010942 Lycopersicon esculentum mRNA for hexose t... 815 0.0
40 gb|L21753|SCFGLUTRAB Saccharum hybrid cultivar H65-7052 glucose ... 222 e-176
gb|U38651|MTU38651 Medicago truncatula sugar transporter mRNA, co... 354 e-174
gb|L08196|RCCSCP Ricinus communis (clone PST293) sugar carrier p... 371 e-173
emb|Y09590|VVHEXTRAN V.vinifera mRNA for hexose transporter. 356 e-170
emb|AF061106|AF061106 Petunia x hybrida putative monosaccharide ... 255 e-170
45 gb|L08188|RCCHCP Ricinus communis (clone ST330) hexose carrier p... 203 e-163
emb|Z83829|PAMST1 P.abies mRNA for monosaccharide transporter Ms... 211 e-154
emb|Z93775|VFZ93775 V.faba mRNA for hexose transporter. 362 e-129
emb|X66856|NTMST1 N.tabacum MST1 mRNA. 215 e-129
gb|L08197|RCCSCPS Ricinus communis (clone PST9) sugar carrier pr... 210 e-114
50 emb|AI775535|AI775535 EST256635 tomato resistant, Cornell Lycope... 401 e-111
gb|L21752|SCFGLUTRAA Saccharum hybrid cultivar H65-7052 glucose ... 193 2e-99
emb|AI775204|AI775204 EST256304 tomato resistant, Cornell Lycope... 352 7e-98
emb|AI772312|AI772312 EST253412 tomato resistant, Cornell Lycope... 214 6e-82
emb|AJ132225|LES132225 Lycopersicon esculentum mRNA for hexose t... 188 5e-79
55 emb|AF173655|AF173655 Beta vulgaris clone GTRTUNI glucose transp... 156 1e-73
emb|AJ001061|VVHEXOSET Vitis vinifera hexose transporter gene. 276 3e-73
emb|AI778344|AI778344 EST259223 tomato susceptible, Cornell Lyco... 259 1e-70
emb|AV407522|AV407522 AV407522 Lotus japonicus young plants (two... 253 2e-66
gb|L31352|RCCHEX9HC Ricinus communis hexose carrier (Hex9) mRNA,... 253 2e-66
60 emb|AW684560|AW684560 NF018C12NR1F1000 Nodulated root Medicago t... 208 9e-61
emb|AI727659|AI727659 BNLGHi8536 Six-day Cotton fiber Gossypium ... 229 5e-59

- emb|AW737777|AW737777 EST339204 tomato flower buds, anthesis, Co... 223 3e-57
 emb|AI772048|AI772048 EST253148 tomato resistant, Cornell Lycopen... 206 1e-55
 emb|AI772049|AI772049 EST253149 tomato resistant, Cornell Lycopen... 206 1e-55
 emb|AJ132223|LES132223 Lycopersicon esculentum mRNA for hexose t... 196 2e-54
 5 emb|AI774617|AI774617 EST255717 tomato resistant, Cornell Lycopen... 188 4e-52
 emb|AI776698|AI776698 EST257786 tomato resistant, Cornell Lycopen... 191 8e-52
 gb|BE020128|BE020128 sm41e08.y1 Gm-cl028 Glycine max cDNA clone ... 149 1e-51
 emb|AW684408|AW684408 NF016F05NR1F1000 Nodulated root Medicago t... 204 2e-51
 emb|AW596416|AW596416 sj12b09.y1 Gm-cl032 Glycine max cDNA clone... 197 2e-51
 10 emb|AW349933|AW349933 GM210006A20H11R Gm-r1021 Glycine max cDNA ... 189 2e-49
 emb|AI460634|AI460634 sa71d03.y1 Gm-cl004 Glycine max cDNA clone... 189 2e-49
 emb|AJ248339|AJ248339 AJ248339 Medicago sativa subsp. x varia yo... 196 3e-49
 emb|AW458444|AW458444 sh09c11.y1 Gm-cl016 Glycine max cDNA clone... 190 6e-49
 15 emb|AW705527|AW705527 sk61c02.y1 Gm-cl016 Glycine max cDNA clone... 193 1e-48
 emb|AA660304|AA660304 00173 MtrHE Medicago truncatula cDNA 5' si... 133 3e-48
 emb|AW704934|AW704934 sk56d08.y1 Gm-cl019 Glycine max cDNA clone... 188 7e-47
 emb|AV412511|AV412511 AV412511 Lotus japonicus young plants (two... 188 1e-46
 gb|BE021812|BE021812 sm62g03.y1 Gm-cl028 Glycine max cDNA clone ... 187 2e-46
 20 emb|AW691511|AW691511 NF045G06ST1F1000 Developing stem Medicago ... 125 3e-46
 emb|AW720443|AW720443 LjNEST19b1r Lotus japonicus nodule library... 158 3e-46
 emb|AW737506|AW737506 EST338933 tomato flower buds, anthesis, Co... 169 2e-45
 emb|AI731272|AI731272 BNLGHi9072 Six-day Cotton fiber Gossypium ... 172 3e-45
 emb|AW092826|AW092826 EST286006 tomato mixed elicitor, BTI Lycop... 173 6e-45
 25 emb|AI730904|AI730904 BNLGHi8171 Six-day Cotton fiber Gossypium ... 156 2e-43
 emb|AW737195|AW737195 EST338622 tomato flower buds, anthesis, Co... 173 3e-42
 gb|L31353|RCCHEX10HC Ricinus communis hexose carrier (Hex10) mRN... 173 4e-42
 emb|AW680072|AW680072 WS1_3_B09.g1_A002 Water-stressed 1 (WS1) S... 170 2e-41
 emb|AI938772|AI938772 sb58g08.y1 Gm-cl018 Glycine max cDNA clone... 104 3e-41
 30 emb|AI930883|AI930883 sb43g12.y1 Gm-cl015 Glycine max cDNA clone... 117 4e-38
 gb|L08189|RCCSCP B Ricinus communis (clone PDG15) sugar carrier p... 158 1e-37
 gb|L08191|RCCSCP D Ricinus communis (clone PDG19) sugar carrier p... 157 2e-37
 emb|AW774154|AW774154 EST333237 KV3 Medicago truncatula cDNA clo... 153 4e-37
 gb|L08194|RCCSCPG Ricinus communis (clone PDGK4) sugar carrier p... 155 6e-37
 35 gb|U22525|KLU22525 Kluyveromyces lactis high affinity glucose tr... 109 3e-36
 emb|AW234900|AW234900 sf20e02.y1 Gm-cl028 Glycine max cDNA clone... 152 8e-36
 emb|AW455278|AW455278 EST311938 tomato root during/after fruit s... 152 8e-36
 emb|AW040775|AW040775 EST283639 tomato mixed elicitor, BTI Lycop... 141 2e-35
 emb|X96876|SCCHRI VFY S.cerevisiae DNA of cosmid from chromosome ... 81 2e-35
 40 emb|Z74186|SCYDL138W S.cerevisiae chromosome IV reading frame OR... 81 2e-35
 gb|BE059128|BE059128 sn25f09.y1 Gm-cl016 Glycine max cDNA clone ... 146 3e-35
 emb|AW687897|AW687897 NF014F11RT1F1094 Developing root Medicago ... 124 3e-35
 emb|AW185053|AW185053 se86b03.y1 Gm-cl023 Glycine max cDNA clone... 149 4e-35
 gb|L08193|RCCSCPF Ricinus communis (clone PDG58) sugar carrier p... 149 7e-35
 45 emb|AI780094|AI780094 EST260973 tomato susceptible, Cornell Lyco... 139 7e-35
 emb|AF149282|AF149282 Phaseolus vulgaris clone pBHEX2 hexose car... 148 1e-34
 emb|AW756300|AW756300 sl18g04.y1 Gm-cl036 Glycine max cDNA clone... 140 2e-33
 emb|AF168773|AF168773 Betula pendula hexose transport protein (H... 141 1e-32
 gb|L08195|RCCSCPH Ricinus communis (clone PDGB14) sugar carrier ... 141 1e-32
 50 gb|BE126141|BE126141 DG1_66_B09.b1_A002 Dark Grown 1 (DG1) Sorgh... 114 2e-32
 emb|AW395888|AW395888 sh07a07.y1 Gm-cl016 Glycine max cDNA clone... 130 4e-32
 gb|L08190|RCCSCPC Ricinus communis (clone PDG16) sugar carrier p... 139 6e-32
 emb|AI729864|AI729864 BNLGHi5432 Six-day Cotton fiber Gossypium ... 124 1e-31
 emb|AF168772|AF168772 Betula pendula hexose transport protein (H... 137 2e-31
 55 emb|AW432874|AW432874 sh99b03.y1 Gm-cl016 Glycine max cDNA clone... 130 5e-31
 emb|AW756360|AW756360 sl19g10.y1 Gm-cl036 Glycine max cDNA clone... 128 9e-29
 gb|L08192|RCCSCPE Ricinus communis (clone PDG40) sugar carrier p... 128 1e-28
 emb|AW830453|AW830453 sm27c06.y1 Gm-cl028 Glycine max cDNA clone... 125 8e-28
 emb|AW934681|AW934681 EST353573 tomato flower buds 0-3 mm, Corne... 79 1e-27
 60 emb|AV407618|AV407618 AV407618 Lotus japonicus young plants (two... 78 2e-24
 emb|AW875010|AW875010 00131 leafy spurge Lambda HybriZAP 2.1 two... 113 4e-24

- emb|AI728506|AI728506 BNLGHi10921 Six-day Cotton fiber Gossypium... 98 1e-23
 gb|T41488|T41488 EST057 Soybean, M Bhattacharyya Glycine max cDN... 102 3e-23
 emb|AF215852|AF215852 Nicotiana tabacum hexose transporter (pGlc... 69 3e-23
 emb|AW255075|AW255075 ML137 peppermint glandular trichome Mentha... 95 7e-23
 5 emb|AV425362|AV425362 AV425362 Lotus japonicus young plants (two... 109 7e-23
 gb|U43629|BVU43629 Beta vulgaris integral membrane protein mRNA,... 68 1e-22
 emb|AF000952|AF000952 Prunus armeniaca putative sugar transporte... 68 2e-21
 emb|AW677475|AW677475 DG1_7_H05.g1_A002 Dark Grown 1 (DG1) Sorgh... 104 2e-21
 emb|AF215851|AF215851 Spinacia oleracea hexose transporter mRNA,... 71 6e-21
 10 emb|AW255633|AW255633 ML692 peppermint glandular trichome Mentha... 101 1e-20
 emb|Z98530|SPAC4F8 S.pombe chromosome I cosmid c4F8. 89 7e-20
 emb|X98622|SPITR1 S.pombe itr1 gene. 89 7e-20
 emb|AW684920|AW684920 NF023B01NR1F1000 Nodulated root Medicago t... 96 7e-20
 emb|AI778758|AI778758 EST259637 tomato susceptible, Cornell Lyco... 89 1e-19
 15 emb|AI778757|AI778757 EST259636 tomato susceptible, Cornell Lyco... 89 1e-19
 gb|BE060390|BE060390 HVSMEg0012C22f Hordeum vulgare pre-anthesis... 99 1e-19

- 20 Query= AC002340.147_at 14609_at /id_source genbank /description
 gb|aac02748.1| (ac002340) putative cytochrome p450 [arabidopsis
 thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002340|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002340|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002340|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac002340>
 25 (1612 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

- 30 Searching:.....done

Score E
 Sequences producing significant alignments: (bits) Value

- 35 gb|M32885|AVOCYP Avocado cytochrome P-450LXXIA1 (cyp71A1) mRNA, ... 137 e-103
 emb|X70981|SMCYPEG2 S.melongena CYP71A1 mRNA for P450 hydroxylase. 127 6e-99
 emb|Y09423|NRCYP71A5 Nepeta racemosa mRNA for cytochrome P450, C... 136 8e-98
 emb|X71654|SMCYP71B3 S.melongena CYP71A2 mRNA for hydroxylase. 124 9e-95
 dbj|D14990|POTCPEG4 Eggplant mRNA for cytochrome P-450EG4, compl... 124 9e-95
 40 emb|Y10489|GMC450CP1 G.max mRNA for putative cytochrome P450, cl... 90 1e-84
 emb|X70982|SMCYPEG3 S.melongena CYP71A3 mRNA for P450 hydroxylase. 126 3e-74
 emb|Y09424|NRCYP71A6 N.racemosa mRNA for cytochrome P450, CYP71A... 154 3e-65
 dbj|E13663|E13663 cDNA encoding cytochrome P450 which is induced... 71 9e-63
 dbj|D83968|SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)... 71 9e-63
 45 emb|AF022157|AF022157 Glycine max cytochrome P450 monooxygenase ... 126 3e-61
 emb|AW053855|AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp... 103 1e-53
 emb|Y09920|HT7EC0DET Helianthus tuberosus mRNA for 7-ethoxycouma... 94 1e-50
 emb|Y10098|HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... 94 1e-50
 emb|AF022459|AF022459 Glycine max cytochrome P450 monooxygenase ... 105 4e-50
 50 emb|AJ238612|CRO238612 Catharanthus roseus mRNA for cytochrome P... 89 2e-49
 emb|AF029858|AF029858 Sorghum bicolor cytochrome P450 CYP71E1 (C... 139 3e-49
 gb|U48434|SCU48434 Solanum chacoense cytochrome P450 mRNA, compl... 117 2e-48
 emb|AF166332|AF166332 Nicotiana tabacum cytochrome P450 gene, co... 114 4e-47
 emb|AW223719|AW223719 EST300530 tomato fruit red ripe, TAMU Lyco... 88 4e-46
 55 emb|Y10490|GMC450CP3 G.max mRNA for putative cytochrome P450, cl... 104 6e-46
 emb|X71658|SMCYPEG8 S.melongena CYP76A1 mRNA. 88 2e-45
 emb|AF122821|AF122821 Capsicum annuum cytochrome P450 (PepCYP) m... 118 4e-45
 emb|Z33875|CYMPCP450 M.piperita gene for cytochrome P-450 oxidase. 88 7e-45
 emb|AI897763|AI897763 EST267206 tomato ovary, TAMU Lycopersicon ... 84 1e-44
 60 emb|AW830233|AW830233 sm24f03.y1 Gm-cl028 Glycine max cDNA clone... 139 5e-44
 gb|U48435|SCU48435 Solanum chacoense putative cytochrome P450 ge... 95 2e-43

- emb|AF029857|AF029857 Sorghum bicolor cytochrome P450 CYP99A1 (C... 127 2e-43
emb|X71657|SMCYPEG7 S.melongena CYP76A2 mRNA for hydroxylase. 87 3e-43
emb|AJ249799|CAR249799 Cicer arietinum partial mRNA for cytochro... 79 8e-43
emb|X96784|NTP450GEN N.tabacum cytochrome P-450 gene. 105 1e-42
5 emb|AW034502|AW034502 EST278118 tomato callus, TAMU Lycopersicon... 107 2e-42
emb|AF124815|AF124815 Mentha spicata cytochrome p450 mRNA, compl... 81 3e-42
emb|AI484957|AI484957 EST243220 tomato ovary, TAMU Lycopersicon ... 84 4e-42
gb|L24438|THLCYP450A Thlaspi arvense germline cytochrome P450 mR... 94 7e-42
emb|AF124816|AF124816 Mentha x piperita cytochrome p450 isoform ... 87 3e-41
10 emb|AW774664|AW774664 EST333815 KV3 Medicago truncatula cDNA clo... 102 6e-41
emb|AW234222|AW234222 sf22f08.y1 Gm-c1028 Glycine max cDNA clone... 88 1e-40
emb|AF155332|AF155332 Petunia x hybrida flavonoid 3'-hydroxylase... 112 6e-40
emb|AW394470|AW394470 sh05e04.y1 Gm-c1016 Glycine max cDNA clone... 89 1e-39
emb|AF029856|AF029856 Sorghum bicolor cytochrome P450 CYP98A1 (C... 95 1e-39
15 dbj|D14590|D14590 Campanula medium mRNA for flavonoid 3',5'-hydr... 82 2e-39
gb|BE054146|BE054146 GA_Ea0034H12f Gossypium arboreum 7-10 dpa ... 72 3e-39
emb|AI727092|AI727092 BNLGHi7313 Six-day Cotton fiber Gossypium ... 87 4e-39
emb|AW223657|AW223657 EST300468 tomato fruit red ripe, TAMU Lyco... 122 4e-39
emb|AW255477|AW255477 ML502 peppermint glandular trichome Mentha... 82 5e-39
20 emb|AI779370|AI779370 EST260249 tomato susceptible, Cornell Lyco... 91 6e-39
emb|AI488646|AI488646 EST246985 tomato ovary, TAMU Lycopersicon ... 79 7e-39
emb|Y10493|GMC450CP7 G.max mRNA for putative cytochrome P450, cl... 114 1e-38
emb|AF022458|AF022458 Glycine max cytochrome P450 monooxygenase ... 92 3e-38
emb|AF124817|AF124817 Mentha x piperita cytochrome p450 isoform ... 89 4e-38
25 emb|AW132351|AW132351 se03a02.y1 Gm-c1013 Glycine max cDNA clone... 159 5e-38
emb|AW832652|AW832652 sm15g02.y1 Gm-c1027 Glycine max cDNA clone... 159 5e-38
emb|AF156976|AF156976 Gerbera hybrida flavone synthase II (CYP93... 68 9e-38
emb|AF022460|AF022460 Glycine max cytochrome P450 monooxygenase ... 113 1e-37
emb|AF014800|AF014800 Eschscholzia californica (S)-N-methylcocla... 75 2e-37
30 emb|AF014801|AF014801 Eschscholzia californica (S)-N-methylcocla... 75 2e-37
emb|AI897760|AI897760 EST267203 tomato ovary, TAMU Lycopersicon ... 71 2e-37
emb|AF135485|AF135485 Glycine max cytochrome P450 monooxygenaseC... 104 3e-37
emb|AI730111|AI730111 BNLGHi6162 Six-day Cotton fiber Gossypium ... 84 4e-37
emb|AI726383|AI726383 BNLGHi5702 Six-day Cotton fiber Gossypium ... 84 4e-37
35 emb|AI896171|AI896171 EST265614 tomato callus, TAMU Lycopersicon... 89 7e-37
emb|AW256010|AW256010 MW364 peppermint glandular trichome Mentha... 89 7e-37
emb|AW832315|AW832315 sm07e11.y1 Gm-c1027 Glycine max cDNA clone... 116 1e-36
emb|AW705746|AW705746 sk51c10.y1 Gm-c1019 Glycine max cDNA clone... 154 2e-36
emb|AW442182|AW442182 EST311578 tomato fruit red ripe, TAMU Lyco... 88 4e-36
40 emb|AW680602|AW680602 WS1_6_C01.b1_A002 Water-stressed 1 (WS1) S... 102 4e-36
emb|AF000403|AF000403 Lotus japonicus putative cytochrome P450 ... 113 5e-36
emb|AI938505|AI938505 sb46e03.y1 Gm-c1015 Glycine max cDNA clone... 94 2e-35
emb|AI779369|AI779369 EST260248 tomato susceptible, Cornell Lyco... 91 3e-35
dbj|D86351|D86351 Glycine max CYP93A2 mRNA for cytochrome P-450,... 68 3e-35
45 emb|AW255799|AW255799 ML868 peppermint glandular trichome Mentha... 68 8e-35
emb|AW617225|AW617225 EST323636 L. hirsutum trichome, Cornell Un... 138 3e-34
emb|AW278865|AW278865 sf99g03.y1 Gm-c1019 Glycine max cDNA clone... 147 3e-34
emb|AF188612|AF188612 Callistephus chinensis flavone synthase II... 72 3e-34
emb|X95342|NTHSR515 N.tabacum mRNA for HSR515 protein. 91 4e-34
50 emb|AW728587|AW728587 GA_Ea0017C12 Gossypium arboreum 7-10 dpa ... 82 5e-34
emb|AW728802|AW728802 GA_Ea0028I12 Gossypium arboreum 7-10 dpa ... 80 5e-34
emb|AW038994|AW038994 EST280967 tomato mixed elicitor, BTI Lycop... 91 7e-34
gb|BE125733|BE125733 DG1_54_G12.g1_A002 Dark Grown 1 (DG1) Sorgh... 145 1e-33
emb|AW923050|AW923050 DG1_48_G09.g1_A002 Dark Grown 1 (DG1) Sorg... 91 1e-33
55 emb|AJ010324|PAJ10324 Populus trichocarpa cv trichobel mRNA for ... 95 2e-33
emb|AF150881|AF150881 Lycopersicon esculentum x Lycopersicon per... 100 2e-33
emb|AF014802|AF014802 Eschscholzia californica (S)-N-methylcocla... 86 3e-33
emb|AW349428|AW349428 GM210007A20E11R Gm-r1021 Glycine max cDNA ... 85 3e-33
emb|AW459662|AW459662 sh90c05.y1 Gm-c1016 Glycine max cDNA clone... 89 3e-33
60 emb|AB032833|AB032833 Cicer arietinum CYP76D1 mRNA for cytochrom... 77 4e-33
emb|AW688786|AW688786 NF011F03ST1F1000 Developing stem Medicago ... 129 4e-33

emb|AF134590|AF134590 Papaver somniferum (S)-N-methylcoclaurine ... 83 6e-33
emb|AW255181|AW255181 ML169 peppermint glandular trichome Mentha... 142 6e-33
emb|AF191772|AF191772 Papaver somniferum (S)-N-methylcoclaurine ... 82 1e-32
emb|AJ777331|AJ777331 EST263739 tomato seed, TAMU Lycopersicon e... 86 1e-32
5 dbj|D85184|D85184 Gentiana triflora mRNA for flavonoid 3',5'-hyd... 72 2e-32
emb|Y10492|GMC450CP5 G.max mRNA for putative cytochrome P450, cl... 67 2e-32
emb|AW733734|AW733734 sk77e06.y1 Gm-c1016 Glycine max cDNA clone... 70 2e-32
emb|AW832405|AW832405 sm09e01.y1 Gm-c1027 Glycine max cDNA clone... 88 2e-32
emb|AW254778|AW254778 ML1061 peppermint glandular trichome Mentha... 141 2e-32
10 emb|AW255299|AW255299 ML307 peppermint glandular trichome Mentha... 88 2e-32
emb|AF195801|AF195801 Medicago sativa isoflavone synthase 2 (ifs... 64 3e-32
emb|AJ243804|CAR243804 Cicer arietinum mRNA for cytochrome P450 ... 66 3e-32
Query= AC004165.66_at 14614_at /id_source genbank /description
gb|aac16958.1| (ac004165) putative glucosyltransferase [arabidopsis
15 thaliana] /blast_score 0 /ec_number /family glucosyltransferase /chip
nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004165| /ncgi
http://www.ncgr.org/cgi-bin/ff?ac004165
20 (1368 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

25 Searching.....done

Score E
Sequences producing significant alignments: (bits) Value

30 emb|AW256802|AW256802 EST304939 KV2 Medicago truncatula cDNA clo... 112 5e-46
emb|AW268009|AW268009 EST306231 DSIR Medicago truncatula cDNA cl... 102 3e-39
emb|AF190634|AF190634 Nicotiana tabacum UDP-glucose:salicylic ac... 101 3e-37
emb|AB000623|AB000623 Nicotiana tabacum mRNA for glucosyl transf... 101 3e-36
emb|AB012116|AB012116 Vigna mungo UFGlyT mRNA for UDP-glucose:fl... 82 2e-34
35 emb|AB013598|AB013598 Verbena hybrida HGT8 mRNA for UDP-glucose:... 104 2e-34
emb|AW776132|AW776132 EST335197 DSIL Medicago truncatula cDNA cl... 99 3e-33
emb|AW459541|AW459541 sh42h03.y1 Gm-c1017 Glycine max cDNA clone... 98 2e-32
emb|AV408145|AV408145 AV408145 Lotus japonicus young plants (two... 85 2e-32
emb|AW216808|AW216808 EST295522 tomato callus, TAMU Lycopersicon... 101 3e-32
40 emb|AW398421|AW398421 EST298268 L. pennellii trichome, Cornell U... 84 6e-32
emb|AW349414|AW349414 GM210007A20D2R Gm-r1021 Glycine max cDNA 3... 97 1e-31
emb|AW035896|AW035896 EST282403 tomato callus, TAMU Lycopersicon... 100 1e-31
gb|BE022282|BE022282 sm72b01.y1 Gm-c1028 Glycine max cDNA clone ... 102 4e-31
emb|AB013596|AB013596 Perilla frutescens PF3R4 mRNA for UDP-gluc... 93 7e-31
45 emb|AB013597|AB013597 Perilla frutescens PF3R6 mRNA for UDP-gluc... 93 1e-30
emb|AI771830|AI771830 EST252930 tomato ovary, TAMU Lycopersicon ... 93 1e-30
emb|AB027455|AB027455 Petunia x hybrida PH1 mRNA for anthocyanin... 89 6e-30
emb|AW459258|AW459258 sh22f07.y1 Gm-c1016 Glycine max cDNA clone... 69 4e-29
emb|AW928895|AW928895 EST337683 tomato flower buds 8 mm to pre-a... 90 4e-29
50 emb|X85138|LETW11 L.esculentum twil mRNA. 81 1e-28
emb|AB033758|AB033758 Citrus unshiu LGTase mRNA for limonoid UDP... 89 2e-28
emb|X72729|LEERT1B L.esculentum (ERT 1b) ripening-related mRNA. 87 9e-28
emb|A62529|A62529 Sequence 34 from Patent WO9716559. 96 1e-27
emb|X77461|MECGT2 M.esculenta Crantz CGT2 mRNA for UTP-glucose g... 78 1e-27
55 emb|AQ580287|AQ580287 T135903b shotgun sub-library of BAC clone ... 93 1e-27
emb|X77460|MECGT4 M.esculenta Crantz CGT4 mRNA for UTP-glucose g... 84 2e-27
emb|AW621210|AW621210 EST312008 tomato root during/after fruit s... 98 4e-27
emb|AW036493|AW036493 EST282992 tomato seed, TAMU Lycopersicon e... 92 5e-27
emb|AW695243|AW695243 NF093A08ST1F1056 Developing stem Medicago ... 74 6e-27
60 emb|AQ368131|AQ368131 tox0001H06r CUGI Tomato BAC Library Lycop... 84 7e-27
emb|AF199453|AF199453 Sorghum bicolor UDP-glucose glucosyltransf... 76 9e-27

- emb|AI488782|AI488782 EST247121 tomato ovary, TAMU Lycopersicon ... 80 1e-26
emb|AI729108|AI729108 BNLGHi12670 Six-day Cotton fiber Gossypium... 82 1e-26
gb|BE126076|BE126076 DG1_65_E03.g1_A002 Dark Grown 1 (DG1) Sorgh... 106 1e-26
dbj|D85186|D85186 Gentiana triflora mRNA for UDP-glucose:flavono... 86 3e-26
5 emb|X77369|SMGT S.melongena GT mRNA for glycosyltransferase. 97 5e-26
dbj|E12713|E12713 Solanum melongena cDNA encoding flavonoid-3-gl... 97 5e-26
emb|AW223197|AW223197 EST300008 tomato fruit red ripe, TAMU Lyco... 79 6e-26
emb|AI485027|AI485027 EST243307 tomato ovary, TAMU Lycopersicon ... 84 6e-26
emb|AF127218|AF127218 Forsythia x intermedia flavonoid 3-O-gluco... 95 1e-25
10 emb|AF101972|AF101972 Phaseolus lunatus zeatin O-glucosyltransfe... 87 2e-25
emb|X77462|MECGT5 M.esculenta Crantz CGT5 mRNA for UTP-glucose g... 83 2e-25
emb|Y18871|DBE18871 Dorotheanthus bellidiformis mRNA for betanid... 81 3e-25
emb|X15694|HVBRNZ1H Barley bronze 1 homologue for UDPglucose fla... 80 5e-25
emb|AB027454|AB027454 Petunia x hybrida PGT8 mRNA for anthocyani... 99 8e-25
15 emb|AF116858|AF116858 Phaseolus vulgaris zeatin O-xylosyltransfe... 84 8e-25
emb|AW573699|AW573699 EST316290 GVN Medicago truncatula cDNA clo... 78 1e-24
emb|AW442772|AW442772 EST307702 tomato mixed elicitor, BTI Lycop... 84 1e-24
emb|AI898951|AI898951 EST268394 tomato ovary, TAMU Lycopersicon ... 83 1e-24
emb|AW040941|AW040941 EST283805 tomato mixed elicitor, BTI Lycop... 83 1e-24
20 emb|AW221893|AW221893 EST298704 tomato fruit red ripe, TAMU Lyco... 84 2e-24
emb|AW933199|AW933199 EST359042 tomato fruit mature green, TAMU ... 93 2e-24
emb|AW981156|AW981156 EST392350 DSIL Medicago truncatula cDNA cl... 83 4e-24
emb|AW625781|AW625781 EST319688 tomato radicle, 5 d post-imbibit... 84 4e-24
emb|X77459|MECGT1 M.esculenta Crantz CGT1 mRNA for UDP-glucose g... 66 4e-24
25 emb|AW034671|AW034671 EST278402 tomato callus, TAMU Lycopersicon... 81 5e-24
emb|AI487283|AI487283 EST245605 tomato ovary, TAMU Lycopersicon ... 89 1e-23
emb|AQ580273|AQ580273 T135889b shotgun sub-library of BAC clone ... 93 2e-23
emb|AW329251|AW329251 N200469e rootphos(-) Medicago truncatula c... 93 2e-23
emb|AI780684|AI780684 EST261479 tomato susceptible, Cornell Lyco... 79 2e-23
30 emb|AI486974|AI486974 EST245296 tomato ovary, TAMU Lycopersicon ... 83 3e-23
emb|AI483783|AI483783 EST249654 tomato ovary, TAMU Lycopersicon ... 79 5e-23
emb|AW348549|AW348549 GM210002B12H12R Gm-r1021 Glycine max cDNA ... 82 5e-23
emb|AW649880|AW649880 EST328334 tomato germinating seedlings, TA... 87 9e-23
emb|AJ400861|CAR400861 Cicer arietinum partial mRNA for putative... 80 1e-22
35 emb|X77463|MECGT6 M.esculenta Crantz CGT6 mRNA for UTP-glucose g... 74 2e-22
emb|AI487582|AI487582 EST245904 tomato ovary, TAMU Lycopersicon ... 82 2e-22
emb|AW759836|AW759836 sl54f11.y1 Gm-cl027 Glycine max cDNA clone... 91 2e-22
emb|AW350921|AW350921 GM210010B10C8R Gm-r1021 Glycine max cDNA 3... 82 3e-22
emb|AF165148|AF165148 Petunia x hybrida UDP-galactose:flavonol 3... 86 4e-22
40 emb|AW394450|AW394450 sh05d10.y1 Gm-cl016 Glycine max cDNA clone... 75 8e-22
emb|AB009370|AB009370 Vigna mungo UF3GaT mRNA for flavonoid 3-O-... 80 1e-21
emb|AF000372|AF000372 Vitis vinifera UDP glucose:flavonoid 3-o-g... 85 1e-21
emb|AF000371|AF000371 Vitis vinifera UDP glucose:flavonoid 3-o-g... 85 1e-21
emb|X77464|MECGT7 M.esculenta Crantz CGT7 mRNA for UTP-glucose g... 88 1e-21
45 emb|AB012114|AB012114 Vigna mungo UFGlyT mRNA for UDP-glycose:fl... 73 2e-21
emb|AI894979|AI894979 EST264422 tomato callus, TAMU Lycopersicon... 74 4e-21
emb|AW650189|AW650189 EST328643 tomato germinating seedlings, TA... 90 5e-21
emb|AW127679|AW127679 M110425 DSLC Medicago truncatula cDNA clon... 102 7e-21
gb|U82367|STU82367 Solanum tuberosum UDP-glucose glucosyltransfe... 73 9e-21
50 emb|AW650188|AW650188 EST328642 tomato germinating seedlings, TA... 89 9e-21
emb|AW617410|AW617410 EST323821 L. hirsutum trichome, Cornell Un... 81 1e-20
emb|AF006081|AF006081 Solanum berthaultii UDPG glucosyltransfera... 69 3e-20
emb|AI487484|AI487484 EST245806 tomato ovary, TAMU Lycopersicon ... 74 3e-20
emb|AW776615|AW776615 EST335680 DSIL Medicago truncatula cDNA cl... 100 4e-20
55 emb|AW687523|AW687523 NF010E07RT1F1054 Developing root Medicago ... 100 4e-20
emb|AI489089|AI489089 EST247428 tomato ovary, TAMU Lycopersicon ... 84 6e-20
emb|AW317745|AW317745 sg56g04.y1 Gm-cl007 Glycine max cDNA clone... 57 8e-20
emb|AI780671|AI780671 EST261466 tomato susceptible, Cornell Lyco... 62 1e-19
emb|AW092049|AW092049 EST285325 tomato mixed elicitor, BTI Lycop... 88 4e-19
60 gb|BE055475|BE055475 GA_Ea0035I12f Gossypium arboreum 7-10 dpa ... 69 5e-19
emb|AF117267|AF117267 Malus domestica UDP glucose:flavonoid 3-O-... 80 7e-19

- emb|AW781424|AW781424 sl78a07.y1 Gm-c1037 Glycine max cDNA clone... 95 9e-19
 emb|Z25802|PHUDPRHAX P.hybrida mRNA for UDP rhamnose: anthocyani... 68 9e-19
 emb|AI967768|AI967768 Ljirnp11-882-f3 Ljirnp Lambda HybriZap ... 95 1e-18
 emb|AB002818|AB002818 Perilla frutescens mRNA for flavonoid 3-O-... 90 1e-18
 5 emb|AB012115|AB012115 Vigna mungo UFGlyT mRNA for UDP-glycose:fl... 89 1e-18
 emb|AI485737|AI485737 EST244058 tomato ovary, TAMU Lycopersicon ... 71 2e-18
 emb|AW677595|AW677595 DG1_8_E07.g1_A002 Dark Grown 1 (DG1) Sorgh... 94 2e-18
- 10 Query= AL021961.3_at 15042_at /id_source genbank /description
 emb|caal7549.1| (al021961) cinnamyl alcohol dehydrogenase - like
 protein [arabidopsis thaliana] /blast_score 1.00e-167 /ec_number
 /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 15 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021961|/ncgi
 http://www.ncgr.org/cgi-bin/ff?al021961
 (1074 letters)
- Database: plantfungal
 20 661,018 sequences; 426,114,510 total letters
- Searching.....done
- Score E
 25 Sequences producing significant alignments: (bits) Value
- dbj|D13991|AAICAD A. cordata mRNA for cinnamyl alcohol dehydroge... 279 e-152
 emb|X62343|NTCAD14MR N.tabacum CAD14 mRNA for cinnamyl alcohol d... 314 e-150
 emb|Z19568|PDCIALDHA P.deltoides encoding cinnamyl alcohol dehyd... 310 e-146
 30 emb|A24083|A24083 pPOPCAD1 cinnamyl alcohol dehydrogenase cDNA. 311 e-146
 emb|AF217957|AF217957 Populus tremuloides cinnamyl alcohol dehyd... 309 e-145
 emb|X62344|NTCAD19MR N.tabacum CAD19 mRNA for cinnamyl alcohol d... 302 e-145
 emb|AF038561|AF038561 Eucalyptus globulus cinnamyl alcohol dehyd... 318 e-141
 emb|X65631|EGCADMR E.gunnii mRNA cad for cinnamyl alcohol dehydr... 319 e-141
 35 emb|A24084|A24084 pEUCAD1 cinnamyl alcohol dehydrogenase cDNA. 319 e-141
 emb|AF083332|AF083332 Medicago sativa cinnamyl-alcohol dehydroge... 326 e-140
 emb|Z19573|MSCIALDHA M.sativa encoding cinnamyl alcohol dehydrog... 325 e-140
 emb|AJ231135|SOF231135 Saccharum officinarum mRNA for cinnamyl a... 384 e-134
 emb|AF010290|AF010290 Lolium perenne cinnamyl alcohol dehydrogen... 262 e-133
 40 emb|X72675|PACINALDA P.abies mRNA for cinnamyl alcohol dehydroge... 240 e-124
 dbj|D86590|D86590 Zinnia elegans mRNA for cinnamyl alcohol dehyd... 264 e-123
 gb|U62394|PRU62394 Pinus radiata cinnamyl alcohol dehydrogenase ... 242 e-122
 emb|Z37992|PTCADBMR P.taeda mRNA for cinnamyl alcohol dehydrogen... 237 e-121
 emb|Z37991|PTCADAMR P.taeda mRNA for cinnamyl alcohol dehydrogen... 237 e-121
 45 gb|U63534|FXU63534 Fragaria x ananassa cinnamyl alcohol dehydrog... 251 9e-89
 emb|AF083333|AF083333 Medicago sativa cinnamyl-alcohol dehydroge... 225 5e-84
 gb|L36823|SSNCAD1A Stylosanthes humilis cinnamyl alcohol dehydro... 226 9e-84
 gb|U24561|AGU24561 Apium graveolens mannitol dehydrogenase (Mtd)... 237 3e-79
 emb|X67817|PCELI3 P.crispum mRNA for Eli3. 240 3e-77
 50 emb|X92855|LEMTD L.esculentum exon 1 of MTD gene. 130 6e-77
 emb|AW255506|AW255506 ML532 peppermint glandular trichome Mentha... 275 6e-73
 emb|AI487388|AI487388 EST245710 tomato ovary, TAMU Lycopersicon ... 274 8e-73
 emb|AF207552|AF207552 Brassica napus cinnamyl alcohol dehydrogen... 155 2e-72
 emb|AF207553|AF207553 Brassica napus cinnamyl alcohol dehydrogen... 156 5e-72
 55 emb|AF207555|AF207555 Brassica rapa cinnamyl alcohol dehydrogena... 155 1e-71
 emb|AF207554|AF207554 Brassica oleracea cinnamyl alcohol dehydro... 156 1e-71
 emb|X92754|HVCADMRNA H.vulgare mRNA for cinnamyl alcohol dehydro... 270 2e-71
 emb|AI489728|AI489728 EST248067 tomato ovary, TAMU Lycopersicon ... 269 3e-71
 emb|AW830216|AW830216 sm24b12.y1 Gm-c1028 Glycine max cDNA clone... 264 6e-70
 60 emb|AW350274|AW350274 GM210007B20B7R Gm-r1021 Glycine max cDNA 3... 262 1e-69
 gb|U79770|MCU79770 Mesembryanthemum crystallinum cinnamyl-alcho... 255 4e-69

- emb|AW031628|AW031628 EST275082 tomato callus, TAMU Lycopersicon... 182 7e-69
 gb|BE021646|BE021646 sm60f08.y1 Gm-cl028 Glycine max cDNA clone ... 259 4e-68
 gb|BE123932|BE123932 EST394057 DSIL Medicago truncatula cDNA clo... 185 7e-65
 emb|AW560160|AW560160 EST315208 DSIR Medicago truncatula cDNA cl... 169 3e-64
 5 emb|AW684815|AW684815 NF021D07NR1F1000 Nodulated root Medicago t... 230 1e-62
 emb|AI162401|AI162401 A017P09U Hybrid aspen plasmid library Popu... 178 5e-62
 emb|AI900147|AI900147 sc01e08.y1 Gm-cl012 Glycine max cDNA clone... 142 2e-61
 emb|AW101492|AW101492 sd78h08.y1 Gm-cl009 Glycine max cDNA clone... 176 3e-61
 emb|AW568106|AW568106 si68e05.y1 Gm-r1030 Glycine max cDNA clone... 136 3e-59
 10 emb|AF146691|AF146691 Lycopersicon esculentum cultivar Rio Grand... 194 1e-58
 emb|AI443116|AI443116 sa84e07.y1 Gm-cl004 Glycine max cDNA clone... 170 1e-54
 emb|AJ001925|PAAJ1925 Picea abies cad7 gene. 115 1e-53
 emb|AJ001926|PAAJ1926 Picea abies cad8 gene. 115 1e-53
 emb|AJ001924|PAAJ1924 Picea abies cad2 gene. 114 1e-53
 15 emb|AI488134|AI488134 EST246456 tomato ovary, TAMU Lycopersicon ... 210 2e-53
 emb|AW981164|AW981164 EST392358 DSIL Medicago truncatula cDNA cl... 133 3e-53
 emb|AI965672|AI965672 sc76g06.y1 Gm-cl018 Glycine max cDNA clone... 209 4e-53
 emb|AW981208|AW981208 EST392298 DSIL Medicago truncatula cDNA cl... 149 3e-52
 emb|AW692803|AW692803 NF059G11ST1F1087 Developing stem Medicago ... 125 4e-52
 20 gb|BE123743|BE123743 NXNV_153_E12_F Nsf Xylem Normal wood Vertic... 187 4e-49
 emb|AL121862|LMFL1063 Leishmania major Friedlin chromosome 23 co... 73 8e-48
 emb|AF109157|AF109157 Eucalyptus globulus cinnamyl alcohol dehyd... 138 2e-46
 emb|X75480|EGCAD E.gunnii CAD gene. 139 3e-46
 dbj|D16624|EGCCAD Eucalyptus botryoides DNA for cinnamyl alcohol... 138 2e-45
 25 emb|AW775567|AW775567 EST334632 DSIL Medicago truncatula cDNA cl... 105 7e-45
 gb|L36456|SSNCAD3 Stylosanthes humilis cinnamyl alcohol dehydrog... 134 1e-44
 emb|AW706922|AW706922 sk08c02.y1 Gm-cl023 Glycine max cDNA clone... 113 1e-43
 gb|BE123884|BE123884 EST394009 DSIL Medicago truncatula cDNA clo... 110 2e-43
 emb|AW201173|AW201173 se98g05.y1 Gm-cl027 Glycine max cDNA clone... 135 3e-43
 30 emb|AI729035|AI729035 BNLGHi12406 Six-day Cotton fiber Gossypium... 174 9e-43
 emb|AW666266|AW666266 sk34e03.y1 Gm-cl028 Glycine max cDNA clone... 108 2e-42
 emb|AW218543|AW218543 EST303726 tomato radicle, 5 d post-imbibit... 88 6e-42
 emb|AW100321|AW100321 sd23a02.y1 Gm-cl012 Glycine max cDNA clone... 130 2e-41
 emb|AI727983|AI727983 BNLGHi9898 Six-day Cotton fiber Gossypium ... 95 2e-40
 35 emb|AV412798|AV412798 AV412798 Lotus japonicus young plants (two... 137 6e-40
 emb|AI731536|AI731536 BNLGHi9665 Six-day Cotton fiber Gossypium ... 94 8e-40
 emb|AW775594|AW775594 EST334659 DSIL Medicago truncatula cDNA cl... 98 8e-40
 emb|AI726959|AI726959 BNLGHi6955 Six-day Cotton fiber Gossypium ... 93 4e-39
 gb|BE124304|BE124304 EST394429 DSIL Medicago truncatula cDNA clo... 94 7e-39
 40 emb|AW776649|AW776649 EST335714 DSIL Medicago truncatula cDNA cl... 94 1e-38
 emb|AI728121|AI728121 BNLGHi9734 Six-day Cotton fiber Gossypium ... 93 2e-38
 emb|AF060491|AF060491 Pinus radiata cinnamyl alcohol dehydrogena... 118 2e-38
 gb|BE036055|BE036055 MO19B09 MO Mesembryanthemum crystallinum cD... 81 4e-38
 emb|AI161452|AI161452 A001P14U Hybrid aspen plasmid library Popu... 125 7e-38
 45 emb|AW648829|AW648829 EST327283 tomato germinating seedlings, TA... 89 3e-37
 gb|BE124289|BE124289 EST394414 DSIL Medicago truncatula cDNA clo... 154 1e-36
 emb|AW348888|AW348888 GM210010A10H2R Gm-r1021 Glycine max cDNA 3... 154 1e-36
 50 emb|AI496395|AI496395 sb04b10.y1 Gm-cl004 Glycine max cDNA clone... 154 1e-36
 emb|AW684143|AW684143 NF012H08NR1F1000 Nodulated root Medicago t... 121 3e-36
 emb|AI899871|AI899871 sb94e03.y1 Gm-cl017 Glycine max cDNA clone... 100 3e-36
 emb|AW650552|AW650552 EST329006 tomato germinating seedlings, TA... 148 4e-36
 emb|AW928461|AW928461 EST337249 tomato flower buds 8 mm to pre-a... 89 3e-34
 emb|AV417794|AV417794 AV417794 Lotus japonicus young plants (two... 140 1e-32
 55 emb|AF067082|AF067082 Apium graveolens mannitol dehydrogenase (M... 127 9e-32
 emb|AW234172|AW234172 sE22a12.y1 Gm-cl028 Glycine max cDNA clone... 134 1e-30
 emb|AI165779|AI165779 A091p26u Hybrid aspen plasmid library Popu... 94 2e-30
 emb|AW686753|AW686753 NF042C07NR1F1000 Nodulated root Medicago t... 93 2e-30
 emb|AW256719|AW256719 EST304856 KV2 Medicago truncatula cDNA clo... 78 3e-30
 60 emb|AW625821|AW625821 EST319728 tomato radicle, 5 d post-imbibit... 132 4e-30
 emb|AI166747|AI166747 xylem.est.549 Poplar xylem Lambda ZAPII li... 94 5e-30

emb|AW218822|AW218822 EST301302 tomato root during/after fruit s... 84 2e-29
 emb|AI960981|AI960981 sc93e08.y1 Gm-cl019 Glycine max cDNA clone... 85 4e-29
 emb|AW617779|AW617779 EST324178 L. hirsutum trichome, Cornell Un... 89 1e-28
 emb|AI165405|AI165405 A083p34u Hybrid aspen plasmid library Popu... 127 1e-28
 5 emb|AW648072|AW648072 EST326526 tomato germinating seedlings, TA... 79 2e-27

Query= AL078637.213_s_at 15523_s_at /id_source genbank /description
 emb|cab45071.1| (al078637) putative protein [arabidopsis thaliana]
 10 /blast_score 8.00e-48 /ec_number /family /chip nova /gb_link /ncgi
 (336 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

15 Searching.....done

		Score	E	
				(bits) Value
20	Sequences producing significant alignments:			
	emb AW394463 AW394463 sh32h06.y1 Gm-cl017 Glycine max cDNA clone...	80	1e-17	
	gb BE023782 BE023782 sm92d02.y1 Gm-cl015 Glycine max cDNA clone ...	73	2e-15	
	emb AW395908 AW395908 sh07c05.y1 Gm-cl016 Glycine max cDNA clone...	80	7e-15	
	emb AW733452 AW733452 sk73g05.y1 Gm-cl016 Glycine max cDNA clone...	77	4e-14	
25	gb BE058639 BE058639 sn18g09.y1 Gm-cl016 Glycine max cDNA clone ...	77	6e-14	
	emb AW156195 AW156195 se20g08.y1 Gm-cl015 Glycine max cDNA clone...	76	1e-13	
	emb AW563817 AW563817 LG1_261_C02.g1_A002 Light Grown 1 (LG1) So...	76	1e-13	
	emb AW677327 AW677327 DG1_5_D03.g1_A002 Dark Grown 1 (DG1) Sorgh...	76	1e-13	
	emb AW424028 AW424028 sh59f09.y1 Gm-cl015 Glycine max cDNA clone...	62	1e-12	
30	gb BE022753 BE022753 sm88a02.y1 Gm-cl015 Glycine max cDNA clone ...	62	2e-12	
	emb AW677332 AW677332 DG1_5_F03.g1_A002 Dark Grown 1 (DG1) Sorgh...	71	3e-12	
	gb BE035944 BE035944 MO22E07 MO Mesembryanthemum crystallinum cD...	69	1e-11	
	emb AW119934 AW119934 sd54g12.y1 Gm-cl016 Glycine max cDNA clone...	55	3e-10	
	gb L20233 POPVEGSTR P.trichocarpa x P.deltoides vegetative stor...	64	4e-10	
35	emb AW119941 AW119941 sd54h12.y1 Gm-cl016 Glycine max cDNA clone...	47	4e-08	
	emb AW092074 AW092074 EST285350 tomato mixed elicitor, BTI Lycop...	57	4e-08	
	emb AW127599 AW127599 M110330 DSLC Medicago truncatula cDNA clon...	43	5e-07	
	emb AI822191 AI822191 L0-668T3 Ice plant Lambda Uni-Zap XR expre...	52	6e-07	
	gb BE035204 BE035204 MO02A04 MO Mesembryanthemum crystallinum cD...	51	2e-06	
40	gb BE035225 BE035225 MO02E03 MO Mesembryanthemum crystallinum cD...	51	2e-06	
	gb BE036341 BE036341 MO23E06 MO Mesembryanthemum crystallinum cD...	51	2e-06	
	gb BE037208 BE037208 MP18A03 MP Mesembryanthemum crystallinum cD...	51	2e-06	
	gb BE037538 BE037538 MP19G11 MP Mesembryanthemum crystallinum cD...	48	9e-06	
	gb BE034872 BE034872 ML05E09 ML Mesembryanthemum crystallinum cD...	45	2e-04	
45	emb AW458345 AW458345 sh86h01.y1 Gm-cl016 Glycine max cDNA clone...	31	9e-04	
	emb AU036852 AU036852 AU036852 Cryptomeria japonica seedling lea...	41	0.003	
	gb S59422 S59422 Populus x canadensis major storage protein mRNA...	41	0.003	
	gb M77504 POPBSP Populus deltoides bark storage protein mRNA, co...	41	0.003	
	emb AC000133 ENAC000133 Emericella nidulans cosmid SW06E08, comp...	33	0.77	
50	emb AW287856 AW287856 N100699e rootphos(-) Medicago truncatula c...	31	1.0	
	emb AQ851083 AQ851083 LMAJFV1_lm38d08.y1 Leishmania major FV1 ra...	33	1.1	
	emb AW329091 AW329091 N200297e rootphos(-) Medicago truncatula c...	31	1.2	
	emb AW329193 AW329193 N200405e rootphos(-) Medicago truncatula c...	31	1.3	
	emb AQ398028 AQ398028 mgxb0017N12f CUGI Rice Blast BAC Library P...	32	1.4	
55	emb AI068626 AI068626 mgae0003cD01f Magnaporthe grisea Appressor...	32	1.4	
	emb AW981194 AW981194 EST392388 DSIL Medicago truncatula cDNA cl...	31	1.5	
	emb AW695905 AW695905 NF100E05ST1F1038 Developing stem Medicago ...	31	1.5	
	dbj D50414 D50414 Cannabis sativa male-associated DNA sequence.	29	1.7	
	emb X70064 PDBSPA P.deltoides gene for poplar bark storage protein.	32	2.0	
60	emb Z64354 SPAC23D3 S.pombe chromosome I cosmid c23D3.	32	2.0	
	emb X83853 NTPAR1A N.tabacum mRNA for PAR-1a.	32	2.0	

emb|AW268020|AW268020 EST306242 DSIR Medicago truncatula cDNA cl... 32 2.0
 emb|AA550547|AA550547 1710m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 32 2.0
 emb|AL078627|SPBC365 S.pombe chromosome II cosmid c365. 31 2.7
 gb|U05613|CBU05613 Crepidomanes birmanicum chloroplast large sub... 31 3.7
 5 emb|AI050216|AI050216 TENU1464 T. cruzi epimastigote normalized ... 31 3.7
 emb|AI065375|AI065375 TENU2262 T. cruzi epimastigote normalized ... 31 3.7
 emb|AI065371|AI065371 TENU2258 T. cruzi epimastigote normalized ... 31 3.7
 emb|AT000167|AT000167 AT000167 Apple young fruit cDNA library Ma... 29 4.0
 emb|AJ388714|AJ388714 AJ388714 Medicago truncatula R108 Medicago... 29 4.3
 10 emb|AQ361816|AQ361816 mgxb0005A07f CUGI Rice Blast BAC Library P... 30 5.1
 emb|AQ162953|AQ162953 mgxb0021G21r CUGI Rice Blast BAC Library P... 30 5.1
 emb|Z67998|SPAC1F7 S.pombe chromosome I cosmid c1F7. 30 5.1
 emb|AF148676|AF148676 Zizaniopsis villanensis maturase (matK) ge... 30 7.1
 emb|AW684956|AW684956 NF023E05NR1F1000 Nodulated root Medicago t... 30 7.1
 15 emb|AZ216404|AZ216404 Sheared DNA-121G9.TF Sheared DNA Trypanoso... 30 7.1
 emb|AQ942697|AQ942697 Sheared DNA-42J8.TR Sheared DNA Trypanosom... 30 7.1
 emb|AI163063|AI163063 A031p30u Hybrid aspen plasmid library Popu... 30 7.1
 gb|BE058445|BE058445 sn16b09.y1 Gm-c1016 Glycine max cDNA clone ... 30 7.1
 gb|BE023592|BE023592 sm82e07.y1 Gm-c1015 Glycine max cDNA clone ... 30 7.1
 20 emb|AZ220034|AZ220034 Sheared DNA-63D11.TR Sheared DNA Trypanoso... 30 7.1
 emb|AI110319|AI110319 TENU3289 T. cruzi epimastigote normalized ... 30 7.1
 emb|AW870077|AW870077 NXNV_123_G11_F Nsf Xylem Normal wood Verti... 30 7.1
 emb|AI057841|AI057841 TENU1932 T. cruzi epimastigote normalized ... 30 7.1
 emb|X83851|NTPAR1B N.tabacum mRNA for PAR-1b. 30 7.1
 25 gb|M18538|POPPOP3A Populus balsamifera subsp. trichocarpa X Popu... 30 7.1
 emb|AW203632|AW203632 sf36d11.y1 Gm-c1028 Glycine max cDNA clone... 30 7.1
 emb|AQ640232|AQ640232 927P1-18B11.TV 927P1 Trypanosoma brucei ge... 30 7.1
 emb|AI779122|AI779122 EST260001 tomato susceptible, Cornell Lyco... 27 8.3
 emb|AW096641|AW096641 EST289821 tomato mixed elicitor, BTI Lycop... 27 8.9
 30 gb|N98085|N98085 2245C3 czapPFDd2.1, Debopam Chakrabarti Plasmod... 29 9.7
 emb|AW929160|AW929160 EST337948 tomato flower buds 8 mm to pre-a... 29 9.7
 emb|AW037807|AW037807 EST279436 tomato mixed elicitor, BTI Lycop... 29 9.7
 emb|AW729409|AW729409 GA_Ea0024O24 Gossypium arboreum 7-10 dpa ... 29 9.7
 emb|AF193903|AF193903 Cafeteria roenbergensis mitochondrial DNA,... 29 9.7
 35

Query= AL078637.191_r_at 15532_r_at /id_source genbank /description
 emb|cab45069.1| (al078637) putative protein [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link
 40 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al078637|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al078637|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al078637|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?al078637>
 (990 letters)

45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

50 Score E
 Sequences producing significant alignments: (bits) Value

emb|AW092074|AW092074 EST285350 tomato mixed elicitor, BTI Lycop... 145 1e-69
 emb|AI778762|AI778762 EST259641 tomato susceptible, Cornell Lyco... 149 1e-49
 55 gb|BE035944|BE035944 MO22E07 MO Mesembryanthemum crystallinum cD... 120 9e-49
 emb|AW618184|AW618184 EST314234 L. pennellii trichome, Cornell U... 138 2e-46
 emb|AI778761|AI778761 EST259640 tomato susceptible, Cornell Lyco... 133 6e-45
 emb|AW618179|AW618179 EST314229 L. pennellii trichome, Cornell U... 114 3e-39
 gb|S59422|S59422 Populus x canadensis major storage protein mRNA... 99 6e-32
 60 gb|M77504|POPBSP Populus deltoides bark storage protein mRNA, co... 99 3e-30
 emb|AW395908|AW395908 sh07c05.y1 Gm-c1016 Glycine max cDNA clone... 125 5e-28

- emb|AW733452|AW733452 sk73g05.y1 Gm-cl016 Glycine max cDNA clone... 122 3e-27
 gb|BE058639|BE058639 sn18g09.y1 Gm-cl016 Glycine max cDNA clone ... 122 4e-27
 emb|AW394463|AW394463 sh32h06.y1 Gm-cl017 Glycine max cDNA clone... 111 4e-26
 emb|AW563817|AW563817 LG1_261_C02.g1_A002 Light Grown 1 (LG1) So... 104 4e-25
 5 emb|AI822191|AI822191 L0-668T3 Ice plant Lambda Uni-Zap XR expre... 114 1e-24
 gb|BE036341|BE036341 MO23E06 MO Mesembryanthemum crystallinum cD... 112 3e-24
 gb|BE035204|BE035204 MO02A04 MO Mesembryanthemum crystallinum cD... 112 3e-24
 gb|BE037538|BE037538 MP19G11 MP Mesembryanthemum crystallinum cD... 112 3e-24
 gb|BE035225|BE035225 MO02E03 MO Mesembryanthemum crystallinum cD... 112 3e-24
 10 gb|BE059090|BE059090 sn25b08.y1 Gm-cl016 Glycine max cDNA clone ... 75 2e-23
 emb|AW395168|AW395168 sh40g07.y1 Gm-cl017 Glycine max cDNA clone... 68 3e-21
 gb|BE037512|BE037512 MP04B06 MP Mesembryanthemum crystallinum cD... 95 4e-20
 emb|AW623629|AW623629 EST321574 tomato flower buds 3-8 mm, Corne... 92 3e-19
 emb|AW625587|AW625587 EST319494 tomato radicle, 5 d post-imbibit... 92 3e-19
 15 emb|AW929488|AW929488 EST338276 tomato flower buds 8 mm to pre-a... 92 3e-19
 emb|AI778197|AI778197 EST259076 tomato susceptible, Cornell Lyco... 92 3e-19
 emb|AW648720|AW648720 EST327090 tomato germinating seedlings, TA... 92 3e-19
 emb|AW625287|AW625287 EST319290 tomato radicle, 5 d post-imbibit... 92 3e-19
 emb|AW648718|AW648718 EST327088 tomato germinating seedlings, TA... 92 3e-19
 20 emb|AW928879|AW928879 EST337667 tomato flower buds 8 mm to pre-a... 92 3e-19
 gb|L20233|POPVEGSTRA P.trichocarpa x P.deltoides vegetative stor... 94 2e-18
 emb|AW733620|AW733620 sk75h08.y1 Gm-cl016 Glycine max cDNA clone... 86 3e-18
 emb|AW677327|AW677327 DG1_5_D03.g1_A002 Dark Grown 1 (DG1) Sorgh... 93 4e-18
 emb|AI163910|AI163910 A051P26U Hybrid aspen plasmid library Popu... 56 1e-17
 25 emb|AW156195|AW156195 se20g08.y1 Gm-cl015 Glycine max cDNA clone... 90 2e-17
 emb|AW775932|AW775932 EST334997 DSIL Medicago truncatula cDNA cl... 84 2e-17
 emb|AW692820|AW692820 NF056A09ST1F1000 Developing stem Medicago ... 84 2e-17
 emb|AW685340|AW685340 NF027C09NR1F1000 Nodulated root Medicago t... 83 4e-17
 emb|AW684469|AW684469 NF017C09NR1F1000 Nodulated root Medicago t... 75 1e-16
 30 gb|BE037208|BE037208 MP18A03 MP Mesembryanthemum crystallinum cD... 84 2e-15
 gb|BE023782|BE023782 sm92d02.y1 Gm-cl015 Glycine max cDNA clone ... 72 4e-14
 gb|BE036234|BE036234 MO21C12 MO Mesembryanthemum crystallinum cD... 78 1e-13
 emb|AW286123|AW286123 LG1_261_F11.b1_A002 Light Grown 1 (LG1) So... 64 5e-13
 emb|AW626069|AW626069 EST319976 tomato radicle, 5 d post-imbibit... 69 1e-12
 35 gb|BE095283|BE095283 00344 leafy spurge Lambda HybriZAP 2.1 two-... 62 1e-12
 emb|AW677160|AW677160 DG1_5_D03.b1_A002 Dark Grown 1 (DG1) Sorgh... 62 2e-12
 emb|AW677332|AW677332 DG1_5_F03.g1_A002 Dark Grown 1 (DG1) Sorgh... 70 2e-11
 gb|BE022753|BE022753 sm88a02.y1 Gm-cl015 Glycine max cDNA clone ... 61 5e-11
 emb|AW424028|AW424028 sh59f09.y1 Gm-cl015 Glycine max cDNA clone... 62 8e-11
 40 emb|X70064|PDBSPA P.deltoides gene for poplar bark storage protein. 63 3e-09
 emb|AW119934|AW119934 sd54g12.y1 Gm-cl016 Glycine max cDNA clone... 54 4e-09
 emb|AW677125|AW677125 DG1_5_F03.b1_A002 Dark Grown 1 (DG1) Sorgh... 43 5e-07
 gb|BE058421|BE058421 sn15h03.y1 Gm-cl016 Glycine max cDNA clone ... 56 6e-07
 emb|AW119941|AW119941 sd54h12.y1 Gm-cl016 Glycine max cDNA clone... 46 1e-06
 45 gb|BE037054|BE037054 MP13H01 MP Mesembryanthemum crystallinum cD... 55 1e-06
 gb|BE036004|BE036004 MO17H11 MO Mesembryanthemum crystallinum cD... 51 1e-06
 gb|BE035382|BE035382 MO03G01 MO Mesembryanthemum crystallinum cD... 54 2e-06
 emb|AW127599|AW127599 M110330 DSLC Medicago truncatula cDNA clon... 44 3e-06
 gb|BE095282|BE095282 00343 leafy spurge Lambda HybriZAP 2.1 two-... 52 5e-06
 50 emb|AW287592|AW287592 LG1_244_A09.b1_A002 Light Grown 1 (LG1) So... 40 6e-06
 emb|AA557101|AA557101 943 Loblolly pine N Pinus taeda cDNA clone... 47 2e-04
 gb|BE037091|BE037091 MP14F10 MP Mesembryanthemum crystallinum cD... 47 2e-04
 gb|M25340|POPCHIC Populus sp. chitinase mRNA fragment, clone 4. 46 6e-04
 gb|BE036753|BE036753 MP04H07 MP Mesembryanthemum crystallinum cD... 46 6e-04
 55 gb|BE037437|BE037437 MP21A08 MP Mesembryanthemum crystallinum cD... 34 8e-04
 gb|BE037490|BE037490 MP21G12 MP Mesembryanthemum crystallinum cD... 45 9e-04
 emb|AU036852|AU036852 AU036852 Cryptomeria japonica seedling lea... 41 0.015
 emb|AA556425|AA556425 280 Loblolly pine C Pinus taeda cDNA clone... 41 0.015
 gb|BE036626|BE036626 MP02H12 MP Mesembryanthemum crystallinum cD... 40 0.021
 60 emb|AW458345|AW458345 sh86h01.y1 Gm-cl016 Glycine max cDNA clone... 30 0.052
 gb|BE034872|BE034872 ML05E09 ML Mesembryanthemum crystallinum cD... 38 0.10

emb|AW729858|AW729858 GA__Ea0026H02 Gossypium arboreum 7-10 dpa ... 36 0.37
emb|AQ953583|AQ953583 Sheared DNA-53H18.TF Sheared DNA Trypanoso... 36 0.51
gb|BE036480|BE036480 MP03G10 MP Mesembryanthemum crystallinum cD... 36 0.51
emb|Z00044|CHNTXX Nicotiana tabacum chloroplast genome DNA. 35 0.70
5 emb|AL160939|L1356CX Leishmania major Friedlin cosmid L1356.3 t3... 34 1.8
gb|BE036897|BE036897 MP08B09 MP Mesembryanthemum crystallinum cD... 34 1.8
emb|AI730722|AI730722 BNLGHi7729 Six-day Cotton fiber Gossypium ... 34 1.8
emb|AB030726|AB030726 Nicotiana tabacum mRNA for DNA (cytosine-5... 34 2.5
emb|AW397331|AW397331 sg77e08.y1 Gm-c1007 Glycine max cDNA clone... 34 2.5
10 emb|AI210350|AI210350 i0c03a1.r1 Aspergillus nidulans 24hr asexu... 34 2.5
emb|AA786346|AA786346 l3g09a1.fl Aspergillus nidulans 24hr asexu... 34 2.5
emb|AW397063|AW397063 sg66e08.y1 Gm-c1007 Glycine max cDNA clone... 34 2.5
emb|AI327733|AI327733 i0c03a1.fl Aspergillus nidulans 24hr asexu... 34 2.5
emb|AW672119|AW672119 LG1_357_F07.b1_A002 Light Grown 1 (LG1) So... 33 3.4
15 emb|AJ270207|ECA270207 Entodinium caudatum partial mRNA fro puta... 33 3.4
emb|AW672133|AW672133 LG1_357_D07.b1_A002 Light Grown 1 (LG1) So... 33 3.4
emb|AQ847463|AQ847463 LMAJFV1_lm34c05.y1 Leishmania major FV1 ra... 33 4.7
emb|AZ212142|AZ212142 Sheared DNA-70G10.TF Sheared DNA Trypanoso... 32 6.4
emb|AI163630|AI163630 A045p06u Hybrid aspen plasmid library Popu... 32 6.4
20 emb|AL354532|LMFL1177 Leishmania major Friedlin chromosome 21 co... 30 6.9
emb|AJ243516|NCR243516 Neurospora crassa partial nca-3 gene for ... 32 8.8
emb|AL116648|CNS01DCG Botrytis cinerea strain T4 cDNA library un... 27 9.3
Query= X71794.2_s_at 15970_s_at /id_source genbank /description
emb|caa50677.1| (x71794) peroxidase [arabidopsis thaliana]
25 /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
(1236 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

30

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

35

gb|M60729|HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge... 744 0.0

emb|A00741|A00741 A.rusticana synthetic gene (reverse complement... 692 0.0

emb|A00740|A00740 A.rusticana synthetic gene for peroxidase. 692 0.0

dbj|E01651|E01651 cDNA encoding horseradish peroxidase. 692 0.0

40

gb|M37157|HRAHRPCB A.rusticana peroxidase isoenzyme C (HPR C) ge... 371 e-133

emb|X97349|PTPXP2PER P.trichocarpa mRNA for anionic peroxidase P... 473 e-132

emb|X97350|PTPXP3PER P.trichocarpa mRNA for anionic peroxidase P... 469 e-131

dbj|D83224|POPP01 Populus nigra mRNA for peroxidase, complete cds. 468 e-131

gb|M37156|HRAHRPCA A.rusticana peroxidase isoenzyme C (HPR C) ge... 363 e-130

45

emb|X97348|PTPXP1PER P.trichocarpa mRNA for anionic peroxidase P... 463 e-129

dbj|D30652|POPPA Populus kitakamiensis mRNA for peroxidase, part... 441 e-123

emb|X97351|PTPXP4PER P.trichocarpa mRNA for anionic peroxidase P... 383 e-120

dbj|D30653|POPPB Populus kitakamiensis mRNA for peroxidase, part... 356 e-112

emb|AF149277|AF149277 Phaseolus vulgaris peroxidase 1 precursor ... 227 e-107

50

gb|L36157|ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple... 229 e-107

emb|AF007211|AF007211 Glycine max peroxidase precursor (GMIPER1)... 229 e-106

gb|L07554|LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA... 381 e-105

emb|X90692|MSRNAPE1A M.sativa mRNA for peroxidase 1A. 211 e-105

dbj|D90115|HRAPRXC2 Horseradish prxC2 gene encoding peroxidase i... 296 e-103

55

emb|AJ242742|IBA242742 Ipomoea batatas mRNA for peroxidase (pod ... 138 2e-97

emb|AF149280|AF149280 Phaseolus vulgaris peroxidase 5 precursor ... 142 4e-97

emb|X90693|MSRNAPE1B M.sativa mRNA for peroxidase 1B. 231 1e-95

emb|X90694|MSRNAPE1C M.sativa mRNA for peroxidase 1C. 226 7e-94

gb|L36111|SSNPEROXIB Stylosanthes humilis peroxidase mRNA. 210 2e-89

60

emb|AI959837|AI959837 sc94h07.y1 Gm-c1019 Glycine max cDNA clone... 228 6e-89

emb|AF244924|AF244924 Spinacia oleracea peroxidase prx15 precurs... 208 9e-88

- emb|AW559660|AW559660 EST314772 DSIR Medicago truncatula cDNA cl... 236 1e-87
emb|AW774581|AW774581 EST333732 KV3 Medicago truncatula cDNA clo... 236 7e-87
emb|AF155124|AF155124 Gossypium hirsutum bacterial-induced perox... 215 2e-86
5 emb|AW981426|AW981426 EST392579 DSIL Medicago truncatula cDNA cl... 236 2e-85
emb|AB042103|AB042103 Asparagus officinalis AspPOX1 mRNA for per... 209 2e-85
emb|AF244923|AF244923 Spinacia oleracea peroxidase prx14 precurs... 205 9e-85
emb|AJ250121|PAB250121 Picea abies mRNA for SPI2 protein (spi2 g... 253 1e-83
emb|AW775762|AW775762 EST334827 DSIL Medicago truncatula cDNA cl... 236 6e-83
emb|Y10466|SOPR XR5 S.oleracea mRNA for peroxidase, clone PC18. 218 3e-82
10 emb|AW775425|AW775425 EST334490 DSIL Medicago truncatula cDNA cl... 208 1e-81
emb|AW685437|AW685437 NF029D09NR1F1000 Nodulated root Medicago t... 230 9e-80
emb|AB024439|AB024439 Scutellaria baicalensis mRNA for peroxidas... 209 2e-79
emb|AF244922|AF244922 Spinacia oleracea peroxidase prx13 precurs... 212 3e-79
emb|X57564|ARNEUPERO A.rusticana mRNA for neutral peroxidase. 115 6e-78
15 emb|AW776273|AW776273 EST335338 DSIL Medicago truncatula cDNA cl... 222 1e-77
emb|AW267813|AW267813 EST305941 DSIR Medicago truncatula cDNA cl... 200 1e-76
emb|X91232|MARNAPRX M.annua mRNA for peroxidase. 196 5e-76
emb|AF049881|AF049881 Linum usitatissimum peroxidase FLXPER4 (PE... 207 7e-76
emb|AW256487|AW256487 EST304624 KV2 Medicago truncatula cDNA clo... 200 9e-76
20 emb|AW775890|AW775890 EST334955 DSIL Medicago truncatula cDNA cl... 200 3e-74
emb|AW257195|AW257195 EST305332 KV2 Medicago truncatula cDNA clo... 214 5e-74
gb|M91373|CUSPREPER Cucumis sativus peroxidase mRNA, complete cds. 86 2e-73
gb|U41657|GMU41657 Glycine max seed coat peroxidase isozyme (SPO... 159 3e-73
emb|AB027752|AB027752 Nicotiana tabacum mRNA for peroxidase, com... 197 5e-73
25 gb|L36110|SSNPEROXIA Stylosanthes humilis peroxidase mRNA. 199 5e-73
gb|M37636|ARCPNC1 Arachis hypogaea cationic peroxidase (PNC1) mR... 204 7e-73
emb|AW685235|AW685235 NF027H10NR1F1000 Nodulated root Medicago t... 236 9e-73
emb|AW278775|AW278775 sf97d02.y1 Gm-c1019 Glycine max cDNA clone... 155 1e-72
emb|X71593|LECEVI1A L.esculentum CEVI-1 mRNA. 99 2e-72
30 gb|J02979|TOBPXDLF Nicotiana tabacum lignin-forming peroxidase m... 100 2e-72
emb|AW559945|AW559945 EST314993 DSIR Medicago truncatula cDNA cl... 233 2e-72
emb|AW980744|AW980744 EST391897 GVN Medicago truncatula cDNA clo... 235 5e-70
emb|Y10467|SOPR XR6 S.oleracea mRNA for peroxidase, clone PC23. 105 1e-69
dbj|D83225|POPP02 Populus nigra peroxidase gene, complete cds. 196 2e-69
35 gb|M74103|TOBANPER Nicotiana sylvestris anionic peroxidase mRNA,... 205 6e-69
emb|AF043234|AF043234 Striga asiatica ferriprotein porphyrin-con... 211 1e-68
gb|BE034991|BE034991 MM01A12 MM Mesembryanthemum crystallinum cD... 202 6e-68
emb|AW574244|AW574244 EST316835 GVN Medicago truncatula cDNA clo... 202 1e-67
emb|Y10465|SOPR XR4 S.oleracea mRNA for peroxidase, clone PC44. 98 3e-67
40 emb|AW686084|AW686084 NF038B07NR1F1000 Nodulated root Medicago t... 236 5e-67
emb|AW561032|AW561032 EST316080 DSIR Medicago truncatula cDNA cl... 203 7e-67
emb|X56011|TAPERO Wheat mRNA for peroxidase. 111 2e-66
emb|AW185769|AW185769 se59d08.y1 Gm-c1019 Glycine max cDNA clone... 219 4e-65
emb|Y17192|CPY17192 Cucurbita pepo mRNA for peroxidase. 96 2e-64
45 gb|BE033422|BE033422 ME01E09 ME Mesembryanthemum crystallinum cD... 184 4e-64
emb|AB024438|AB024438 Scutellaria baicalensis mRNA for peroxidas... 205 7e-64
gb|M91374|CUSPREPERA Cucumis sativus peroxidase mRNA, complete cds. 76 2e-63
gb|L24120|LINFLXP Linum usitatissimum peroxidase precursor (FLXP... 167 2e-63
gb|M91372|CUSPREPERB Cucumis sativus peroxidase mRNA, complete cds. 134 2e-63
50 emb|AF043235|AF043235 Striga asiatica ferriprotein porphyrin-con... 199 3e-63
emb|AW288002|AW288002 N100846e rootphos(-) Medicago truncatula c... 182 7e-63
emb|AW126121|AW126121 N100318e rootphos(-) Medicago truncatula c... 216 1e-62
gb|L36093|BLYPRX Barley peroxidase mRNA, complete cds. 133 5e-62
emb|AW687443|AW687443 NF009F07RT1F1062 Developing root Medicago ... 235 1e-61
55 emb|AW687957|AW687957 NF001D11ST1F1000 Developing stem Medicago ... 236 3e-61
emb|AB024437|AB024437 Scutellaria baicalensis mRNA for peroxidas... 163 3e-61
emb|X58396|HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7). 133 5e-61
emb|AI496388|AI496388 sb04a11.y1 Gm-c1004 Glycine max cDNA clone... 224 6e-61
emb|AW686765|AW686765 NF042E07NR1F1000 Nodulated root Medicago t... 222 8e-61
60 dbj|D38050|POPP1 Aspen prxA3a gene for peroxidase, complete cds. 121 9e-61
emb|AW704659|AW704659 sk54h10.y1 Gm-c1019 Glycine max cDNA clone... 149 9e-61

emb|Y10464|SOPR XR3 S.oleracea mRNA for peroxidase, clone PC42. 80 3e-60
 emb|AW705730|AW705730 sk51b02.y1 Gm-c1019 Glycine max cDNA clone... 149 8e-60
 gb|U51191|GMU51191 Glycine max peroxidase precursor (sEPa1) mRNA... 100 9e-60
 gb|U12314|CCU12314 Cenchrus ciliaris clone PX7 peroxidase mRNA, ... 105 9e-60
 5 emb|AI938533|AI938533 sb46h09.y1 Gm-c1015 Glycine max cDNA clone... 145 1e-59
 emb|AW705617|AW705617 sk50d03.y1 Gm-c1019 Glycine max cDNA clone... 149 2e-59
 emb|AI781859|AI781859 EST262738 tomato susceptible, Cornell Lyco... 102 2e-59
 emb|AF149278|AF149278 Phaseolus vulgaris peroxidase 3 precursor ... 90 3e-59
 gb|U51192|GMU51192 Glycine max peroxidase precursor (sEPa2) mRNA... 102 4e-59
 10 emb|AW441632|AW441632 EST311028 tomato fruit red ripe, TAMU Lyco... 105 7e-59
 emb|AF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 156 8e-59
 gb|M32742|CUSCUPER C.sativus peroxidase (put.) (CuPer2) mRNA, 3'... 107 2e-58
 emb|AW705946|AW705946 sk52h07.y1 Gm-c1019 Glycine max cDNA clone... 224 6e-58

15

Query= X68592.6_at 15978_at /id_source genbank /description
 emb|caa48579.1| (x68592) adenosine nucleotide translocator
 [arabidopsis thaliana] /blast_score 0 /ec_number /family translocase
 /chip nova /gb_link

20

[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x68592|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|x68592|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x68592|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?x68592>
 (1530 letters)

25

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

30

Score E
 Sequences producing significant alignments: (bits) Value

emb|AF006489|AF006489 Gossypium hirsutum adenine nucleotide tran... 325 0.0
 emb|X62123|STANTG S.tuberosum ant gene for ADP/ATP translocator. 328 0.0
 35 gb|U89839|LEU89839 Lycopersicon esculentum ADP/ATP translocator ... 327 0.0
 emb|X57557|STANT1 S.tuberosum PANT1 mRNA for adenine nucleotide ... 635 0.0
 emb|AJ003197|LAJ3197 Lupinus albus mRNA for adenine nucleotide ... 331 e-175
 emb|X80023|TTADPATP T.turgidum mRNA for ADP/ATP carrier. 322 e-172
 emb|X65194|CRANT C.reinhardtii mRNA CRANT for mitochondrial ADP/... 348 e-149
 40 emb|AL023634|SPBC530 S.pombe chromosome II cosmid c530. 265 e-139
 emb|Z49974|SPANCI1GN S.pombe ANC1 gene for adenine nucleotide car... 265 e-139
 emb|AF085429|AF085429 Candida parapsilosis ADP/ATP carrier prote... 311 e-134
 dbj|D89102|D89102 Schizosaccharomyces pombe mRNA, partial cds, c... 265 e-133
 gb|L33797|YSKAAC Kluyveromyces lactis ADP/ATP translocase (AAC) ... 259 e-132
 45 emb|AF237675|AF237675 Yarrowia lipolytica ADP/ATP carrier protei... 247 e-132
 emb|AJ277099|CUT277099 Candida utilis anc gene for mitochondrial... 253 e-131
 emb|AJ277098|CUT277098 Candida utilis anc gene for mitochondrial... 253 e-131
 gb|M34075|YSCAAC3 S.cerevisiae ADP/ATP-translocator protein (AAC... 252 e-129
 emb|X77291|SCIILDNA S.cerevisiae YBL0421, YBL0438, YBL0418, YBL0... 252 e-129
 50 emb|Z35791|SCYBL030C S.cerevisiae chromosome II reading frame OR... 252 e-129
 emb|X74427|SCADNUCA S.cerevisiae gene for adenine nucleotide car... 252 e-129
 gb|J04021|YSCAAC2 S.cerevisiae ADP/ATP carrier protein (AAC2) ge... 252 e-129
 emb|X00363|NCADPATP Neurospora crassa mRNA for mitochondrial ADP... 280 e-126
 emb|Z49703|SC9796 S.cerevisiae chromosome XIII cosmid 9796. 248 e-125
 55 gb|M12514|YSCPET9 S.cerevisiae ADP/ATP translocator protein (AAC... 248 e-125
 emb|Z35954|SCYBR085W S.cerevisiae chromosome II reading frame OR... 247 e-125
 gb|M34076|YSCAAC2A S.cerevisiae ADP/ATP-translocator protein (AA... 247 e-125
 emb|AW774326|AW774326 EST333477 KV3 Medicago truncatula cDNA clo... 288 e-124
 emb|AL111975|CNS019QN Botrytis cinerea strain T4 cDNA library un... 254 e-122
 60 emb|AW647699|AW647699 EST307178 tomato germinating seedlings, TA... 299 e-120

- emb|AW349848|AW349848 GM210006A11G9R Gm-r1021 Glycine max cDNA 3... 326 e-118
- emb|AW624842|AW624842 EST313671 tomato radicle, 5 d post-imbibit... 229 e-116
- emb|X95863|TTANT1 T.turgidum ant gene (1549bp). 195 e-114
- 5 emb|AW041186|AW041186 EST284050 tomato mixed elicitor, BTI Lycop... 239 e-114
- emb|X95864|TTANT2 T.turgidum ant gene (1494bp). 191 e-112
- emb|AW706324|AW706324 sj54h05.y1 Gm-c1033 Glycine max cDNA clone... 245 e-110
- emb|AL157416|LMFL6066 Leishmania major Friedlin chromosome 19 co... 233 e-108
- emb|AW160172|AW160172 EST290029 L. pennellii trichome, Cornell U... 328 e-108
- 10 emb|AW928728|AW928728 EST337516 tomato flower buds 8 mm to pre-a... 247 e-107
- emb|AW218544|AW218544 EST303727 tomato radicle, 5 d post-imbibit... 325 e-105
- emb|AW830381|AW830381 sm26a12.y1 Gm-c1028 Glycine max cDNA clone... 268 e-105
- emb|AW201674|AW201674 sf05h11.y1 Gm-c1027 Glycine max cDNA clone... 309 e-104
- emb|AI812944|AI812944 22G12 Pine Lambda Zap Xylem library Pinus ... 251 e-103
- 15 emb|AI777865|AI777865 EST258744 tomato susceptible, Cornell Lyco... 284 e-102
- emb|AW234033|AW234033 sf33d01.y1 Gm-c1028 Glycine max cDNA clone... 237 e-101
- emb|AW831587|AW831587 sm28b02.y1 Gm-c1028 Glycine max cDNA clone... 300 e-101
- emb|AW668198|AW668198 GA__Ea0013C13 Gossypium arboreum 7-10 dpa ... 331 e-100
- emb|AF049130|AF049130 Trypanosoma brucei brucei ADP/ATP carrier ... 238 1e-98
- 20 emb|AI898886|AI898886 EST268329 tomato ovary, TAMU Lycopersicon ... 213 2e-98
- gb|U32987|TBU32987 Trypanosoma brucei rhodesiense ADP/ATP carrie... 238 3e-98
- emb|AW223982|AW223982 EST300793 tomato fruit red ripe, TAMU Lyco... 327 1e-96
- emb|AW624951|AW624951 EST313780 tomato radicle, 5 d post-imbibit... 327 1e-96
- emb|AW348348|AW348348 GM210002A13A5R Gm-r1021 Glycine max cDNA 3... 328 2e-96
- 25 emb|AW441243|AW441243 EST310639 tomato fruit red ripe, TAMU Lyco... 324 1e-95
- emb|AW223973|AW223973 EST300784 tomato fruit red ripe, TAMU Lyco... 321 7e-95
- emb|AW931569|AW931569 EST357412 tomato fruit mature green, TAMU ... 328 2e-94
- emb|AW218871|AW218871 EST301353 tomato root during/after fruit s... 327 8e-94
- 30 emb|AL116444|CNS01D6S Botrytis cinerea strain T4 cDNA library un... 267 4e-93
- emb|AW831561|AW831561 sm34f06.y1 Gm-c1028 Glycine max cDNA clone... 312 2e-92
- emb|AI484151|AI484151 EST248958 tomato resistant, Cornell Lycope... 264 3e-91
- emb|AW925414|AW925414 HVSMEg0001L02 Hordeum vulgare pre-anthesis... 299 6e-91
- emb|AI731594|AI731594 BNLGHi10182 Six-day Cotton fiber Gossypium... 335 7e-91
- 35 emb|AW730597|AW730597 GA__Ea0027H02 Gossypium arboreum 7-10 dpa ... 333 1e-90
- emb|AW647665|AW647665 EST307143 tomato germinating seedlings, TA... 317 1e-90
- emb|AW395111|AW395111 sh40a06.y1 Gm-c1017 Glycine max cDNA clone... 303 6e-90
- emb|AI725588|AI725588 BNLGHi12376 Six-day Cotton fiber Gossypium... 288 1e-89
- emb|AW934656|AW934656 EST353548 tomato flower buds 0-3 mm, Corne... 328 2e-89
- 40 emb|AW757478|AW757478 874001D11.y1 C. reinhardtii CC-1690, Lambd... 202 3e-89
- emb|AW725897|AW725897 GA__Ea0020B06 Gossypium arboreum 7-10 dpa ... 328 8e-89
- emb|AW647757|AW647757 EST326211 tomato germinating seedlings, TA... 301 1e-88
- emb|AW509174|AW509174 sh92b04.y1 Gm-c1016 Glycine max cDNA clone... 297 4e-88
- emb|AW666654|AW666654 GA__Ea0005E11 Gossypium arboreum 7-10 dpa ... 279 7e-88
- 45 emb|AL114553|CNS01BQ9 Botrytis cinerea strain T4 cDNA library un... 231 3e-87
- gb|BE021489|BE021489 sm59b05.y1 Gm-c1028 Glycine max cDNA clone ... 322 5e-87
- emb|AW507801|AW507801 si45c02.y1 Gm-r1030 Glycine max cDNA clone... 259 2e-86
- emb|AW733916|AW733916 sk85a11.y1 Gm-c1035 Glycine max cDNA clone... 306 2e-86
- emb|AW096468|AW096468 EST289648 tomato mixed elicitor, BTI Lycop... 292 6e-86
- 50 emb|AW156741|AW156741 se30b08.y1 Gm-c1015 Glycine max cDNA clone... 184 1e-85
- emb|AI729625|AI729625 BNLGHi13824 Six-day Cotton fiber Gossypium... 276 4e-85
- emb|AW034214|AW034214 EST277785 tomato callus, TAMU Lycopersicon... 304 5e-85
- emb|AJ273864|AJ273864 AJ273864 Metarhizium anisopliae ARSEF 2575... 184 1e-84
- emb|AI775647|AI775647 EST256747 tomato resistant, Cornell Lycope... 297 1e-84
- 55 emb|AI822682|AI822682 L0-1204T3 Ice plant Lambda Uni-Zap XR expr... 314 2e-84
- emb|AW625107|AW625107 EST313924 tomato radicle, 5 d post-imbibit... 314 2e-84
- emb|AI726147|AI726147 BNLGHi5085 Six-day Cotton fiber Gossypium ... 263 6e-83
- emb|AW755396|AW755396 sl03d11.y1 Gm-c1036 Glycine max cDNA clone... 306 3e-82
- emb|AI728088|AI728088 BNLGHi9938 Six-day Cotton fiber Gossypium ... 259 5e-82
- 60 emb|AW979992|AW979992 EST310378 tomato root deficiency, Cornell ... 285 8e-82
- emb|AW333018|AW333018 S16C3 AGS-1 Pneumocystis carinii f. sp. ca... 278 1e-81

- emb|AI780394|AI780394 EST261273 tomato susceptible, Cornell Lyco... 284 2e-81
 emb|AW691046|AW691046 NF037A12ST1F1000 Developing stem Medicago ... 266 2e-81
 emb|AW924717|AW924717 WS1_71_A04.b1_A002 Water-stressed 1 (WS1) ... 303 3e-81
 emb|AI731287|AI731287 BNLGHi9093 Six-day Cotton fiber Gossypium ... 262 5e-81
 5 emb|AW760027|AW760027 sl57b04.y1 Gm-cl027 Glycine max cDNA clone... 301 1e-80
 emb|AW667101|AW667101 GA__Ea0007F21 Gossypium arboreum 7-10 dpa ... 300 2e-80
 emb|AW622023|AW622023 EST312821 tomato root during/after fruit s... 280 4e-80
 emb|AV388663|AV388663 AV388663 Chlamydomonas reinhardtii C9 Chla... 284 8e-80
 emb|AW650428|AW650428 EST328882 tomato germinating seedlings, TA... 278 4e-79
 10 emb|AI775628|AI775628 EST256728 tomato resistant, Cornell Lycops... 295 7e-79
 gb|BE024093|BE024093 sm96f04.y1 Gm-cl015 Glycine max cDNA clone ... 293 2e-78
 emb|AJ273749|AJ273749 AJ273749 Metarhizium anisopliae ARSEF 2575... 256 1e-77
 emb|AW737446|AW737446 EST338789 tomato flower buds, anthesis, Co... 290 2e-77

15

Query= Y14251.4_i_at 16053_i_at /id_source genbank /description
 emb|caa74639.1| (y14251) glutathione s-transferase [arabidopsis
 thaliana] /blast_score 1.00e-110 /ec_number /family transferase /chip
 nova /gb_link

20

[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|y14251|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|y14251|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|y14251|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?y14251>
 (630 letters)

25

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

30

Score E
 Sequences producing significant alignments: (bits) Value

- emb|X78203|HMGST H.muticus mRNA for glutathione S-transferase. 271 4e-72
 emb|AW727692|AW727692 GA__Ea0015I24 Gossypium arboreum 7-10 dpa ... 146 9e-71
 35 emb|AF002692|AF002692 Solanum commersonii glutathione S-transfer... 264 3e-70
 dbj|D10524|TOBPARB Nicotiana tabacum mRNA for glutathione S-tran... 262 2e-69
 emb|AW731360|AW731360 GA__Ea0030G14 Gossypium arboreum 7-10 dpa ... 142 3e-69
 dbj|D29680|TOBAPI2B Tobacco api2 mRNA (which expression is induc... 261 4e-69
 emb|AW220064|AW220064 EST302547 tomato root during/after fruit s... 260 5e-69
 40 emb|Z71749|NPGSTMR N.plumbaginifolia mRNA for glutathione S-tran... 260 8e-69
 emb|AI774583|AI774583 EST255683 tomato resistant, Cornell Lycops... 258 3e-68
 emb|AW728413|AW728413 GA__Ea0016J18 Gossypium arboreum 7-10 dpa ... 142 7e-68
 emb|AI725552|AI725552 BNLGHi12077 Six-day Cotton fiber Gossypium... 142 4e-67
 emb|AI728937|AI728937 BNLGHi12090 Six-day Cotton fiber Gossypium... 142 4e-67
 45 gb|BE033971|BE033971 MG02G09 MG Mesembryanthemum crystallinum cD... 228 2e-65
 emb|AW735791|AW735791 EST336559 tomato flower buds 0-3 mm, Corne... 248 2e-65
 emb|AF242309|AF242309 Euphorbia esula glutathione S-transferase ... 130 3e-62
 emb|AW726844|AW726844 GA__Ea0022O11 Gossypium arboreum 7-10 dpa ... 140 5e-61
 emb|AI726215|AI726215 BNLGHi5300 Six-day Cotton fiber Gossypium ... 142 5e-61
 50 emb|AW218151|AW218151 EST303332 tomato radicle, 5 d post-imbibit... 232 1e-60
 emb|AW728876|AW728876 GA__Ea0028P14 Gossypium arboreum 7-10 dpa ... 147 2e-60
 gb|M84968|SIPGTSTF Silene cucubalus glutathione-S-transferase mR... 115 5e-59
 emb|AF133894|AF133894 Persea americana glutathione S-transferase... 220 8e-57
 emb|AI352770|AI352770 MB58-4B PZ204.BNlib Brassica napus cDNA cl... 174 7e-55
 55 emb|AW040790|AW040790 EST283654 tomato mixed elicitor, BTI Lycop... 210 6e-54
 emb|AW649890|AW649890 EST328344 tomato germinating seedlings, TA... 202 2e-51
 emb|AW862639|AW862639 00097 leafy spurge Lambda HybriZAP 2.1 two... 128 2e-48
 emb|AI943409|AI943409 MF02B7 MF Mesembryanthemum crystallinum cD... 190 1e-47
 emb|AV411409|AV411409 AV411409 Lotus japonicus young plants (two... 187 6e-47
 60 emb|AW684286|AW684286 NF015A06NR1F1000 Nodulated root Medicago t... 186 1e-46
 emb|AW039384|AW039384 EST281641 tomato mixed elicitor, BTI Lycop... 185 2e-46

- gb|BE033640|BE033640 MF05D04 MF Mesembryanthemum crystallinum cD... 185 2e-46
emb|AW777169|AW777169 Str3-D4 Sugar Beet germination cDNA librar... 185 3e-46
emb|AW667591|AW667591 GA_Ea0009N18 Gossypium arboreum 7-10 dpa ... 112 4e-46
emb|AV414359|AV414359 AV414359 Lotus japonicus young plants (two... 182 2e-45
5 gb|BE034473|BE034473 MH05E04 MH Mesembryanthemum crystallinum cD... 181 4e-45
gb|BE033466|BE033466 ME02E04 ME Mesembryanthemum crystallinum cD... 170 7e-45
emb|AW623451|AW623451 EST321396 tomato flower buds 3-8 mm, Corne... 179 2e-44
emb|AV408851|AV408851 AV408851 Lotus japonicus young plants (two... 173 9e-43
emb|AV417287|AV417287 AV417287 Lotus japonicus young plants (two... 173 9e-43
10 emb|AI486597|AI486597 EST244918 tomato ovary, TAMU Lycopersicon ... 173 1e-42
emb|AV417605|AV417605 AV417605 Lotus japonicus young plants (two... 172 2e-42
emb|AW667380|AW667380 GA_Ea0009C08 Gossypium arboreum 7-10 dpa ... 147 2e-42
gb|C96149|C96149 C96149 Marchantia polymorpha immature sex organ... 145 1e-41
emb|AI054936|AI054936 c0au0002J02 Cotton Boll Abscission Zone cD... 142 2e-40
15 dbj|D49526|TOBPBARBA Tobacco chimeric parB promoter/beta-glucuron... 163 1e-39
emb|AI774099|AI774099 EST255199 tomato resistant, Cornell Lycope... 163 1e-39
emb|AV418074|AV418074 AV418074 Lotus japonicus young plants (two... 160 6e-39
gb|BE020725|BE020725 sm52b05.y1 Gm-cl028 Glycine max cDNA clone ... 148 5e-38
emb|AI162894|AI162894 A026P40U Hybrid aspen plasmid library Popu... 155 4e-37
20 emb|Y07721|PHGLSTRAN P.hybrida mRNA for glutathione S-transferase. 151 5e-36
gb|BE053268|BE053268 GA_Ea0035A09f Gossypium arboreum 7-10 dpa ... 137 7e-36
gb|M84969|SIPGTSTFA Silene cucubalus glutathione-S-transferase g... 78 1e-35
emb|AW507753|AW507753 si44f10.y1 Gm-r1030 Glycine max cDNA clone... 149 2e-35
emb|AW596451|AW596451 sj12e11.y1 Gm-cl032 Glycine max cDNA clone... 149 2e-35
25 emb|AW926756|AW926756 HVSMEg0008B23 Hordeum vulgare pre-anthesis... 92 3e-35
emb|AJ279691|BPE279691 Betula pendula partial mRNA for glutathio... 144 8e-34
emb|AV427165|AV427165 AV427165 Lotus japonicus young plants (two... 142 3e-33
emb|AJ010451|AMY010451 Alopecurus myosuroides mRNA for glutathio... 97 4e-33
emb|AF184059|AF184059 Triticum aestivum glutathione S-transferas... 81 5e-33
30 emb|AW164336|AW164336 se71b09.y1 Gm-cl023 Glycine max cDNA clone... 139 1e-32
emb|AJ010454|AMY010454 Alopecurus myosuroides mRNA for glutathio... 95 2e-32
emb|AJ010452|AMY010452 Alopecurus myosuroides mRNA for glutathio... 94 3e-32
emb|AW678048|AW678048 WS1_13_A09.b1_A002 Water-stressed 1 (WS1) ... 84 3e-32
gb|BE021219|BE021219 sm56c09.y1 Gm-cl028 Glycine max cDNA clone ... 99 7e-32
35 emb|AW561921|AW561921 IPPGHZ0010 Cotton fiber and embryo Lambda ... 137 7e-32
emb|AW458936|AW458936 sh16g07.y1 Gm-cl016 Glycine max cDNA clone... 137 7e-32
emb|AW218152|AW218152 EST303333 tomato radicle, 5 d post-imbibit... 137 1e-31
emb|AV426478|AV426478 AV426478 Lotus japonicus young plants (two... 137 1e-31
emb|AI823144|AI823144 L30-1027T3 Ice plant Lambda Uni-Zap XR exp... 112 4e-31
40 emb|AI823131|AI823131 L30-1014T3 Ice plant Lambda Uni-Zap XR exp... 112 4e-31
gb|BE058603|BE058603 sn18c06.y1 Gm-cl016 Glycine max cDNA clone ... 134 5e-31
emb|AI773198|AI773198 EST254298 tomato resistant, Cornell Lycope... 133 1e-30
emb|AI778224|AI778224 EST259103 tomato susceptible, Cornell Lyco... 111 2e-30
emb|AW745644|AW745644 WS1_36_D11.b1_A002 Water-stressed 1 (WS1) ... 84 4e-30
45 emb|AW279568|AW279568 sf95d06.y1 Gm-cl019 Glycine max cDNA clone... 131 4e-30
emb|AW054044|AW054044 L30-2014T3 Ice plant Lambda Uni-Zap XR exp... 106 3e-29
emb|AW202090|AW202090 sf11a03.y1 Gm-cl027 Glycine max cDNA clone... 106 1e-28
emb|AI440830|AI440830 sa86f05.y1 Gm-cl004 Glycine max cDNA clone... 126 1e-28
emb|AW678628|AW678628 WS1_1_B05.b1_A002 Water-stressed 1 (WS1) S... 85 2e-28
50 emb|AW677650|AW677650 WS1_10_F04.b1_A002 Water-stressed 1 (WS1) ... 80 6e-28
emb|AW678706|AW678706 WS1_1_B05.b2_A002 Water-stressed 1 (WS1) S... 85 8e-28
emb|AW677798|AW677798 WS1_11_H05.b1_A002 Water-stressed 1 (WS1) ... 76 2e-27
emb|AW053375|AW053375 L30-1572T3 Ice plant Lambda Uni-Zap XR exp... 99 2e-27
emb|AV426523|AV426523 AV426523 Lotus japonicus young plants (two... 122 2e-27
55 emb|AV427075|AV427075 AV427075 Lotus japonicus young plants (two... 122 2e-27
emb|AV415440|AV415440 AV415440 Lotus japonicus young plants (two... 122 2e-27
emb|AT000441|AT000441 AT000441 Brassica rapa guard cell Brassica... 122 3e-27
emb|AI442436|AI442436 sa26h04.y1 Gm-cl004 Glycine max cDNA clone... 111 4e-27
gb|BE034032|BE034032 MG03G03 MG Mesembryanthemum crystallinum cD... 90 6e-26
60 emb|AW689646|AW689646 NF022G04ST1F1000 Developing stem Medicago ... 66 3e-25
gb|BE060798|BE060798 HVSMEg0013G13f Hordeum vulgare pre-anthesis... 92 6e-25

gb|BE060847|BE060847 HVSMeg0013J11f Hordeum vulgare pre-anthesis... 64 3e-24
 emb|AW171715|AW171715 N100609e rootphos(-) Medicago truncatula c... 112 3e-24
 emb|AW348131|AW348131 GM210001A21A6R Gm-r1021 Glycine max cDNA 3... 98 4e-24
 emb|AW680604|AW680604 WS1_6_C03.b1_A002 Water-stressed 1 (WS1) S... 84 4e-24
 5 emb|AI352728|AI352728 MB47-17 PZ204.BNlib Brassica napus cDNA cl... 110 1e-23
 emb|AW127163|AW127163 M110099 GVN Medicago truncatula cDNA clone... 110 1e-23
 emb|AW924273|AW924273 WS1_51_A04.b1_A002 Water-stressed 1 (WS1) ... 95 1e-23
 emb|AW680779|AW680779 WS1_7_D01.b1_A002 Water-stressed 1 (WS1) S... 97 1e-23
 emb|AI444064|AI444064 sa31g12.y1 Gm-c1004 Glycine max cDNA clone... 109 2e-23
 10 emb|AW459151|AW459151 sh21c07.y1 Gm-c1016 Glycine max cDNA clone... 66 6e-23

Query= X77500.2_at 16522_at /id_source genbank /description
 emb|caa54631.1| (x77500) amino acid transporter [arabidopsis thaliana]
 15 /blast_score 0 /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|x77500|/ncgi
 http://www.ncgr.org/cgi-bin/ff?x77500
 (1619 letters)

20 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

25 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

30 emb|AJ007574|RCO7574 Ricinus communis mRNA for amino acid carrier. 410 0.0
 emb|Y09591|VFAMACTRA V.faba mRNA for amino acid transporter. 392 0.0
 emb|AJ132228|RCO132228 Ricinus communis mRNA for amino acid carr... 342 0.0
 emb|AF080543|AF080543 Nepenthes alata amino acid transporter (AA... 641 0.0
 emb|Y09826|STAAP2 S.tuberosum mRNA for amino acid transporter AA... 354 0.0
 emb|AF080544|AF080544 Nepenthes alata amino acid transporter (AA... 596 0.0
 35 emb|Y09825|STAAP1 S.tuberosum mRNA for amino acid transporter AA... 288 e-158
 emb|Z68759|RCAACMR R.communis mRNA for amino acid carrier. 334 e-155
 emb|AF080542|AF080542 Nepenthes alata amino acid transporter (AA... 239 e-145
 emb|AF061435|AF061435 Vicia faba amino acid transporter b (AAPB)... 501 e-141
 emb|Y11121|RCAACARR Ricinus communis mRNA for amino acid carrier... 264 e-123
 40 emb|AF061434|AF061434 Vicia faba amino acid transporter a (AAPA)... 290 e-107
 emb|AF061436|AF061436 Vicia faba amino acid transporter c (AAPC)... 259 5e-95
 emb|AW560155|AW560155 EST315203 DSIR Medicago truncatula cDNA cl... 293 4e-86
 emb|AW203255|AW203255 sf27a03.y1 Gm-c1028 Glycine max cDNA clone... 312 4e-84
 emb|AI166826|AI166826 xylem.est.62 Poplar xylem Lambda ZAPII lib... 188 2e-68
 45 emb|AW648039|AW648039 EST326493 tomato germinating seedlings, TA... 226 2e-67
 emb|AI974813|AI974813 T113295e KV2 Medicago truncatula cDNA clon... 153 2e-66
 emb|AW926173|AW926173 HVSMeg0006I08 Hordeum vulgare pre-anthesis... 243 3e-66
 emb|AW648857|AW648857 EST327311 tomato germinating seedlings, TA... 219 3e-65
 emb|AV428014|AV428014 AV428014 Lotus japonicus young plants (two... 248 6e-65
 50 emb|AW277711|AW277711 sf85f01.y1 Gm-c1019 Glycine max cDNA clone... 242 5e-63
 emb|AW774110|AW774110 EST333340 KV3 Medicago truncatula cDNA clo... 238 7e-62
 emb|AW720246|AW720246 LjNEST17f12r Lotus japonicus nodule librar... 235 6e-61
 emb|AI930612|AI930612 sb37c02.y1 Gm-c1013 Glycine max cDNA clone... 167 5e-60
 emb|AW399595|AW399595 EST310095 L. pennellii trichome, Cornell U... 192 8e-58
 55 emb|AW737124|AW737124 EST338551 tomato flower buds, anthesis, Co... 217 2e-55
 emb|AW691461|AW691461 NF045C01ST1F1000 Developing stem Medicago ... 206 7e-55
 emb|AW432416|AW432416 sh73f10.y1 Gm-c1015 Glycine max cDNA clone... 89 8e-51
 emb|AW255060|AW255060 ML1355 peppermint glandular trichome Menth... 111 1e-50
 emb|AW685782|AW685782 NF035B03NR1F1000 Nodulated root Medicago t... 201 1e-50
 60 gb|BE125804|BE125804 DG1_57_F07.b1_A002 Dark Grown 1 (DG1) Sorgh... 178 3e-50
 emb|AW307506|AW307506 sf57g11.y1 Gm-c1009 Glycine max cDNA clone... 181 2e-49

- emb|AW349599|AW349599 GM210005A21G12R Gm-r1021 Glycine max cDNA ... 140 5e-49
- emb|AI487167|AI487167 EST245489 tomato ovary, TAMU Lycopersicon ... 122 2e-48
- emb|AW737784|AW737784 EST339211 tomato flower buds, anthesis, Co... 192 6e-48
- 5 emb|AW309945|AW309945 sf27a03.x1 Gm-c1028 Glycine max cDNA clone... 149 5e-47
- emb|AW738557|AW738557 EST339984 tomato flower buds, anthesis, Co... 188 8e-47
- emb|AQ842052|AQ842052 T134338 Soybean RFLP probe Glycine max gen... 148 2e-44
- emb|AF074703|AF074703 Glycine max pA381 marker, sequence tagged ... 149 1e-43
- emb|AW649763|AW649763 EST328217 tomato germinating seedlings, TA... 127 3e-43
- 10 gb|BE022301|BE022301 sm73b09.y1 Gm-c1028 Glycine max cDNA clone ... 176 4e-43
- emb|AW597381|AW597381 si92b03.y1 Gm-c1031 Glycine max cDNA clone... 175 1e-42
- emb|AW310916|AW310916 sg29h08.x1 Gm-c1024 Glycine max cDNA clone... 172 5e-42
- emb|AW306512|AW306512 se51h04.y1 Gm-c1017 Glycine max cDNA clone... 140 1e-41
- emb|AW395873|AW395873 sh01d01.y1 Gm-c1026 Glycine max cDNA clone... 112 4e-41
- 15 emb|AW201454|AW201454 sf03c12.y1 Gm-c1027 Glycine max cDNA clone... 127 9e-41
- emb|AW684816|AW684816 NF021D09NR1F1000 Nodulated root Medicago t... 164 2e-39
- emb|AZ051221|AZ051221 Gm_UMb001_166_P11R UMN Soybean BAC Library... 159 7e-38
- emb|AI779305|AI779305 EST260184 tomato susceptible, Cornell Lyco... 155 1e-36
- emb|AI779304|AI779304 EST260183 tomato susceptible, Cornell Lyco... 155 1e-36
- 20 emb|AW830977|AW830977 sm31a10.y1 Gm-c1028 Glycine max cDNA clone... 149 4e-35
- emb|AW096758|AW096758 EST289938 tomato mixed elicitor, BTI Lycop... 147 3e-34
- emb|AJ004829|STAJ4829 Solanum tuberosum fdh3 pseudogene. 110 3e-33
- emb|AQ841805|AQ841805 T134055 Soybean RFLP probe Glycine max gen... 140 2e-32
- emb|AW736648|AW736648 EST333140 KV3 Medicago truncatula cDNA clo... 138 1e-31
- 25 emb|AV418629|AV418629 AV418629 Lotus japonicus young plants (two... 130 3e-29
- emb|AW442349|AW442349 EST311745 tomato fruit red ripe, TAMU Lyco... 130 3e-29
- emb|AW738564|AW738564 EST339991 tomato flower buds, anthesis, Co... 104 7e-29
- emb|AW561095|AW561095 EST316143 DSIR Medicago truncatula cDNA cl... 126 6e-28
- emb|AW234791|AW234791 sf19c06.y1 Gm-c1028 Glycine max cDNA clone... 124 2e-27
- 30 gb|U31932|NSU31932 Nicotiana sylvestris amino acid permease 1 (N... 61 3e-27
- emb|AI441371|AI441371 sa64f02.y1 Gm-c1004 Glycine max cDNA clone... 72 2e-26
- emb|AW438003|AW438003 ST83D04 Pine TriplEx shoot tip library Pin... 111 2e-23
- emb|AW056573|AW056573 ST52G03 Pine TriplEx shoot tip library Pin... 109 8e-23
- emb|AW923686|AW923686 DG1_57_F07.g1_A002 Dark Grown 1 (DG1) Sorg... 107 3e-22
- 35 emb|AW924285|AW924285 WS1_52_F10.b1_A002 Water-stressed 1 (WS1) ... 106 5e-22
- emb|AJ238635|CPR238635 Chlorella protothecoides partial mRNA for... 75 4e-20
- emb|AW102174|AW102174 sd84c08.y1 Gm-c1009 Glycine max cDNA clone... 100 6e-20
- emb|AW102244|AW102244 sd85c02.y1 Gm-c1009 Glycine max cDNA clone... 92 1e-17
- emb|AW620352|AW620352 sj04b02.y1 Gm-c1032 Glycine max cDNA clone... 92 1e-17
- 40 emb|AW288077|AW288077 N100921e rootphos(-) Medicago truncatula c... 84 2e-15
- emb|AW396191|AW396191 sh02e09.y1 Gm-c1026 Glycine max cDNA clone... 57 2e-14
- emb|AI773761|AI773761 EST254861 tomato resistant, Cornell Lycope... 65 2e-12
- gb|BE020684|BE020684 sm45f08.y1 Gm-c1028 Glycine max cDNA clone ... 74 3e-12
- emb|AF014810|AF014810 Lycopersicon esculentum proline transporte... 54 9e-12
- 45 emb|AI728355|AI728355 BNLGHi10544 Six-day Cotton fiber Gossypium... 70 4e-11
- emb|AW780460|AW780460 sl71b05.y1 Gm-c1027 Glycine max cDNA clone... 70 6e-11
- emb|AF014808|AF014808 Lycopersicon esculentum proline transporte... 55 5e-09
- emb|AF014809|AF014809 Lycopersicon esculentum proline transporte... 52 2e-08
- emb|AW832495|AW832495 sm11e04.y1 Gm-c1027 Glycine max cDNA clone... 60 2e-08
- 50 emb|AW563318|AW563318 LG1_228_A07.g1_A002 Light Grown 1 (LG1) So... 48 2e-07
- gb|U64823|NSU64823 Nicotiana sylvestris amino acid permease (nsa... 37 2e-06
- emb|AI489487|AI489487 EST247826 tomato ovary, TAMU Lycopersicon ... 52 1e-05
- emb|AV417239|AV417239 AV417239 Lotus japonicus young plants (two... 52 1e-05
- emb|AI772468|AI772468 EST253568 tomato resistant, Cornell Lycope... 52 1e-05
- 55 gb|BE023644|BE023644 sm83e05.y1 Gm-c1015 Glycine max cDNA clone ... 51 2e-05
- emb|AW102341|AW102341 sd86d12.y1 Gm-c1009 Glycine max cDNA clone... 49 9e-05
- emb|AW560837|AW560837 EST315885 DSIR Medicago truncatula cDNA cl... 47 3e-04
- emb|AW720608|AW720608 LjNEST20d11rc Lotus japonicus nodule libra... 47 4e-04
- emb|AW720138|AW720138 LjNEST15d10r Lotus japonicus nodule librar... 47 4e-04
- 60 emb|AV409658|AV409658 AV409658 Lotus japonicus young plants (two... 47 4e-04
- emb|AW691465|AW691465 NF045C04ST1F1000 Developing stem Medicago ... 44 8e-04

	emb AW428965 AW428965 EST306505 tomato flower buds 0-3 mm, Corne...	35	0.001
	emb AJ004959 CAA004959 Cicer arietinum mRNA for hypothetical pro...	45	0.002
	emb AW757005 AW757005 sl02a06.y1 Gm-cl036 Glycine max cDNA clone...	45	0.002
	emb Z49501 SCYJR001W S.cerevisiae chromosome X reading frame ORF...	44	0.003
5	emb X87611 SCXCOSM83 S.cerevisiae chromosome X DNA (cosmid 83).	44	0.003
	emb AW677443 AW677443 DG1_7_D10.b1_A002 Dark Grown 1 (DG1) Sorgh...	44	0.004
	emb AQ841996 AQ841996 T134282 Soybean RFLP probe Glycine max gen...	44	0.004
10	Query= AL049500.57_s_at 16914_s_at /id_source genbank /description emb cab39936.1 (al049500) osmotin precursor [arabidopsis thaliana] /blast_score 1.00e-143 /ec_number /family /chip nova /gb_link /ncgi (735 letters)		
15	Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching.....done		
20	Score E		
	Sequences producing significant alignments:	(bits)	Value
	emb AW685448 AW685448 NF029F08NR1F1000 Nodulated root Medicago t...	409	e-114
	emb AJ010501 CAR010501 Cicer arietinum L. mRNA for thaumatin-lik...	409	e-114
25	emb AW573922 AW573922 EST316513 GVN Medicago truncatula cDNA clo...	409	e-113
	emb AW685184 AW685184 NF026H08NR1F1000 Nodulated root Medicago t...	338	e-105
	emb AW348587 AW348587 GM210002B22C8R Gm-r1021 Glycine max cDNA 3...	365	e-101
	emb AW685583 AW685583 NF029C04NR1F1000 Nodulated root Medicago t...	320	e-100
	emb X15224 NTE22TLP Tobacco E22 gene for a thaumatin-like protein.	201	4e-99
30	emb X12739 NTPRRMAJ N. tabacum mRNA for pathogenesis-related pro...	201	4e-99
	emb AF003007 AF003007 Vitis vinifera thaumatin-like protein VVTL...	214	7e-98
	emb X15223 NTE2TLP Tobacco E2 gene for a thaumatin-like protein.	195	2e-97
	emb X03913 NTTHAUR Tobacco mRNA for TMV induced protein homologo...	195	2e-97
	emb AW684755 AW684755 NF021G01NR1F1000 Nodulated root Medicago t...	348	3e-95
35	emb AV428977 AV428977 AV428977 Lotus japonicus young plants (two...	343	7e-94
	emb Y10992 VVOSM1 V.vinifera mRNA for osmotin-like protein.	224	3e-90
	emb AF199508 AF199508 Fragaria x ananassa osmotin-like protein (...)	220	1e-89
	emb X72928 SC13OLP S.commersonii (pOSML13) gene for osmotin-like...	200	1e-88
	emb X67121 SCOSMLP S.commersonii mRNA for osmotin-like protein.	200	1e-88
40	emb X70787 LEPRPA L.esculentum pr p23 mRNA for pathogenesis-rela...	200	1e-88
	emb AW039873 AW039873 EST282346 tomato mixed elicitor, BTI Lycop...	200	1e-88
	emb X66416 LETPM1M L.esculentum tpm 1 mRNA.	199	1e-88
	emb AW218786 AW218786 EST301266 tomato root during/after fruit s...	197	9e-88
	dbj D76437 TOBNP50 Nicotiana sylvestris DNA for neutral PR-5 (os...	193	8e-87
45	emb X95308 NTOSPR N.tabacum osmotin gene.	195	8e-87
	gb S40046 S40046 abscisic acid-activated [Nicotiana tabacum L.=t...	195	1e-86
	emb X65701 NTAP24G N.tabacum ap24 gene.	195	1e-86
	emb X65700 NTAP24 N.tabacum mRNA ap24.	195	1e-86
	gb S44889 S44889 osmotin=pathogenesis-related protein homolog [N...	195	1e-86
50	emb A16782 A16782 osmotin-like protein gene without 20 C- termin...	195	1e-86
	emb A16780 A16780 osmotin-like protein gene seq ID No: 5.	195	1e-86
	emb A83550 A83550 Sequence 1 from Patent WO9849331.	195	1e-86
	gb M64081 TOBOLP Nicotiana tabacum osmotin-like protein (OLP1) m...	193	1e-86
	dbj E03321 E03321 DNA encoding osmotin-like protein.	193	1e-86
55	emb X72927 SC81OLP S.commersonii (pOSML81) gene for osmotin-like...	193	7e-86
	emb AW218785 AW218785 EST301265 tomato root during/after fruit s...	200	7e-86
	emb AF093743 AF093743 Lycopersicon esculentum pathogenesis-relat...	193	1e-85
	gb M21346 TOMNP24 Tomato NP24 protein mRNA, 3' end.	193	1e-85
	emb AW035171 AW035171 EST280433 tomato callus, TAMU Lycopersicon...	193	1e-85
60	emb AW223970 AW223970 EST300781 tomato fruit red ripe, TAMU Lyco...	193	1e-85
	emb AW223507 AW223507 EST300318 tomato fruit red ripe, TAMU Lyco...	193	1e-85

- emb|AW222204|AW222204 EST299015 tomato fruit red ripe, TAMU Lyco... 193 1e-85
emb|AW217005|AW217005 EST295719 tomato callus, TAMU Lycopersicon... 193 1e-85
emb|AW622159|AW622159 EST312957 tomato root during/after fruit s... 193 1e-85
emb|AW684839|AW684839 NF022B04NR1F1000 Nodulated root Medicago t... 316 1e-85
5 emb|AI855542|AI855542 sc20e11.y1 Gm-cl013 Glycine max cDNA clone... 185 1e-85
emb|X67244|CSOSLP S.commersonii mRNA for osmotin-like protein. 193 2e-85
emb|AW216590|AW216590 EST295304 tomato callus, TAMU Lycopersicon... 193 3e-85
emb|X72926|SCA81OLP S.commersonii (pA81) mRNA for osmotin-like p... 189 6e-85
emb|AF001528|AF001528 Musa acuminata ripening-associated protein... 307 8e-85
10 emb|AW622107|AW622107 EST312905 tomato root during/after fruit s... 192 9e-85
emb|AW218972|AW218972 EST301454 tomato root during/after fruit s... 191 1e-84
emb|AW033829|AW033829 EST277400 tomato callus, TAMU Lycopersicon... 193 2e-84
emb|AW221921|AW221921 EST298732 tomato fruit red ripe, TAMU Lyco... 187 4e-84
emb|AF109653|AF109653 AF109653 Capsicum annuum root susceptible ... 192 9e-84
15 emb|AW621924|AW621924 EST312722 tomato root during/after fruit s... 192 2e-83
emb|AW650675|AW650675 EST329129 tomato germinating seedlings, TA... 193 1e-82
emb|AW034088|AW034088 EST277583 tomato callus, TAMU Lycopersicon... 193 1e-81
emb|AW219330|AW219330 EST301812 tomato root during/after fruit s... 193 1e-81
emb|AW034433|AW034433 EST278004 tomato callus, TAMU Lycopersicon... 175 2e-80
20 emb|AI895910|AI895910 EST265353 tomato callus, TAMU Lycopersicon... 177 3e-80
emb|AW625009|AW625009 EST313838 tomato radicle, 5 d post-imbibit... 193 4e-80
emb|AI896330|AI896330 EST265773 tomato callus, TAMU Lycopersicon... 193 4e-80
emb|AJ277064|LES277064 Lycopersicon esculentum PR-5 gene for pat... 192 3e-79
gb|M29279|TOBOSM N.tabacum osmotin mRNA, complete cds. 242 4e-79
25 emb|AW029746|AW029746 EST273001 tomato callus, TAMU Lycopersicon... 168 2e-78
emb|AW029798|AW029798 EST273053 tomato callus, TAMU Lycopersicon... 168 2e-78
emb|AW650717|AW650717 EST329171 tomato germinating seedlings, TA... 165 2e-77
emb|AW094053|AW094053 EST287233 tomato mixed elicitor, BTI Lycop... 166 3e-77
emb|X61679|NTOSMOTIN N.tabacum mRNA for osmotin. 193 8e-77
30 emb|AW686653|AW686653 NF043G01NR1F1000 Nodulated root Medicago t... 265 1e-76
emb|AW220061|AW220061 EST302544 tomato root during/after fruit s... 193 1e-76
emb|AW830631|AW830631 sm04e12.y1 Gm-cl027 Glycine max cDNA clone... 230 2e-76
emb|AW099440|AW099440 sd40e08.y1 Gm-cl016 Glycine max cDNA clone... 227 2e-76
emb|AW458142|AW458142 sh78g09.y1 Gm-cl016 Glycine max cDNA clone... 185 2e-75
35 emb|AJ131731|PME131731 Pseudotsuga menziesii mRNA for Thaumatin-... 237 3e-74
gb|BE033983|BE033983 MG02H11 MG Mesembryanthemum crystallinum cD... 155 2e-73
gb|BE034303|BE034303 MH03A01 MH Mesembryanthemum crystallinum cD... 139 4e-73
emb|AW686245|AW686245 NF035F09NR1F1000 Nodulated root Medicago t... 274 7e-73
emb|A15671|A15671 proprothaumatine. 116 4e-72
40 gb|J01209|TDATHAU2 T.daniellii preprothaumatin-2 mRNA, complete ... 116 4e-72
emb|A15673|A15673 proprothaumatine and the coding strand of its ... 116 4e-72
emb|A15677|A15677 proprothaumatine and the coding stand of its s... 116 4e-72
emb|AF110151|AF110151 AF110151 Capsicum annuum root 1st-branched... 192 4e-72
emb|A15675|A15675 proprothaumatine and the coding strand of its ... 116 2e-71
45 emb|A15660|A15660 Mature thaumatin. 116 2e-71
emb|A46806|A46806 Sequence 3 from Patent EP0684312. 115 5e-71
emb|AF121776|AF121776 Juniperus ashei allergen Jun a 3 mRNA, com... 144 1e-70
emb|AF016327|AF016327 Hordeum vulgare Barperml (perml) mRNA, par... 221 3e-70
emb|AW031249|AW031249 EST274624 tomato callus, TAMU Lycopersicon... 200 3e-70
50 emb|AI896554|AI896554 EST265997 tomato callus, TAMU Lycopersicon... 140 5e-70
emb|AF108890|AF108890 AF108890 Capsicum annuum root 1st-branched... 177 9e-70
emb|AV423642|AV423642 AV423642 Lotus japonicus young plants (two... 263 1e-69
emb|AI055586|AI055586 coau0004G15 Cotton Boll Abscission Zone cD... 262 2e-69
emb|AW032915|AW032915 EST276474 tomato callus, TAMU Lycopersicon... 200 2e-69
55 emb|A46810|A46810 Sequence 7 from Patent EP0684312. 108 1e-68
emb|AW441774|AW441774 EST311170 tomato fruit red ripe, TAMU Lyco... 193 1e-68
emb|AW223623|AW223623 EST300434 tomato fruit red ripe, TAMU Lyco... 193 1e-68
emb|AW032317|AW032317 EST275771 tomato callus, TAMU Lycopersicon... 193 1e-68
emb|AW224329|AW224329 EST301140 tomato fruit red ripe, TAMU Lyco... 193 1e-68
60 emb|AI895353|AI895353 EST264796 tomato callus, TAMU Lycopersicon... 193 1e-68
emb|AA824730|AA824730 CT028.SK Tomato Leaf cDNA from cv. VFNT ch... 193 1e-68

Query= U35829.2_s_at 16981_s_at /id_source genbank /description
 gb|aac49356.1| (u35829) thioredoxin h [arabidopsis thaliana]
 5 /blast_score 4.00e-64 /ec_number /family /chip nova /gb_link /ncgi
 (357 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

10

Searching.....done

	Score	E	(bits)	Value
15	Sequences producing significant alignments:			
	emb X89759 BOPC17	B.oleracea mRNA for thioredoxin h-like, pollen...	194	2e-49
	gb U59379 BNU59379	Brassica napus thioredoxin-h-like-1 (THL-1) m...	194	2e-49
	emb AB010434 AB010434	Brassica rapa PEC-2 mRNA for Thioredoxin, ...	192	9e-49
	emb AW255457 AW255457	ML480 peppermint glandular trichome Mentha...	190	3e-48
20	emb AW569018 AW569018	si74e02.y1 Gm-cl031 Glycine max cDNA clone...	185	1e-46
	emb AI988470 AI988470	sd02f07.y1 Gm-cl020 Glycine max cDNA clone...	185	1e-46
	emb Z70677 RCTHIORXN	R.communis mRNA for thioredoxin.	183	5e-46
	emb AI161830 AI161830	A007P52U Hybrid aspen plasmid library Popu...	182	9e-46
	gb BE053835 BE053835	GA__Ea0009P21f Gossypium arboreum 7-10 dpa ...	182	9e-46
25	emb AW677726 AW677726	WS1_10_F03.g1_A002 Water-stressed 1 (WS1) ...	181	2e-45
	emb AW924685 AW924685	WS1_71_B11.b1_A002 Water-stressed 1 (WS1) ...	181	2e-45
	emb AW565750 AW565750	LG1_349_G02.g1_A002 Light Grown 1 (LG1) So...	181	2e-45
	emb AW671668 AW671668	LG1_349_G02.b1_A002 Light Grown 1 (LG1) So...	181	2e-45
	emb AW677651 AW677651	WS1_10_F03.b1_A002 Water-stressed 1 (WS1) ...	181	2e-45
30	emb AW349345 AW349345	GM210007A20B10R Gm-r1021 Glycine max cDNA ...	179	6e-45
	emb AI938238 AI938238	sc41e05.y1 Gm-cl014 Glycine max cDNA clone...	179	6e-45
	emb AI461219 AI461219	sa76f11.y1 Gm-cl004 Glycine max cDNA clone...	179	6e-45
	emb AJ009762 TAE9762	Triticum aestivum mRNA for thioredoxin H.	179	9e-45
35	emb AW164730 AW164730	se77a02.y1 Gm-cl023 Glycine max cDNA clone...	179	9e-45
	gb T24347 T24347	crs1466 lambdaZAPST Ricinus communis cDNA clone...	177	3e-44
	gb BE054543 BE054543	GA__Ea0026K15f Gossypium arboreum 7-10 dpa ...	177	4e-44
	dbj D87984 D87984	Fagopyrum esculentum mRNA for thioredoxin, com...	177	4e-44
	emb AW983331 AW983331	HVSMEg0010D20f Hordeum vulgare pre-anthesi...	177	4e-44
40	emb AW329521 AW329521	N200767e rootphos(-) Medicago truncatula c...	176	6e-44
	gb BE053246 BE053246	GA__Ea0021K08f Gossypium arboreum 7-10 dpa ...	176	8e-44
	emb AW255195 AW255195	ML185 peppermint glandular trichome Mentha...	176	8e-44
	emb X69915 TATHIORDH	T.aestivum mRNA for thioredoxine H.	175	1e-43
	emb AW164347 AW164347	se71c11.y1 Gm-cl023 Glycine max cDNA clone...	175	1e-43
45	emb AW781479 AW781479	sl79e04.y1 Gm-cl037 Glycine max cDNA clone...	175	1e-43
	emb A48516 A48516	Sequence 4 from Patent WO9603505.	175	1e-43
	emb AW705063 AW705063	sk57b09.y1 Gm-cl019 Glycine max cDNA clone...	175	1e-43
	emb AW568753 AW568753	si72f07.y1 Gm-cl031 Glycine max cDNA clone...	175	1e-43
	emb AI165128 AI165128	A076P57U Hybrid aspen plasmid library Popu...	175	1e-43
50	emb AJ001903 TDAJ1903	Triticum durum mRNA for thioredoxin H.	175	1e-43
	emb A48520 A48520	Sequence 8 from Patent WO9603505.	175	1e-43
	emb A48514 A48514	Sequence 2 from Patent WO9603505.	175	1e-43
	emb A48519 A48519	Sequence 7 from Patent WO9603505.	175	1e-43
	emb AW329764 AW329764	N201033e rootphos(-) Medicago truncatula c...	174	2e-43
55	emb AW983305 AW983305	HVSMEg0010C12f Hordeum vulgare pre-anthesi...	174	3e-43
	emb AW626018 AW626018	EST319925 tomato radicle, 5 d post-imbibit...	174	3e-43
	emb AW982237 AW982237	HVSMEg0002G18f Hordeum vulgare pre-anthesi...	174	3e-43
	emb X58527 NTTRNA	N.tabacum mRNA for thioredoxin.	173	5e-43
	gb U59380 BNU59380	Brassica napus thioredoxin-h-like-2 (THL-2) m...	101	5e-43
60	gb C95504 C95504	C95504 Citrus unshiu Miyagawa-wase maturation s...	172	7e-43
	emb AW277335 AW277335	sf80b02.y1 Gm-cl019 Glycine max cDNA clone...	171	1e-42

- emb|AI441505|AI441505 sa87c03.y1 Gm-cl004 Glycine max cDNA clone... 171 1e-42
 emb|AW349509|AW349509 GM210005A21B12R Gm-r1021 Glycine max cDNA ... 171 1e-42
- 5 emb|AW096472|AW096472 EST289652 tomato mixed elicitor, BTI Lycop... 171 3e-42
 emb|AI775760|AI775760 EST256860 tomato resistant, Cornell Lycop... 171 3e-42
 emb|AI773303|AI773303 EST254403 tomato resistant, Cornell Lycop... 171 3e-42
 emb|AI776110|AI776110 EST257198 tomato resistant, Cornell Lycop... 171 3e-42
 emb|AW650009|AW650009 EST328463 tomato germinating seedlings, TA... 171 3e-42
 emb|AW040011|AW040011 EST282502 tomato mixed elicitor, BTI Lycop... 171 3e-42
- 10 emb|AW040001|AW040001 EST282492 tomato mixed elicitor, BTI Lycop... 171 3e-42
 emb|AW621673|AW621673 EST312471 tomato root during/after fruit s... 171 3e-42
 emb|AI780240|AI780240 EST261119 tomato susceptible, Cornell Lyco... 171 3e-42
 emb|AW041395|AW041395 EST284259 tomato mixed elicitor, BTI Lycop... 171 3e-42
 emb|AW038141|AW038141 EST279798 tomato mixed elicitor, BTI Lycop... 171 3e-42
- 15 emb|AW038924|AW038924 EST280880 tomato mixed elicitor, BTI Lycop... 171 3e-42
 emb|AW037831|AW037831 EST279460 tomato mixed elicitor, BTI Lycop... 171 3e-42
 emb|AW094525|AW094525 EST287705 tomato mixed elicitor, BTI Lycop... 171 3e-42
 emb|AW625957|AW625957 EST319852 tomato radicle, 5 d post-imbibit... 171 3e-42
 emb|AI781827|AI781827 EST262706 tomato susceptible, Cornell Lyco... 171 3e-42
- 20 emb|AI778940|AI778940 EST259819 tomato susceptible, Cornell Lyco... 171 3e-42
 emb|AW625331|AW625331 EST319154 tomato radicle, 5 d post-imbibit... 171 3e-42
 emb|AW597424|AW597424 si92g01.y1 Gm-cl031 Glycine max cDNA clone... 169 9e-42
 emb|AW040201|AW040201 EST282700 tomato mixed elicitor, BTI Lycop... 168 1e-41
 emb|AW040195|AW040195 EST282694 tomato mixed elicitor, BTI Lycop... 168 1e-41
- 25 emb|AW038564|AW038564 EST280247 tomato mixed elicitor, BTI Lycop... 168 1e-41
 gb|BE057793|BE057793 sn07c11.y1 Gm-cl016 Glycine max cDNA clone ... 168 1e-41
 emb|AW217307|AW217307 EST296026 tomato flower buds 0-3 mm, Corne... 165 2e-40
 emb|AW289622|AW289622 NXNV003H05F Nsf Xylem Normal wood Vertical... 164 2e-40
 emb|AW064893|AW064893 ST37B02 Pine TriplEx shoot tip library Pin... 162 8e-40
- 30 emb|AW065132|AW065132 ST40A08 Pine TriplEx shoot tip library Pin... 162 1e-39
 emb|AF051206|AF051206 Picea mariana probable thioredoxin H (Sb09... 162 1e-39
 emb|AW010199|AW010199 ST03C05 Pine TriplEx shoot tip library Pin... 162 1e-39
 emb|AW042699|AW042699 ST23E01 Pine TriplEx shoot tip library Pin... 162 1e-39
 emb|AW043379|AW043379 ST32F12 Pine TriplEx shoot tip library Pin... 162 1e-39
- 35 emb|AW043214|AW043214 ST30F08 Pine TriplEx shoot tip library Pin... 162 1e-39
 emb|AW043171|AW043171 ST30B09 Pine TriplEx shoot tip library Pin... 162 1e-39
 emb|AW497847|AW497847 PC02B02 Pine TriplEx pollen cone library P... 161 1e-39
 emb|AW736931|AW736931 NXNV_081_G02_F Nsf Xylem Normal wood Verti... 161 1e-39
 emb|AW680877|AW680877 WS1_7_D07.g1_A002 Water-stressed 1 (WS1) S... 161 2e-39
- 40 emb|AW680784|AW680784 WS1_7_D07.b1_A002 Water-stressed 1 (WS1) S... 161 2e-39
 emb|AW011327|AW011327 ST19E02 Pine TriplEx shoot tip library Pin... 160 3e-39
 emb|AW011046|AW011046 ST16A08 Pine TriplEx shoot tip library Pin... 160 4e-39
 emb|AI736736|AI736736 sb32g12.y1 Gm-cl012 Glycine max cDNA clone... 93 6e-39
 emb|AW010836|AW010836 ST14F05 Pine TriplEx shoot tip library Pin... 159 7e-39
- 45 emb|AW290231|AW290231 NXNV015E05F Nsf Xylem Normal wood Vertical... 159 1e-38
 emb|AW011498|AW011498 ST21E10 Pine TriplEx shoot tip library Pin... 158 2e-38
 emb|AA740038|AA740038 803 PtIFG2 Pinus taeda cDNA clone 9266M 3'... 157 3e-38
 emb|AW009991|AW009991 ST01A09 Pine TriplEx shoot tip library Pin... 157 3e-38
 emb|AW684766|AW684766 NF021G12NR1F1000 Nodulated root Medicago t... 124 3e-38
- 50 emb|AW706540|AW706540 sj57g11.y1 Gm-cl033 Glycine max cDNA clone... 156 7e-38
 emb|AI461254|AI461254 sa60f10.y1 Gm-cl004 Glycine max cDNA clone... 155 9e-38
 emb|AW745883|AW745883 WS1_38_B01.b1_A002 Water-stressed 1 (WS1) ... 154 2e-37
 emb|AW923038|AW923038 DG1_48_B02.g1_A002 Dark Grown 1 (DG1) Sorg... 154 2e-37
 emb|AW754729|AW754729 PC07B04 Pine TriplEx pollen cone library P... 154 2e-37
- 55 emb|AW681036|AW681036 WS1_8_D05.b1_A002 Water-stressed 1 (WS1) S... 154 2e-37
 emb|AW679524|AW679524 WS1_29_F05.g1_A002 Water-stressed 1 (WS1) ... 154 2e-37

60 Query= AC002391.188_at 16995_at /id_source genbank /description
 gb|aab87114.1| (ac002391) unknown protein [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link

<http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002391|/ncgi>
<http://www.ncgr.org/cgi-bin/ff?ac002391>
 (1896 letters)

5

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

10

Score E
 Sequences producing significant alignments: (bits) Value

	emb AF123503 AF123503 Nicotiana tabacum Nt-gh3 deduced protein m...	484	0.0
15	emb X60033 GMGH3G G.max GH3 gene for auxin-regulated protein.	406	0.0
	emb AI489187 AI489187 EST247526 tomato ovary, TAMU Lycopersicon ...	421	e-116
	emb AI489278 AI489278 EST247617 tomato ovary, TAMU Lycopersicon ...	410	e-113
	emb AW223544 AW223544 EST300355 tomato fruit red ripe, TAMU Lyco...	385	e-106
	emb AI729810 AI729810 BNLGHi5260 Six-day Cotton fiber Gossypium ...	225	e-103
20	emb AW455302 AW455302 EST311840 tomato root during/after fruit s...	358	6e-98
	emb AW307114 AW307114 sf52h11.y1 Gm-cl009 Glycine max cDNA clone...	357	2e-97
	emb AW730905 AW730905 GA__Ea0029G23 Gossypium arboreum 7-10 dpa ...	321	2e-95
	emb AW737090 AW737090 EST338517 tomato flower buds, anthesis, Co...	228	3e-94
	gb BE053589 BE053589 GA__Ea0013N22f Gossypium arboreum 7-10 dpa ...	298	1e-79
25	emb AW164615 AW164615 se74c04.y1 Gm-cl023 Glycine max cDNA clone...	169	1e-78
	emb AW686313 AW686313 NF040C09NR1F1000 Nodulated root Medicago t...	211	7e-78
	emb AW035201 AW035201 EST280463 tomato callus, TAMU Lycopersicon...	153	2e-77
	emb AW720296 AW720296 LjNEST20d3r Lotus japonicus nodule library...	290	3e-77
	emb AW559498 AW559498 EST314546 DSIR Medicago truncatula cDNA cl...	169	3e-76
30	emb AW774169 AW774169 EST333252 KV3 Medicago truncatula cDNA clo...	169	1e-75
	emb AW125947 AW125947 N100142e rootphos(-) Medicago truncatula c...	274	1e-72
	emb AW668277 AW668277 GA__Ea0013G22 Gossypium arboreum 7-10 dpa ...	271	1e-71
	emb AW980820 AW980820 EST391973 GVN Medicago truncatula cDNA clo...	254	2e-66
	emb AW221739 AW221739 EST298550 tomato fruit red ripe, TAMU Lyco...	180	6e-63
35	emb AW929039 AW929039 EST337743 tomato flower buds 8 mm to pre-a...	144	6e-62
	emb AV410002 AV410002 AV410002 Lotus japonicus young plants (two...	232	9e-61
	emb AW720379 AW720379 LjNEST22a11r Lotus japonicus nodule librar...	175	2e-59
	emb AW928468 AW928468 EST337256 tomato flower buds 8 mm to pre-a...	200	3e-59
	emb AW163964 AW163964 Ljirnpes17-383-g11 Ljirnp Lambda HybriZap...	198	6e-57
40	emb AW185677 AW185677 se58c02.y1 Gm-cl019 Glycine max cDNA clone...	219	5e-56
	emb AI773943 AI773943 EST255043 tomato resistant, Cornell Lycope...	133	5e-54
	emb AI054856 AI054856 coau0002F14 Cotton Boll Abscission Zone cD...	97	8e-53
	emb AV426547 AV426547 AV426547 Lotus japonicus young plants (two...	135	1e-51
	emb AW684512 AW684512 NF017G09NR1F1000 Nodulated root Medicago t...	197	2e-49
45	emb AW428928 AW428928 Ljirnpes25-068-h9 Ljirnp Lambda HybriZap ...	107	5e-49
	emb AI484627 AI484627 EST242888 tomato ovary, TAMU Lycopersicon ...	194	1e-48
	emb AW676760 AW676760 DG1_14_F09.g1_A002 Dark Grown 1 (DG1) Sorg...	167	2e-47
	emb AW647702 AW647702 EST307181 tomato germinating seedlings, TA...	130	2e-44
	emb AW160191 AW160191 EST290048 L. pennellii trichome, Cornell U...	137	6e-44
50	emb AI775892 AI775892 EST256992 tomato resistant, Cornell Lycope...	177	2e-43
	emb AW031091 AW031091 EST274398 tomato callus, TAMU Lycopersicon...	104	4e-43
	emb AI437757 AI437757 sa39b12.y1 Gm-cl004 Glycine max cDNA clone...	144	6e-43
	emb AW647700 AW647700 EST307179 tomato germinating seedlings, TA...	129	7e-43
	gb BE122431 BE122431 Ljirnpes26-072-a2 Ljirnp Lambda HybriZap t...	107	1e-42
55	emb AW349113 AW349113 GM210004B21A1R Gm-r1021 Glycine max cDNA 3...	131	4e-41
	emb AI737532 AI737532 T110159e KV0 Medicago truncatula cDNA clon...	165	1e-39
	emb AV420807 AV420807 AV420807 Lotus japonicus young plants (two...	154	7e-39
	emb AW622684 AW622684 EST306821 tomato flower buds 3-8 mm, Corne...	105	7e-38
60	emb AW217219 AW217219 EST295933 tomato callus, TAMU Lycopersicon...	157	2e-37
	emb AI771570 AI771570 EST252670 tomato ovary, TAMU Lycopersicon ...	112	3e-37

- emb|AI483575|AI483575 EST249425 tomato ovary, TAMU Lycopersicon ... 112 3e-37
 emb|AW781778|AW781778 sl92c01.y1 Gm-c1037 Glycine max cDNA clone... 110 1e-35
 emb|AW932607|AW932607 EST358450 tomato fruit mature green, TAMU ... 116 3e-35
 emb|AW596402|AW596402 sj12a06.y1 Gm-c1032 Glycine max cDNA clone... 103 9e-35
 5 emb|AI487477|AI487477 EST245799 tomato ovary, TAMU Lycopersicon ... 113 8e-34
 emb|AW568731|AW568731 si72d08.y1 Gm-c1031 Glycine max cDNA clone... 104 1e-33
 emb|AW037990|AW037990 EST279634 tomato mixed elicitor, BTI Lycop... 91 2e-31
 emb|AW442518|AW442518 EST307448 tomato mixed elicitor, BTI Lycop... 92 1e-30
 emb|AV408894|AV408894 AV408894 Lotus japonicus young plants (two... 132 1e-29
 10 emb|AW597236|AW597236 si91a07.y1 Gm-c1031 Glycine max cDNA clone... 91 1e-29
 emb|AB005877|AB005877 Nicotiana tabacum mRNA for BYJ14, partial ... 131 2e-29
 emb|AI483752|AI483752 EST249623 tomato ovary, TAMU Lycopersicon ... 104 6e-29
 emb|AW234030|AW234030 sf33c09.y1 Gm-c1028 Glycine max cDNA clone... 79 2e-28
 emb|AW156137|AW156137 se20a04.y1 Gm-c1015 Glycine max cDNA clone... 125 1e-27
 15 emb|AI900868|AI900868 sb95e02.y1 Gm-c1012 Glycine max cDNA clone... 104 1e-26
 emb|AI779963|AI779963 EST260842 tomato susceptible, Cornell Lyco... 122 1e-26
 emb|AI898974|AI898974 EST268417 tomato ovary, TAMU Lycopersicon ... 99 3e-24
 emb|AI778687|AI778687 EST259566 tomato susceptible, Cornell Lyco... 113 5e-24
 emb|AW981373|AW981373 EST392526 DSIL Medicago truncatula cDNA cl... 101 1e-23
 20 emb|AI441355|AI441355 sa55f08.y1 Gm-c1004 Glycine max cDNA clone... 59 8e-22
 emb|AI974524|AI974524 T110474e KV0 Medicago truncatula cDNA clon... 105 2e-21
 emb|AI899093|AI899093 EST268536 tomato ovary, TAMU Lycopersicon ... 104 2e-21
 emb|AI777312|AI777312 EST258277 tomato resistant, Cornell Lycope... 103 6e-21
 emb|AW398897|AW398897 EST309397 L. pennellii trichome, Cornell U... 74 1e-20
 25 emb|AI166806|AI166806 xylem.est.601 Poplar xylem Lambda ZAPII li... 84 9e-20
 emb|AW224185|AW224185 EST301092 tomato fruit red ripe, TAMU Lyco... 98 2e-19
 emb|AA824951|AA824951 CT234.UNI Tomato Leaf cDNA from cv. VFNT c... 93 3e-19
 emb|AW458783|AW458783 sh14c06.y1 Gm-c1016 Glycine max cDNA clone... 95 1e-18
 emb|AW038098|AW038098 EST279755 tomato mixed elicitor, BTI Lycop... 62 4e-16
 30 emb|AW618367|AW618367 EST320353 L. pennellii trichome, Cornell U... 85 2e-15
 emb|AI776968|AI776968 EST252060 tomato callus, TAMU Lycopersicon... 85 2e-15
 emb|AW622772|AW622772 EST306758 tomato flower buds 3-8 mm, Come... 55 3e-15
 emb|AI777546|AI777546 EST258520 tomato susceptible, Cornell Lyco... 63 4e-15
 emb|AW618243|AW618243 EST314293 L. pennellii trichome, Cornell U... 66 5e-15
 35 emb|AW278756|AW278756 sf97b03.y1 Gm-c1019 Glycine max cDNA clone... 82 1e-14
 emb|AW092080|AW092080 EST285356 tomato mixed elicitor, BTI Lycop... 71 8e-14
 emb|AW282596|AW282596 LG1_310_F07.g1_A002 Light Grown 1 (LG1) So... 61 1e-13
 emb|AW705294|AW705294 sk59b10.y1 Gm-c1019 Glycine max cDNA clone... 78 3e-13
 emb|AW738104|AW738104 EST339531 tomato flower buds, anthesis, Co... 77 4e-13
 40 emb|AW459172|AW459172 sh21e10.y1 Gm-c1016 Glycine max cDNA clone... 77 6e-13
 gb|BE035111|BE035111 MM03C07 MM Mesembryanthemum crystallinum cD... 66 6e-12
 emb|AW442808|AW442808 EST307738 tomato mixed elicitor, BTI Lycop... 62 8e-12
 emb|AW706842|AW706842 sk04g06.y1 Gm-c1023 Glycine max cDNA clone... 72 1e-11
 emb|AI773706|AI773706 EST254806 tomato resistant, Cornell Lycope... 49 2e-11
 45 emb|AI897063|AI897063 EST266506 tomato ovary, TAMU Lycopersicon ... 66 8e-10
 emb|AW032584|AW032584 EST276143 tomato callus, TAMU Lycopersicon... 64 3e-09
 emb|AW683199|AW683199 NF008H01LF1F1014 Developing leaf Medicago ... 63 8e-09
 gb|BE059206|BE059206 sn27f04.y1 Gm-c1016 Glycine max cDNA clone ... 62 1e-08
 emb|AW616334|AW616334 EST322745 L. hirsutum trichome, Cornell Un... 61 3e-08
 50 emb|AI483553|AI483553 EST249402 tomato ovary, TAMU Lycopersicon ... 59 1e-07
 emb|AI773748|AI773748 EST254848 tomato resistant, Cornell Lycope... 59 1e-07
 emb|AW038769|AW038769 EST280630 tomato mixed elicitor, BTI Lycop... 56 9e-07
 gb|L38057|L38057 BNAF0397E Mustard flower buds Brassica rapa cDN... 53 8e-06
 55
 Query= AC006585.212_at 17008_at /id_source genbank /description
 gb|aad23027.1|ac006585_22 (ac006585) putative tyrosine
 aminotransferase [arabidopsis thaliana] /blast_score 0 /ec_number
 /family transaminase /chip nova /gb_link
 60 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006585|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006585|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006585|/ncgi)

<http://www.ncgr.org/cgi-bin/ff?ac006585>
(1582 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	
10	Sequences producing significant alignments:	(bits)	Value
	dbj D88273 D88273 Hordeum vulgare naat-A mRNA for nicotianamine ...	446	e-124
	emb AB005788 AB005788 Hordeum vulgare mRNA for nicotianamine ami...	433	e-120
	emb AB024006 AB024006 Hordeum vulgare naat-B and naat-A genes fo...	184	3e-78
15	emb AW760137 AW760137 sl58e07.y1 Gm-cl027 Glycine max cDNA clone...	270	1e-72
	emb AW508844 AW508844 si41a10.y1 Gm-r1030 Glycine max cDNA clone...	191	7e-61
	emb AW348839 AW348839 GM210003B11G12R Gm-r1021 Glycine max cDNA ...	233	2e-60
	emb AW832427 AW832427 sm10c03.y1 Gm-cl027 Glycine max cDNA clone...	233	3e-60
20	emb AW760284 AW760284 sl48d01.y1 Gm-cl027 Glycine max cDNA clone...	206	6e-55
	emb AW620771 AW620771 sj09d03.y1 Gm-cl032 Glycine max cDNA clone...	209	5e-53
	emb AW568831 AW568831 si61g09.y1 Gm-r1030 Glycine max cDNA clone...	199	5e-50
	emb AW030722 AW030722 EST273977 tomato callus, TAMU Lycopersicon...	198	9e-50
	emb AW306460 AW306460 se51a02.y1 Gm-cl017 Glycine max cDNA clone...	178	8e-44
25	emb AW459166 AW459166 sh21e03.y1 Gm-cl016 Glycine max cDNA clone...	170	3e-41
	emb AW030650 AW030650 EST273905 tomato callus, TAMU Lycopersicon...	96	4e-38
	emb AW202348 AW202348 sf14a04.y1 Gm-cl027 Glycine max cDNA clone...	96	1e-33
	emb AW760709 AW760709 sl36a11.y1 Gm-cl027 Glycine max cDNA clone...	138	8e-32
	gb BE020273 BE020273 sm42g02.y1 Gm-cl028 Glycine max cDNA clone ...	91	3e-31
30	gb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine aminotransf...	97	1e-26
	emb AW102390 AW102390 sd87b05.y1 Gm-cl009 Glycine max cDNA clone...	119	5e-26
	emb AW928492 AW928492 EST337280 tomato flower buds 8 mm to pre-a...	78	9e-25
	emb AI930964 AI930964 sb45d08.y1 Gm-cl015 Glycine max cDNA clone...	115	1e-24
	emb AW678964 AW678964 WS1_21_A12.g1_A002 Water-stressed 1 (WS1) ...	115	1e-24
35	emb AW928458 AW928458 EST337246 tomato flower buds 8 mm to pre-a...	85	3e-23
	emb AI487927 AI487927 EST246249 tomato ovary, TAMU Lycopersicon ...	70	7e-23
	emb AW737817 AW737817 EST339244 tomato flower buds, anthesis, Co...	79	2e-22
	emb AW924630 AW924630 WS1_70_A07.g1_A002 Water-stressed 1 (WS1) ...	106	5e-22
	emb AW832131 AW832131 sm20a05.y1 Gm-cl027 Glycine max cDNA clone...	105	9e-22
40	emb AW221912 AW221912 EST298723 tomato fruit red ripe, TAMU Lyco...	70	9e-19
	emb AI562691 AI562691 TENS2678 T. cruzi epimastigote normalized ...	92	1e-18
	emb AI562604 AI562604 TENS2761 T. cruzi epimastigote normalized ...	95	2e-18
	emb AW782202 AW782202 sm02g12.y1 Gm-cl027 Glycine max cDNA clone...	70	1e-16
	emb Z48758 SC9727 S.cerevisiae chromosome IV cosmid 9727.	54	2e-16
45	emb AV421843 AV421843 AV421843 Lotus japonicus young plants (two...	86	6e-16
	emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c19G10.	57	1e-15
	emb AL096788 SPBC582 S.pombe chromosome II cosmid c582.	57	1e-15
	emb AW034806 AW034806 EST278842 tomato callus, TAMU Lycopersicon...	85	1e-15
	gb U53880 YSCL9449 Saccharomyces cerevisiae chromosome XII cosmi...	51	2e-14
50	emb Z73261 SCYLR089C S.cerevisiae chromosome XII reading frame O...	51	2e-14
	emb AW100534 AW100534 sd56d09.y1 Gm-cl016 Glycine max cDNA clone...	79	7e-14
	emb AW776160 AW776160 EST335225 DSIL Medicago truncatula cDNA cl...	70	6e-13
	emb Z49335 SCYJL060W S.cerevisiae chromosome X reading frame ORF...	63	8e-13
	emb AW329712 AW329712 N200976e rootphos(-) Medicago truncatula c...	75	1e-12
55	emb Z98531 SPAC6B12 S.pombe chromosome I cosmid c6B12.	63	2e-12
	emb AI057693 AI057693 TENU1783 T. cruzi epimastigote normalized ...	74	3e-12
	emb AV419799 AV419799 AV419799 Lotus japonicus young plants (two...	72	2e-11
	emb AW219060 AW219060 EST301542 tomato root during/after fruit s...	71	3e-11
	emb AW756163 AW756163 sl16f12.y1 Gm-cl036 Glycine max cDNA clone...	62	2e-08
60	emb AI667953 AI667953 TENG0919 T. Cruzi epimastigote normalised ...	61	2e-08
	emb AQ911130 AQ911130 GSSTc02564 Trypanosome cruzi random genom...	61	2e-08

	emb AQ904747 AQ904747 GSSTc03969 Trypanosome cruzi random genomi...	61	2e-08
	emb AQ905153 AQ905153 GSSTc03744 Trypanosome cruzi random genomi...	61	2e-08
	emb AI068927 AI068927 mgae0004dB02f Magnaporthe grisea Appressor...	45	5e-08
	emb AQ445624 AQ445624 GSSTc00112 Trypanosoma cruzi random genomi...	56	1e-06
5	emb AI110334 AI110334 TENU3304 T. cruzi epimastigote normalized ...	39	1e-06
	emb AI055475 AI055475 coau0004B14 Cotton Boll Abscission Zone cD...	55	2e-06
	gb U37774 CMU37774 Cucurbita maxima 1-aminocyclopropane-1-carbox...	50	2e-06
	dbj D01033 CUCACCA Cucurbita maxima mRNA for 1-aminocyclopropane...	50	2e-06
	emb AF083816 AF083816 Antirrhinum majus ACC synthase 3 (ACS3) mR...	46	2e-06
10	emb AI080889 AI080889 TENU3747 T. cruzi epimastigote normalized ...	52	9e-06
	emb AB006805 AB006805 Cucumis sativus CS-ACS3 mRNA for ACC synth...	48	1e-05
	gb U59813 CSU59813 Cucumis sativus 1-aminocyclopropane-1-carboxy...	48	1e-05
	emb AW934295 AW934295 EST360138 tomato fruit mature green, TAMU ...	52	1e-05
	emb AW101681 AW101681 sd68f11.y1 Gm-cl008 Glycine max cDNA clone...	51	2e-05
15	emb AW691076 AW691076 NF041A07ST1F1000 Developing stem Medicago ...	44	2e-05
	emb AW477177 AW477177 ga42h10.y1 Moss EST library PPU Physcomitr...	44	2e-05
	emb AV424265 AV424265 AV424265 Lotus japonicus young plants (two...	51	2e-05
	emb AF074929 AF074929 Sinapis arvensis 1-aminocyclopropane-1-car...	46	3e-05
	emb AW033989 AW033989 EST277651 tomato callus, TAMU Lycopersicon...	51	3e-05
20	emb AF074931 AF074931 Sinapis arvensis 1-aminocyclopropane-1-car...	46	3e-05
	emb AI896625 AI896625 EST266068 tomato callus, TAMU Lycopersicon...	50	5e-05
	emb AW695981 AW695981 NF100F04ST1F1042 Developing stem Medicago ...	50	5e-05
	emb AI483496 AI483496 EST249317 tomato ovary, TAMU Lycopersicon ...	41	5e-05
	emb AI487017 AI487017 EST245339 tomato ovary, TAMU Lycopersicon ...	41	5e-05
25	emb AW032141 AW032141 EST275595 tomato callus, TAMU Lycopersicon...	50	6e-05
	emb AQ906278 AQ906278 GSSTc02322 Trypanosome cruzi random genomi...	50	6e-05
	emb AF074930 AF074930 Sinapis arvensis 1-aminocyclopropane-1-car...	45	9e-05
	emb AI896469 AI896469 EST265900 tomato callus, TAMU Lycopersicon...	49	9e-05
	emb AW033411 AW033411 EST276982 tomato callus, TAMU Lycopersicon...	49	9e-05
30	emb AW685223 AW685223 NF027D03NR1F1000 Nodulated root Medicago t...	49	9e-05
	emb AI896781 AI896781 EST266224 tomato callus, TAMU Lycopersicon...	49	9e-05
	emb AV426435 AV426435 AV426435 Lotus japonicus young plants (two...	49	1e-04
	emb AW690226 AW690226 NF030F01ST1F1000 Developing stem Medicago ...	40	2e-04
	emb AW093940 AW093940 EST287120 tomato mixed elicitor, BTI Lycop...	48	2e-04
35	emb Z26322 HVALAAT H.vulgare mRNA for alanine aminotransferase.	48	2e-04
	emb AW727211 AW727211 GA_Ea0023N19 Gossypium arboreum 7-10 dpa ...	48	2e-04
	emb AV411813 AV411813 AV411813 Lotus japonicus young plants (two...	48	2e-04
	emb X69421 PMPALAAT2 P. miliaceum mRNA for alanine aminotransfer...	48	2e-04
	emb AQ873648 AQ873648 V73B5 mTn-3xHA/lacZ Insertion Library, str...	48	2e-04
40	emb AW217028 AW217028 EST295742 tomato callus, TAMU Lycopersicon...	48	2e-04
	emb AW093939 AW093939 EST287119 tomato mixed elicitor, BTI Lycop...	47	3e-04
	emb AZ217827 AZ217827 Sheared DNA-81E6.TF Sheared DNA Trypanosom...	47	3e-04
	emb AF049137 AF049137 Dianthus caryophyllus 1-aminocyclopropane-...	47	4e-04
	emb AI773775 AI773775 EST254875 tomato resistant, Cornell Lycop...	39	4e-04
45	emb AF052832 AF052832 Trypanosoma cruzi CL Brener cosmid 1b21 ch...	47	4e-04
	emb AF049711 AF049711 Petunia x hybrida pollen-specific 1-aminoc...	42	5e-04
	emb AB010102 AB010102 Malus domestica gene for 1-aminocyclopropa...	41	7e-04
	gb U89156 MDU89156 Malus domestica ACC synthase (MdACS-1) gene, ...	41	7e-04
	gb L31347 MAUACCSYN Malus domestica 1-aminocyclopropane-1-carbox...	41	7e-04
50	emb AB015624 AB015624 Pyrus pyrifolia mRNA for 1-aminocyclopropa...	41	7e-04
	emb AB007449 AB007449 Actinidia deliciosa mRNA for 1-aminocyclop...	42	7e-04

Query= AJ006961.4_s_at 17413_s_at /id_source genbank /description
 55 emb|caa67551.1| (x99097) peroxidase [arabidopsis thaliana]
 /blast_score 2.00e-84 /ec_number /family /chip nova /gb_link /ncgi
 (460 letters)

Database: plantfungal
 60 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	
	(bits) Value		
Sequences producing significant alignments:			
5			
	emb AW035239 AW035239	EST280501	tomato callus, TAMU Lycopersicon... 274 3e-73
	emb AW035958 AW035958	EST282817	tomato callus, TAMU Lycopersicon... 274 3e-73
	emb X94943 LECEVI16G	L.esculentum mRNA for peroxidase.	274 3e-73
	emb AW032485 AW032485	EST276044	tomato callus, TAMU Lycopersicon... 272 1e-72
10	gb M37637 ARCPNC2	A.hypogaea cationic peroxidase mRNA, complete ...	271 2e-72
	emb AF149279 AF149279	Phaseolus vulgaris peroxidase 4 precursor ...	265 1e-70
	emb AI777064 AI777064	EST252031	tomato callus, TAMU Lycopersicon... 261 3e-69
	emb AW216562 AW216562	EST295276	tomato callus, TAMU Lycopersicon... 259 9e-69
	emb AW035446 AW035446	EST281184	tomato callus, TAMU Lycopersicon... 258 2e-68
15	emb AB027753 AB027753	Nicotiana tabacum mRNA for peroxidase, com...	255 1e-67
	emb AW216873 AW216873	EST295587	tomato callus, TAMU Lycopersicon... 251 2e-66
	emb AV414074 AV414074	AV414074	Lotus japonicus young plants (two... 250 5e-66
	emb AI773788 AI773788	EST254888	tomato resistant, Cornell Lycope... 246 9e-65
	gb L36112 SSNPEROXIC	Stylosanthes humilis peroxidase mRNA.	193 3e-64
20	emb Y10468 SOPR XR7	S.oleracea mRNA for peroxidase, clone PC36.	242 8e-64
	emb AW035207 AW035207	EST280469	tomato callus, TAMU Lycopersicon... 237 5e-62
	emb AV422753 AV422753	AV422753	Lotus japonicus young plants (two... 235 1e-61
	emb AW224630 AW224630	EST303073	tomato root, plants pre-anthesis... 235 2e-61
	emb AW224631 AW224631	EST303074	tomato root, plants pre-anthesis... 235 2e-61
25	emb AW219926 AW219926	EST302409	tomato root during/after fruit s... 235 2e-61
	emb AW224632 AW224632	EST303075	tomato root, plants pre-anthesis... 235 2e-61
	emb AW759829 AW759829	sl54f01.y1 Gm-c1027	Glycine max cDNA clone... 231 3e-60
	emb AW219312 AW219312	EST301794	tomato root during/after fruit s... 230 6e-60
	emb AW219314 AW219314	EST301796	tomato root during/after fruit s... 229 1e-59
30	emb AW219112 AW219112	EST301594	tomato root during/after fruit s... 227 3e-59
	emb AI772237 AI772237	EST253337	tomato resistant, Cornell Lycope... 223 5e-58
	emb AW035660 AW035660	EST281492	tomato callus, TAMU Lycopersicon... 223 7e-58
	emb AW035872 AW035872	EST282181	tomato callus, TAMU Lycopersicon... 221 4e-57
	emb AW621675 AW621675	EST312473	tomato root during/after fruit s... 220 7e-57
35	emb AW666030 AW666030	sk31c04.y1 Gm-c1028	Glycine max cDNA clone... 216 8e-56
	emb AI778513 AI778513	EST259392	tomato susceptible, Cornell Lyco... 213 6e-55
	emb AW224633 AW224633	EST303076	tomato root, plants pre-anthesis... 215 6e-55
	gb L77080 SSNCAPEA	Stylosanthes humilis cationic peroxidase gene...	161 9e-55
	emb AW031362 AW031362	EST274816	tomato callus, TAMU Lycopersicon... 205 2e-52
40	emb AV414872 AV414872	AV414872	Lotus japonicus young plants (two... 202 2e-51
	emb AW033820 AW033820	EST277391	tomato callus, TAMU Lycopersicon... 193 7e-49
	emb AW029850 AW029850	EST273105	tomato callus, TAMU Lycopersicon... 191 3e-48
	emb AI895550 AI895550	EST264993	tomato callus, TAMU Lycopersicon... 188 3e-47
	emb AW030052 AW030052	EST273307	tomato callus, TAMU Lycopersicon... 186 8e-47
45	emb AF145349 AF145349	Glycine max peroxidase (Prx3) mRNA, partia...	143 2e-46
	emb AI774511 AI774511	EST255611	tomato resistant, Cornell Lycope... 184 4e-46
	emb X57564 ARNEUPERO	A.rusticana mRNA for neutral peroxidase.	129 2e-45
	emb AW220442 AW220442	EST302925	tomato root during/after fruit s... 108 3e-44
	emb AW625509 AW625509	EST319416	tomato radicle, 5 d post-imbibit... 106 7e-44
50	emb AW569733 AW569733	si79g02.y1 Gm-c1031	Glycine max cDNA clone... 175 2e-43
	emb AW621545 AW621545	EST312343	tomato root during/after fruit s... 108 2e-43
	emb AW694946 AW694946	NF081G11ST1F1087	Developing stem Medicago ... 142 4e-43
	emb AW132575 AW132575	se05h10.y1 Gm-c1013	Glycine max cDNA clone... 138 5e-43
	emb AF109663 AF109663	AF109663	Capsicum annuum root susceptible ... 161 2e-42
55	emb AW622066 AW622066	EST312864	tomato root during/after fruit s... 111 4e-42
	gb U51194 GMU51194	Glycine max peroxidase (sEPb2) mRNA, partial ...	138 4e-42
	gb L13654 TOMTPX1A	Lycopersicon.esculentum peroxidase (TPX1) mRN...	112 5e-42
	gb U51193 GMU51193	Glycine max peroxidase (sEPb1) mRNA, partial ...	133 2e-41
	emb AW219925 AW219925	EST302408	tomato root during/after fruit s... 168 2e-41
60	emb AW622012 AW622012	EST312810	tomato root during/after fruit s... 111 2e-41
	emb AW621198 AW621198	EST311996	tomato root during/after fruit s... 111 2e-41

- emb|AW626302|AW626302 EST320209 tomato radicle, 5 d post-imbibit... 111 2e-41
 emb|AW720673|AW720673 LjNEST4b2rc Lotus japonicus nodule library... 123 2e-41
 emb|AW693737|AW693737 NF068E06ST1F1050 Developing stem Medicago ... 136 3e-41
 emb|AW621449|AW621449 EST312247 tomato root during/after fruit s... 110 5e-41
 5 emb|AW928514|AW928514 EST337302 tomato flower buds 8 mm to pre-a... 95 5e-41
 emb|AW220017|AW220017 EST302500 tomato root during/after fruit s... 111 1e-40
 emb|AI771103|AI771103 EST252203 tomato ovary, TAMU Lycopersicon ... 111 1e-40
 emb|AW649146|AW649146 EST327600 tomato germinating seedlings, TA... 111 1e-40
 emb|AW219955|AW219955 EST302438 tomato root during/after fruit s... 111 1e-40
 10 emb|AF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 103 2e-40
 gb|L13653|TOMTPX2A Lycopersicon esculentum peroxidase (TPX2) mRN... 107 2e-40
 emb|AI773722|AI773722 EST254822 tomato resistant, Cornell Lycopersicon... 165 2e-40
 emb|AW035007|AW035007 EST279236 tomato callus, TAMU Lycopersicon... 165 2e-40
 emb|AI729640|AI729640 BNLGHi13846 Six-day Cotton fiber Gossypium... 155 4e-40
 15 emb|AI725603|AI725603 BNLGHi12435 Six-day Cotton fiber Gossypium... 153 5e-40
 emb|AF155124|AF155124 Gossypium hirsutum bacterial-induced perox... 94 8e-40
 emb|AV426241|AV426241 AV426241 Lotus japonicus young plants (two... 163 9e-40
 emb|AW034987|AW034987 EST279216 tomato callus, TAMU Lycopersicon... 163 9e-40
 emb|AW561204|AW561204 ga76g12.y1 Moss EST library PPU Physcomitr... 148 1e-39
 20 emb|Y10470|SOPR XR9 S.oleracea mRNA for peroxidase, clone PC56. 151 1e-39
 gb|M91373|CUSPREPER Cucumis sativus peroxidase mRNA, complete cds. 124 2e-39
 emb|AW671673|AW671673 LG1_349_F09.b1_A002 Light Grown 1 (LG1) So... 147 2e-39
 emb|AI728549|AI728549 BNLGHi11012 Six-day Cotton fiber Gossypium... 153 2e-39
 emb|AW672124|AW672124 LG1_357_F02.b1_A002 Light Grown 1 (LG1) So... 147 2e-39
 25 emb|AW625780|AW625780 EST319687 tomato radicle, 5 d post-imbibit... 105 2e-39
 emb|AW621202|AW621202 EST312000 tomato root during/after fruit s... 105 2e-39
 emb|Y16778|SPY16778 Spinacia oleracea mRNA for peroxidase, prx11... 130 3e-39
 emb|AI522935|AI522935 sa92c07.y1 Gm-c1004 Glycine max cDNA clone... 126 3e-39
 emb|AW219743|AW219743 EST302225 tomato root during/after fruit s... 111 4e-39
 30 emb|Y17192|CPY17192 Cucurbita pepo mRNA for peroxidase. 121 9e-39
 emb|AW622593|AW622593 EST313393 tomato root during/after fruit s... 105 1e-38
 emb|AW220074|AW220074 EST302557 tomato root during/after fruit s... 113 1e-38
 emb|AW219160|AW219160 EST301642 tomato root during/after fruit s... 107 1e-38
 emb|AW625441|AW625441 EST319348 tomato radicle, 5 d post-imbibit... 107 1e-38
 35 emb|AW625860|AW625860 EST319767 tomato radicle, 5 d post-imbibit... 105 1e-38
 emb|AW219258|AW219258 EST301740 tomato root during/after fruit s... 112 2e-38
 emb|AB024437|AB024437 Scutellaria baicalensis mRNA for peroxidase... 101 3e-38
 emb|AW647641|AW647641 EST307119 tomato germinating seedlings, TA... 107 3e-38
 emb|AI895098|AI895098 EST264541 tomato callus, TAMU Lycopersicon... 111 6e-38
 40 emb|AW032353|AW032353 EST275807 tomato callus, TAMU Lycopersicon... 156 7e-38
 emb|AW719266|AW719266 LjNEST1h8r Lotus japonicus nodule library,... 111 1e-37
 emb|AI055188|AI055188 coau0003E18 Cotton Boll Abscission Zone cD... 99 2e-37
 emb|AW689722|AW689722 NF023F03ST1F1000 Developing stem Medicago ... 123 2e-37
 emb|AW686882|AW686882 NF003E08RT1F1000 Developing root Medicago ... 105 3e-37

45

Query= AC000132.72_at 17464_at /id_source genbank /description
 "gb|aab60752.1| (ac000132) similar to a. thaliana receptor-like
 protein kinase (gb|rlk5_arath). ests gb|atts0475,gb|atts4362 come from
 this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family
 50 kinase /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000132|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000132|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000132|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac000132>
 (2766 letters)

55

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

60 Searching.....done

Score E

	Sequences producing significant alignments:	(bits) Value
	emb AF053127 AF053127 <i>Malus domestica</i> leucine-rich receptor-like... 333 2e-91	
	emb AW036763 AW036763 EST252152 tomato ovary, TAMU Lycopersicon ... 175 3e-77	
5	emb AW036762 AW036762 EST252151 tomato ovary, TAMU Lycopersicon ... 173 3e-76	
	gb U42444 U42444 <i>Lycopersicon pimpinellifolium</i> leucine rich repe... 198 1e-70	
	emb A57130 A57130 Sequence 1 from Patent WO9531564. 198 1e-70	
	gb U42445 U42445 <i>Lycopersicon pimpinellifolium</i> leucine rich repe... 198 1e-70	
	emb A57133 A57133 Sequence 4 from Patent WO9531564. 198 1e-70	
10	emb AF053998 AF053998 <i>Lycopersicon esculentum</i> Hcr2-5D (Hcr2-5D) ... 194 3e-68	
	emb A67434 A67434 Sequence 7 from Patent WO9743429. 194 3e-68	
	gb U77888 INU77888 <i>Ipomoea nil</i> receptor-like protein kinase (inr... 174 2e-66	
	emb AF053995 AF053995 <i>Lycopersicon esculentum</i> Hcr2-0B (Hcr2-0B) ... 195 1e-65	
	emb AF053993 AF053993 <i>Lycopersicon esculentum</i> disease resistance... 198 2e-65	
15	emb A67429 A67429 Sequence 2 from Patent WO9743429. 198 2e-65	
	emb A67428 A67428 Sequence 1 from Patent WO9743429. 198 2e-65	
	emb AI485090 AI485090 EST243394 tomato ovary, TAMU Lycopersicon ... 177 9e-64	
	emb AF053996 AF053996 <i>Lycopersicon pimpinellifolium</i> Hcr2-2A (Hcr... 180 8e-62	
	gb BE034258 BE034258 MH02C02 <i>MH Mesembryanthemum crystallinum</i> cD... 239 9e-62	
20	emb AF053994 AF053994 <i>Lycopersicon esculentum</i> Hcr2-0A (Hcr2-0A) ... 180 1e-61	
	emb AI486438 AI486438 EST244759 tomato ovary, TAMU Lycopersicon ... 230 1e-61	
	emb AF053997 AF053997 <i>Lycopersicon esculentum</i> Hcr2-5B (Hcr2-5B) ... 183 1e-61	
	emb A67432 A67432 Sequence 5 from Patent WO9743429. 183 1e-61	
	emb AI771280 AI771280 EST252296 tomato ovary, TAMU Lycopersicon ... 185 2e-59	
25	emb AF197947 AF197947 Glycine max receptor protein kinase-like p... 144 2e-59	
	emb AI771841 AI771841 EST252941 tomato ovary, TAMU Lycopersicon ... 177 6e-57	
	emb AW726024 AW726024 GA__Ea0020G24 <i>Gossypium arboreum</i> 7-10 dpa ... 193 2e-55	
	emb AI485862 AI485862 EST244183 tomato ovary, TAMU Lycopersicon ... 177 3e-54	
	emb AW224642 AW224642 EST303085 tomato root, plants pre-anthesis... 123 6e-54	
30	emb AI495469 AI495469 sa98d06.y1 Gm-cl004 Glycine max cDNA clone... 209 1e-52	
	emb AF197946 AF197946 Glycine max receptor protein kinase-like p... 146 2e-52	
	emb AB029327 AB029327 <i>Nicotiana tabacum</i> mRNA for elicitor-induci... 181 9e-48	
	emb AI442177 AI442177 sa58c02.y1 Gm-cl004 Glycine max cDNA clone... 158 3e-45	
	emb AW727470 AW727470 GA__Ea0012H16 <i>Gossypium arboreum</i> 7-10 dpa ... 86 5e-41	
35	emb AW979740 AW979740 EST341365 tomato root deficiency, Cornell ... 151 2e-39	
	emb AW010219 AW010219 ST03E03 Pine TriplEx shoot tip library Pin... 164 2e-39	
	emb AI487432 AI487432 EST245754 tomato ovary, TAMU Lycopersicon ... 150 7e-39	
	emb AI490531 AI490531 EST249065 tomato ovary, TAMU Lycopersicon ... 154 6e-38	
	emb AW668045 AW668045 GA__Ea0012G15 <i>Gossypium arboreum</i> 7-10 dpa ... 113 3e-37	
40	emb AW287714 AW287714 LG1_271_E06.b1_A002 Light Grown 1 (LG1) So... 150 3e-37	
	emb AW693988 AW693988 NF071C05ST1F1037 Developing stem <i>Medicago</i> ... 149 8e-35	
	emb AW774582 AW774582 EST333733 KV3 <i>Medicago truncatula</i> cDNA clo... 131 8e-35	
	emb AW650851 AW650851 EST329305 tomato germinating seedlings, TA... 87 1e-34	
	emb AW185015 AW185015 se85e10.y1 Gm-cl023 Glycine max cDNA clone... 89 1e-34	
45	emb AW267958 AW267958 EST306300 DSIR <i>Medicago truncatula</i> cDNA cl... 125 2e-34	
	emb AW667985 AW667985 GA__Ea0012C15 <i>Gossypium arboreum</i> 7-10 dpa ... 117 1e-33	
	emb AI725692 AI725692 BNLGHi12653 Six-day Cotton fiber <i>Gossypium</i> ... 142 1e-32	
	emb Z73295 CRPK1 <i>C.roseus</i> mRNA for receptor-like protein kinase. 125 2e-32	
	emb AW618736 AW618736 EST320722 <i>L. pennellii</i> trichome, Cornell U... 141 2e-32	
50	emb AA557073 AA557073 915 Loblolly pine N <i>Pinus taeda</i> cDNA clone... 85 6e-32	
	emb AI442338 AI442338 sa61b11.y1 Gm-cl004 Glycine max cDNA clone... 138 8e-32	
	emb AI495862 AI495862 sb17b07.y1 Gm-cl004 Glycine max cDNA clone... 138 2e-31	
	emb AW156187 AW156187 se20f08.y1 Gm-cl015 Glycine max cDNA clone... 137 5e-31	
	emb AI967314 AI967314 Ljirmp00-017 Ljirmp Lambda HybriZap two... 88 9e-31	
55	emb AW034426 AW034426 EST277997 tomato callus, TAMU Lycopersicon... 119 1e-30	
	emb AW224303 AW224303 EST301030 tomato fruit red ripe, TAMU Lyco... 128 1e-30	
	emb AW035394 AW035394 EST281132 tomato callus, TAMU Lycopersicon... 136 1e-30	
	emb AW930866 AW930866 EST356709 tomato fruit mature green, TAMU ... 84 1e-30	
	emb AW932515 AW932515 EST358358 tomato fruit mature green, TAMU ... 78 1e-30	
60	emb AI166936 AI166936 xylem.est.719 Poplar xylem Lambda ZAPII li... 85 1e-30	
	emb AV419736 AV419736 AV419736 <i>Lotus japonicus</i> young plants (two... 135 1e-30	

- gb|BE054944|BE054944 GA_Ea0032D07f Gossypium arboreum 7-10 dpa ... 91 2e-30
 emb|AW756743|AW756743 sl26f10.y1 Gm-c1027 Glycine max cDNA clone... 83 9e-30
 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 94 1e-29
 emb|AL354532|LMFL1177 Leishmania major Friedlin chromosome 21 co... 98 1e-29
 5 gb|BE060551|BE060551 HVSMeg0012J19f Hordeum vulgare pre-anthesis... 88 1e-29
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 85 3e-29
 emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 86 3e-29
 emb|AW650232|AW650232 EST328686 tomato germinating seedlings, TA... 85 3e-29
 emb|AW694732|AW694732 NF079D07ST1F1061 Developing stem Medicago ... 89 4e-29
 10 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 129 8e-29
 emb|AI967315|AI967315 Ljirnp00-018 Ljirnp Lambda HybriZap two... 105 2e-28
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 85 2e-28
 emb|AI731035|AI731035 BNLGHi8447 Six-day Cotton fiber Gossypium ... 75 3e-28
 emb|AW735867|AW735867 EST336635 tomato flower buds 0-3 mm, Corne... 127 3e-28
 15 emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 127 3e-28
 emb|AW774553|AW774553 EST333704 KV3 Medicago truncatula cDNA clo... 90 3e-28
 emb|AW094468|AW094468 EST287648 tomato mixed elicitor, BTI Lycop... 126 6e-28
 emb|AW203459|AW203459 sf30e03.y1 Gm-c1028 Glycine max cDNA clone... 75 7e-28
 emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 85 8e-28
 20 emb|AI727547|AI727547 BNLGHi8389 Six-day Cotton fiber Gossypium ... 75 9e-28
 emb|AI730872|AI730872 BNLGHi8131 Six-day Cotton fiber Gossypium ... 73 9e-28
 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 80 1e-27
 emb|AW299082|AW299082 EST305756 KV2 Medicago truncatula cDNA clo... 126 1e-27
 emb|AI937984|AI937984 sc06e07.y1 Gm-c1012 Glycine max cDNA clone... 81 1e-27
 25 emb|AF220602|AF220602 Lycopersicon pimpinellifolium Rio Grande 7... 73 2e-27
 emb|A58270|A58270 Sequence 1 from Patent WO9635790. 90 2e-27
 emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 75 3e-27
 emb|AW736597|AW736597 EST333089 KV3 Medicago truncatula cDNA clo... 105 3e-27
 gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 99 3e-27
 30 emb|AW587497|AW587497 IPPGHZ0085 Cotton fiber and embryo Lambda ... 123 3e-27
 emb|AW705130|AW705130 sk42a08.y1 Gm-c1019 Glycine max cDNA clone... 117 3e-27
 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 78 4e-27
 emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 80 4e-27
 emb|AW587493|AW587493 IPPGHZ0080 Cotton fiber and embryo Lambda ... 122 4e-27
 35 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 77 5e-27
 emb|AW224643|AW224643 EST303086 tomato root, plants pre-anthesis... 123 5e-27
 emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 75 7e-27
 emb|AW982539|AW982539 HVSMeg0003I16f Hordeum vulgare pre-anthesi... 121 8e-27
 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 80 9e-27
 40 emb|AW685504|AW685504 NF030H04NR1F1000 Nodulated root Medicago t... 122 1e-26
 emb|AW287734|AW287734 LG1_271_G05.b1_A002 Light Grown 1 (LG1) So... 104 1e-26

45 Query= Z97340.345_s_at 17485_s_at /id_source genbank /description
 "emb|cab10405.1| (z97340) beta-1, 3-glucanase class i precursor
 [arabidopsis thaliana]" /blast_score 1.00e-169 /ec_number /family
 /chip nova /gb_link /ncgi
 (921 letters)

50 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

55 Score E
 Sequences producing significant alignments: (bits) Value

60 gb|U22147|HBU22147 Hevea brasiliensis beta-1,3-glucanase (HGN1) ... 279 e-123
 emb|AJ133470|HBR133470 Hevea brasiliensis mRNA for beta-1,3-gluc... 276 e-123
 emb|A26453|A26453 Recombinant soya beta-1,3-glucanase plasmid. 259 e-117
 emb|A26449|A26449 Soya mutant beta-1,3-glucanase cDNA. 259 e-117

- emb|A26447|A26447 Soya beta-1,3-glucanase cDNA HindIII-HindIII f... 259 e-117
 emb|A26451|A26451 Soya beta-1,3-glucanase plasmid pBR59 NdeI-Hin... 259 e-117
 emb|X53129|PV13BDGL *P. vulgaris* mRNA for 1,3-beta-D-glucanase. 244 e-111
 emb|X89717|PVB13GLUC *P. vulgaris* beta-1,3-glucanase gene. 247 e-110
 5 emb|X07280|NPGLUCB *Nicotiana plumbaginifolia* mRNA for beta-glucan... 245 e-108
 gb|M23120|TOBGLUCB2 Tobacco (*N. plumbaginifolia*) beta-glucanase m... 245 e-108
 emb|AJ131047|CAR131047 *Cicer arietinum* mRNA for glucan-endo-1,3-... 251 e-107
 gb|L02212|PEABETAGLU Pea beta-1,3-glucanase gene; complete cds. 246 e-106
 gb|S51479|S51479 beta-1,3-glucanase [*Pisum sativum*=peas, cultiva... 246 e-106
 10 gb|U27179|MSU27179 *Medicago sativa* acidic glucanase mRNA, comple... 232 e-104
 emb|AF034109|AF034109 *Glycine max* beta-1,3-glucanase 4 (SGlu4) g... 225 4e-99
 gb|M80608|TOMB13GLUB *Lycopersicon esculentum* beta-1,3-glucanase ... 237 9e-99
 emb|AF067863|AF067863 *Solanum tuberosum* 1,3-beta-glucan glucanoh... 238 7e-97
 gb|U01901|U01901 *Solanum tuberosum* *Datura* endo-1,3-beta-D-glucan... 235 1e-96
 15 emb|X54742|NPB13GG *Nicotiana plumbaginifolia* beta-(1,3)-glucanas... 240 2e-96
 gb|U01900|U01900 *Solanum tuberosum* *Datura* endo-1,3-beta-D-glucan... 236 3e-96
 gb|M60402|TOBGLA13B *Nicotiana tabacum* glucan beta-1,3-glucanase ... 240 6e-95
 emb|X53600|NTGLN2G Tobacco gln2 gene for beta -1,3-glucanase. 240 6e-95
 emb|AF001523|AF001523 *Musa acuminata* beta-1, 3-glucanase mRNA, ... 205 8e-95
 20 emb|AF004838|AF004838 *Musa acuminata* beta-1,3-glucanase mRNA, pa... 205 8e-95
 gb|M60403|TOBGLB13B *Nicotiana tabacum* glucan beta-1,3-glucosidas... 238 2e-94
 emb|AF034117|AF034117 *Glycine max* beta-1,3-glucanase 12 (SGlu12)... 180 3e-94
 gb|M59442|TOBGLUCA *N. tabacum* basic-1,3-glucanase gene, complete cds. 236 7e-94
 emb|A16121|A16121 Intracellular Beta-1, 3 glucanase gene (SEQ ID... 236 7e-94
 25 gb|M59443|TOBGLUCB *N. tabacum* acidic beta-1,3-glucanase gene, com... 150 2e-92
 emb|A16120|A16120 Extracellular Beta-1, 3 glucanase gene (SEQ ID... 150 2e-92
 gb|M60460|TOBPR2A Tobacco PR2 protein mRNA, complete cds. 149 4e-91
 emb|AJ277900|VVI277900 *Vitis vinifera* mRNA for beta 1-3 glucanas... 221 8e-91
 gb|U01902|U01902 *Solanum tuberosum* *Datura* endo-1,3-beta-D-glucan... 238 3e-90
 30 gb|U49454|PPU49454 *Prunus persica* beta-1,3-glucanase (Gns1) gene... 211 2e-89
 emb|AF227953|AF227953 *Capsicum annuum* basic beta-1,3-glucanase (... 224 4e-89
 emb|AF034106|AF034106 *Glycine max* beta-1,3-glucanase 1 (SGlu1) g... 221 2e-88
 emb|AF141654|AF141654 *Nicotiana tabacum* beta-1,3-glucanase (GGL4... 139 3e-88
 gb|M60463|TOBGL153A Tobacco GL153 protein mRNA, complete cds. 139 3e-88
 35 gb|M20620|TOBGLUBC *N. tabacum* beta-1,3-glucanase mRNA, clone pGL43. 238 4e-88
 emb|AF034113|AF034113 *Glycine max* beta-1,3-glucanase 8 (SGlu8) g... 222 1e-87
 emb|X54431|NTSP41B Tobacco sp41b mRNA for (1-3)-beta-glucanase. 136 6e-87
 emb|AF141653|AF141653 *Nicotiana tabacum* beta-1,3-glucanase (GGL1... 136 1e-86
 gb|M60464|TOBB13G Tobacco beta-1,3-glucanase mRNA, complete cds. 136 1e-86
 40 emb|AJ000081|CSAJ81 *Citrus sinensis* mRNA for beta-1,3-glucanase. 113 2e-86
 emb|X81560|NTSP41AGN *N. tabacum* Sp41a gene. 136 4e-86
 emb|X54430|NTSP41A Tobacco sp41a mRNA for (1-3)-beta-glucanase. 135 8e-86
 dbj|E03985|E03985 DNA encoding beta-1,3-endoglucanase. 167 3e-84
 dbj|E02108|E02108 cDNA sequence coding for beta-1,3-endoglucanase. 167 3e-84
 45 gb|M37753|SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple... 167 3e-84
 emb|AJ009932|STAJ9932 *Solanum tuberosum* mRNA for beta-1,3-glucan... 144 4e-84
 emb|AW034632|AW034632 EST278316 tomato callus, TAMU *Lycopersicon*... 188 1e-82
 gb|U41323|GMU41323 *Glycine max* beta-1,3-glucanase (SGN1) gene, c... 169 3e-82
 emb|AW033770|AW033770 EST277341 tomato callus, TAMU *Lycopersicon*... 186 5e-82
 50 gb|M80604|TOMB13GLUA *Lycopersicon esculentum* beta-1,3-glucanase ... 142 5e-82
 emb|X74905|LEQA *L. esculentum* TomQ'a mRNA for beta(1,3)glucanase. 128 4e-79
 emb|AI896001|AI896001 EST265444 tomato callus, TAMU *Lycopersicon*... 175 9e-79
 emb|AW034584|AW034584 EST278268 tomato callus, TAMU *Lycopersicon*... 226 9e-79
 emb|X54456|NTEC32139 *N. tabacum* mRNA for acidic beta-1,3 glucana... 127 2e-78
 55 emb|AJ012751|CAR012751 *Cicer arietinum* mRNA for glucan endo-beta... 126 2e-78
 emb|AW034478|AW034478 EST278049 tomato callus, TAMU *Lycopersicon*... 227 8e-78
 emb|AW031078|AW031078 EST274385 tomato callus, TAMU *Lycopersicon*... 169 4e-77
 emb|AW035235|AW035235 EST280497 tomato callus, TAMU *Lycopersicon*... 179 5e-77
 gb|M60462|TOBPRNA Tobacco PRN protein mRNA, 3' end. 117 5e-76
 60 emb|AW775271|AW775271 EST334336 *DSIL Medicago truncatula* cDNA cl... 163 6e-76
 emb|AW776932|AW776932 EST335997 *DSIL Medicago truncatula* cDNA cl... 156 7e-76

- emb|AW216637|AW216637 EST295351 tomato callus, TAMU Lycopersicon... 164 2e-75
 emb|AW032447|AW032447 EST276006 tomato callus, TAMU Lycopersicon... 227 2e-74
 emb|AW156463|AW156463 se26e04.y1 Gm-c1015 Glycine max cDNA clone... 256 3e-74
 emb|Z68154|GHBGLUCS G.hirsutum mRNA for 1,3-beta-glucanase. 152 1e-73
 5 gb|M63634|TOBGCBREG Nicotiana plumbaginifolia beta(1,3)-glucanas... 250 9e-73
 emb|AW032644|AW032644 EST276203 tomato callus, TAMU Lycopersicon... 189 1e-71
 emb|AF230109|AF230109 Populus alba x Populus tremula beta-1,3 gl... 173 3e-71
 gb|M20618|TOBGLUBA N.tabacum beta-1,3-glucanase mRNA, clones pGL... 238 3e-71
 emb|AI894445|AI894445 EST263900 tomato callus, TAMU Lycopersicon... 231 3e-71
 10 emb|AF034107|AF034107 Glycine max beta-1,3-glucanase 2 (SGlu2) g... 142 7e-71
 emb|AW031387|AW031387 EST274841 tomato callus, TAMU Lycopersicon... 237 7e-71
 emb|AW035366|AW035366 EST280928 tomato callus, TAMU Lycopersicon... 237 7e-71
 emb|AI896035|AI896035 EST265478 tomato callus, TAMU Lycopersicon... 237 7e-71
 15 emb|AW031155|AW031155 EST274589 tomato callus, TAMU Lycopersicon... 237 7e-71
 emb|AW030447|AW030447 EST273702 tomato callus, TAMU Lycopersicon... 236 3e-70
 emb|AF034116|AF034116 Glycine max beta-1,3-glucanase 11 (SGlu11)... 124 9e-70
 emb|AW030277|AW030277 EST273532 tomato callus, TAMU Lycopersicon... 144 2e-69
 emb|AF034110|AF034110 Glycine max beta-1,3-glucanase 5 (SGlu5) g... 122 3e-69
 emb|AW035160|AW035160 EST280422 tomato callus, TAMU Lycopersicon... 142 6e-69
 20 emb|AW032444|AW032444 EST276003 tomato callus, TAMU Lycopersicon... 142 6e-69
 emb|X74906|LEQB L.esculentum TomQ'b mRNA for beta(1,3)glucanase. 101 1e-68
 emb|AJ011769|CIN011769 Cichorium intybus X Cichorium endivia sub... 97 1e-68
 emb|AW030283|AW030283 EST273538 tomato callus, TAMU Lycopersicon... 140 2e-68
 gb|M13237|BLYGLUCB Barley beta glucanase mRNA. 158 7e-68
 25 emb|Z15131|ASBGLUCAN A.sativa mRNA for beta glucanase. 158 9e-68
 emb|AI896042|AI896042 EST265485 tomato callus, TAMU Lycopersicon... 237 1e-67
 gb|M62740|BLYGLB2 Hordeum vulgare 1,3-1,4-beta-D glucan 4-glucan... 158 2e-67
 emb|AW031259|AW031259 EST274634 tomato callus, TAMU Lycopersicon... 136 3e-67
 emb|AW035840|AW035840 EST281994 tomato callus, TAMU Lycopersicon... 136 3e-67
 30 emb|AW032451|AW032451 EST276010 tomato callus, TAMU Lycopersicon... 136 3e-67
 emb|AW031353|AW031353 EST274807 tomato callus, TAMU Lycopersicon... 136 3e-67
 emb|AI895981|AI895981 EST265424 tomato callus, TAMU Lycopersicon... 136 3e-67
 gb|U73709|VVU73709 Vitis vinifera beta-1,3-glucanase mRNA, parti... 244 3e-67
 emb|Z22874|TABETGLUB T.aestivum (1,3;1,4) beta glucanase mRNA, c... 160 3e-67
 35 emb|AF034114|AF034114 Glycine max beta-1,3-glucanase 9 (SGlu9) p... 119 7e-67

Query= U18993.2_s_at 17487_s_at /id_source genbank /description
 gb|aac49117.1|(u18993) tryptophan synthase alpha chain [arabidopsis
 40 thaliana] /blast_score 1.00e-158 /ec_number /family /chip nova
 /gb_link /ncgi
 (939 letters)

Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 50 Sequences producing significant alignments: (bits) Value

- emb|AW730233|AW730233 GA_Ea0014B16 Gossypium arboreum 7-10 dpa ... 352 5e-98
 emb|AW649960|AW649960 EST328414 tomato germinating seedlings, TA... 308 4e-83
 emb|AW621664|AW621664 EST312462 tomato root during/after fruit s... 290 1e-77
 55 emb|AW031327|AW031327 EST274781 tomato callus, TAMU Lycopersicon... 282 3e-75
 gb|U38804|PPU38804 Porphyra purpurea chloroplast, complete genome. 271 4e-72
 emb|AW775853|AW775853 EST334918 DSIL Medicago truncatula cDNA cl... 264 9e-70
 emb|Z21642|CHASTRNA Antithamnion sp. Chloroplast trnK, trnE, trpA... 255 4e-67
 gb|BE124387|BE124387 EST393422 GVN Medicago truncatula cDNA clon... 227 9e-59
 60 gb|BE121873|BE121873 894015F07.y1 C. reinhardtii CC-1690, normal... 227 1e-58
 emb|AF022186|AF022186 Cyanidium caldarium strain RK1 chloroplast... 220 1e-56

- emb|AI782364|AI782364 EST263243 tomato susceptible, Cornell Lyco... 210 1e-53
emb|AW691298|AW691298 NF040B01ST1F1000 Developing stem Medicago ... 193 1e-49
dbj|D63675|D63675 Cyanidioschyzon merolae trnK, trpA, trnT, rps4... 130 1e-49
emb|AV392084|AV392084 AV392084 Chlamydomonas reinhardtii C9 Chla... 195 5e-49
5 emb|AA660642|AA660642 00530 MtRHE Medicago truncatula cDNA 5' si... 190 1e-47
dbj|D17791|CYNPLTRNK C.caldarium chloroplast gene for trnK and g... 121 1e-46
emb|AW034248|AW034248 EST277819 tomato callus, TAMU Lycopersicon... 184 9e-46
dbj|D63676|D63676 Cyanidium caldarium trnK, trpA, trnT, rps4, tr... 122 1e-45
gb|L38526|L38526 BNAF0168E Mustard flower buds Brassica rapa cDN... 177 1e-43
10 emb|V01342|SCTRP5A Yeast gene (trp5) for tryptophan synthetase. 86 9e-42
emb|Z72548|SCYGL026C S.cerevisiae chromosome VII reading frame O... 86 9e-42
emb|AW398861|AW398861 EST309361 L. pennellii trichome, Cornell U... 158 5e-38
emb|AU090244|AU090244 AU090244 Hordeum vulgare subsp. vulgare Up... 149 7e-38
emb|AW650911|AW650911 EST329365 tomato germinating seedlings, TA... 141 1e-32
15 emb|AI773494|AI773494 EST254594 tomato resistant, Cornell Lycope... 138 5e-32
emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8. 74 3e-30
emb|V01343|SCTRP5B Part of the yeast gene for tryptophan synthet... 86 2e-26
emb|AI165371|AI165371 A082p39u Hybrid aspen plasmid library Popu... 81 1e-21
emb|AU090028|AU090028 AU090028 Hordeum vulgare subsp. vulgare Up... 97 2e-19
20 gb|J04594|NEUTRP3A N.crassa tryptophan synthetase (trp3) alpha-2... 78 1e-17
emb|AF084886|AF084886 Neurospora crassa 314-448A mutant tryptoph... 68 9e-11
emb|AF084890|AF084890 Neurospora crassa TD 554-6A mutant tryptop... 53 4e-10
emb|AF084880|AF084880 Neurospora crassa EMSG9-9A mutant tryptoph... 66 5e-10
emb|AF084885|AF084885 Neurospora crassa NG61-6A mutant tryptoph... 64 1e-09
25 emb|AF084884|AF084884 Neurospora crassa 314-722A mutant tryptoph... 64 1e-09
emb|AF084883|AF084883 Neurospora crassa 314-709A mutant tryptoph... 64 1e-09
emb|AF084882|AF084882 Neurospora crassa 314-682A mutant tryptoph... 64 1e-09
emb|AF084881|AF084881 Neurospora crassa 314-693A mutant tryptoph... 64 2e-09
emb|AF084889|AF084889 Neurospora crassa 314-492-2A mutant trypto... 53 3e-09
30 gb|M29094|CCITRP01 Mushroom (C.cinereus) tryptophan synthetase (... 59 4e-08
emb|AU011013|AU011013 AU011013 Schizosaccharomyces pombe late lo... 54 2e-06
emb|AW693052|AW693052 NF059C08ST1F1065 Developing stem Medicago ... 51 1e-05
emb|AV390244|AV390244 AV390244 Chlamydomonas reinhardtii C9 Chla... 49 4e-05
emb|AW616467|AW616467 EST322878 L. hirsutum trichome, Cornell Un... 48 7e-05
35 emb|AL354022|P761R Leishmania major Friedlin PAC P761 right end-... 44 0.002
gb|M91656|CCITRP05 Coprinus cinereus tryptophan synthetase (TRP1... 43 0.005
emb|AQ903789|AQ903789 GSSTc04230 Trypanosome cruzi random genomi... 35 0.24
emb|AW727215|AW727215 GA__Ea0023N23 Gossypium arboreum 7-10 dpa ... 36 0.52
gb|M91654|CCITRP03 Coprinus cinereus tryptophan synthetase (TRP1... 36 0.52
40 emb|AW728975|AW728975 GA__Ea0018P19 Gossypium arboreum 7-10 dpa ... 35 0.64
emb|AL139794|LMFP1105 Leishmania major Friedlin chromosome 4 PAC... 35 0.87
emb|AW926438|AW926438 HVSMEg0007D14 Hordeum vulgare pre-anthesis... 34 1.2
emb|AA965348|AA965348 e9d04a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3
gb|U12630|ENU12630 Emericella nidulans R153 core histone H3 (H3)... 34 1.3
45 emb|AI007494|AI007494 e9c09a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3
emb|AA787433|AA787433 n3d04a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3
emb|X55548|ANH3GENE A.nidulans gene for core histone for H3. 34 1.3
emb|AQ396426|AQ396426 mgxb0013C24f CUGI Rice Blast BAC Library P... 34 1.6
emb|AF262997|AF262997 Ricinus communis NADP-dependent malic prot... 34 1.6
50 gb|M19025|CFUCPOR C.fumago cpo gene encoding chloroperoxidase, c... 34 1.6
emb|AF084888|AF084888 Neurospora crassa 656-2A mutant tryptophan... 31 1.7
emb|AF084887|AF084887 Neurospora crassa TDA78(1-A)9A(TD201) muta... 31 1.7
emb|AW694774|AW694774 NF080A05ST1F1036 Developing stem Medicago ... 34 1.8
emb|Y18012|TVE18012 Trametes versicolor mRNA for laccase. 33 2.3
55 emb|AQ500614|AQ500614 V35B5 mTn-3xHA/lacZ Insertion Library Sacc... 33 2.5
emb|AW187498|AW187498 BNLGHi6414 Six-day Cotton fiber Gossypium ... 33 3.1
emb|AW187530|AW187530 BNLGHi6944 Six-day Cotton fiber Gossypium ... 33 3.1
emb|AW694072|AW694072 NF072B12ST1F1096 Developing stem Medicago ... 33 3.1
emb|AW186883|AW186883 BNLGHi6498 Six-day Cotton fiber Gossypium ... 33 3.1
60 emb|AW187537|AW187537 BNLGHi7006 Six-day Cotton fiber Gossypium ... 33 3.1
emb|AW187474|AW187474 BNLGHi5936 Six-day Cotton fiber Gossypium ... 33 3.1

	emb AA167859 AA167859 CpEST.053 uniZAPCpIOWAsporoLib1 Cryptospor...	33	3.5
	emb AV421993 AV421993 AV421993 Lotus japonicus young plants (two...	33	4.3
	emb AF129874 AF129874 Pichia angusta peroxin-6 (PEX6) gene, comp...	33	4.3
	emb AL112679 CNS01AA7 Botrytis cinerea strain T4 cDNA library un...	33	4.7
5	gb BE028433 BE028433 EtESTea78d07.y1 Eimeria M5-6 Merozoite stag...	32	5.9
	emb AI166784 AI166784 xylem.est.582 Poplar xylem Lambda ZAPII li...	32	5.9
	emb AQ941624 AQ941624 Sheared DNA-53E1.TF Sheared DNA Trypanosom...	32	5.9
	emb AW728623 AW728623 GA__Ea0017G06 Gossypium arboreum 7-10 dpa ...	32	5.9
	gb BE027723 BE027723 EtESTea86c08.y1 Eimeria M5-6 Merozoite stag...	32	5.9
10	emb AI757375 AI757375 EtESTea32d03.y1 Eimeria S5-2 Sporozoite st...	32	5.9
	gb BE027843 BE027843 EtESTea88c05.y1 Eimeria M5-6 Merozoite stag...	32	5.9
	emb AI973878 AI973878 sd13a09.y1 Gm-c1020 Glycine max cDNA clone...	32	5.9
	dbj D85261 D85261 Plasmodium vivax clone TD439B DNA for merozoit...	32	5.9
	dbj D85251 D85251 Plasmodium vivax clone TD207B DNA for merozoit...	32	5.9
15	emb Z69381 SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom...	32	6.5
	emb Z71509 SCYNL233W S.cerevisiae chromosome XIV reading frame O...	32	6.5
	emb AW707662 AW707662 832011E08.y1 C. reinhardtii CC-125 nutrien...	28	7.3
	emb AF083075 AF083075 Fusarium oxysporum f. sp. lycopersici exop...	32	8.1
	emb AV411934 AV411934 AV411934 Lotus japonicus young plants (two...	32	8.1
20	emb AW703740 AW703740 sk23g09.y1 Gm-c1028 Glycine max cDNA clone...	32	8.1
	emb AW703739 AW703739 sk23g08.y1 Gm-c1028 Glycine max cDNA clone...	32	8.1
	emb AV419698 AV419698 AV419698 Lotus japonicus young plants (two...	32	8.1
	emb AV419299 AV419299 AV419299 Lotus japonicus young plants (two...	32	8.1
	emb AV420652 AV420652 AV420652 Lotus japonicus young plants (two...	32	8.1
25	emb AV408860 AV408860 AV408860 Lotus japonicus young plants (two...	32	8.1
	emb AV420989 AV420989 AV420989 Lotus japonicus young plants (two...	32	8.1
	emb AV419314 AV419314 AV419314 Lotus japonicus young plants (two...	32	8.1
	emb AW720540 AW720540 LjNEST18h4r Lotus japonicus nodule library...	32	8.1
30	emb X77895 CPGPRNL28 G.pyrenaica chloroplast trnL gene intron.	32	8.1

Query= Z97339.197_at 17899_at /id_source genbank /description
emb|cab10339.1| (z97339) hypothetical protein [arabidopsis thaliana]
/blast_score 5.00e-55 /ec_number /family /chip nova /gb_link
35 http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|z97339| /ncgi
http://www.ncgr.org/cgi-bin/ff?z97339
(441 letters)

40 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

45	Score E	
	Sequences producing significant alignments:	(bits) Value
	emb AW685774 AW685774 NF035A03NR1F1000 Nodulated root Medicago t...	123 6e-28
	emb AW687017 AW687017 NF005A10RT1F1072 Developing root Medicago ...	123 6e-28
50	emb AW687794 AW687794 NF013E08RT1F1066 Developing root Medicago ...	89 3e-23
	emb AW310121 AW310121 sf31d07.x1 Gm-c1028 Glycine max cDNA clone...	68 3e-19
	emb AW704640 AW704640 sk54f05.y1 Gm-c1019 Glycine max cDNA clone...	68 3e-19
	emb AW395252 AW395252 sh45g06.y1 Gm-c1017 Glycine max cDNA clone...	68 3e-19
	emb AW704612 AW704612 sk54c11.y1 Gm-c1019 Glycine max cDNA clone...	68 3e-19
55	emb AT000508 AT000508 AT000508 Brassica rapa guard cell Brassica...	50 2e-18
	emb AW704218 AW704218 sk17c12.y1 Gm-c1028 Glycine max cDNA clone...	63 3e-17
	emb AW423428 AW423428 sh66f08.y1 Gm-c1015 Glycine max cDNA clone...	63 1e-16
	emb AW687188 AW687188 NF006H09RT1F1079 Developing root Medicago ...	82 3e-15
	emb AW684973 AW684973 NF023G04NR1F1000 Nodulated root Medicago t...	68 1e-13
60	emb AW233878 AW233878 sf31d07.y1 Gm-c1028 Glycine max cDNA clone...	69 3e-13
	emb AW687098 AW687098 NF006A02RT1F1007 Developing root Medicago ...	72 2e-12

	emb AW686346 AW686346 NF040F08NR1F1000 Nodulated root Medicago t...	67	7e-12
	emb AI437669 AI437669 sa38a11.y1 Gm-cl004 Glycine max cDNA clone...	48	1e-11
	emb AW348644 AW348644 GM210003A11A8R Gm-r1021 Glycine max cDNA 3...	48	2e-11
	emb AW687565 AW687565 NF011A04RT1F1024 Developing root Medicago ...	48	2e-11
5	gb BE033951 BE033951 MG02E05 MG Mesembryanthemum crystallinum cD...	44	3e-10
	emb AW185776 AW185776 se59e03.y1 Gm-cl019 Glycine max cDNA clone...	51	2e-08
	emb AI930953 AI930953 sb45c07.y1 Gm-cl015 Glycine max cDNA clone...	48	4e-08
	emb AI440599 AI440599 sa68c05.y1 Gm-cl004 Glycine max cDNA clone...	48	6e-08
	emb AW394608 AW394608 sh33e11.y1 Gm-cl017 Glycine max cDNA clone...	46	2e-07
10	emb AW284126 AW284126 LG1_262_A05.g1_A002 Light Grown 1 (LG1) So...	55	3e-07
	emb AI960446 AI960446 sc84a10.y1 Gm-cl018 Glycine max cDNA clone...	48	4e-06
	emb AI794716 AI794716 sb68b06.y1 Gm-cl019 Glycine max cDNA clone...	48	5e-06
	gb BE024111 BE024111 sm96h03.y1 Gm-cl015 Glycine max cDNA clone ...	48	9e-06
	emb Z99969 MAZ99969 Musa acuminata mRNA for putative beta-1,3-gl...	41	6e-05
15	emb AV412437 AV412437 AV412437 Lotus japonicus young plants (two...	47	9e-05
	emb AV427297 AV427297 AV427297 Lotus japonicus young plants (two...	46	2e-04
	emb AW666090 AW666090 sk32a11.y1 Gm-cl028 Glycine max cDNA clone...	42	2e-04
	emb AW277478 AW277478 sf82e11.y1 Gm-cl019 Glycine max cDNA clone...	37	4e-04
	emb AW775954 AW775954 EST335019 DSIL Medicago truncatula cDNA cl...	42	7e-04
20	gb BE122569 BE122569 Ljimpest29-344-g6 Ljimp Lambda HybriZap t...	43	0.001
	emb AW299135 AW299135 EST305809 KV2 Medicago truncatula cDNA clo...	43	0.002
	emb AW423359 AW423359 sh06g04.y1 Gm-cl016 Glycine max cDNA clone...	41	0.004
	emb AW171748 AW171748 N100642e rootphos(-) Medicago truncatula c...	40	0.014
	emb AW285241 AW285241 LG1_236_C10.g1_A002 Light Grown 1 (LG1) So...	39	0.026
25	emb AW747074 AW747074 WS1_65_A07.g1_A002 Water-stressed 1 (WS1) ...	39	0.026
	emb AW649685 AW649685 EST328139 tomato germinating seedlings, TA...	38	0.036
	emb AW299176 AW299176 EST305986 KV2 Medicago truncatula cDNA clo...	38	0.036
	emb AW220014 AW220014 EST302497 tomato root during/after fruit s...	38	0.050
	gb C96140 C96140 C96140 Marchantia polymorpha immature sex organ...	38	0.050
30	emb AW625648 AW625648 EST319555 tomato radicle, 5 d post-imbibit...	38	0.050
	emb AW926780 AW926780 HVSMEG0008D23 Hordeum vulgare pre-anthesis...	37	0.094
	gb L05906 PMCMMSGF Pneumocystis carinii (clone GP3) major surface...	36	0.18
	emb AW333354 AW333354 S20F5 AGS-1 Pneumocystis carinii f. sp. ca...	36	0.18
	emb Z98595 SPAC11E3 S.pombe chromosome I cosmid c11E3.	35	0.24
35	emb AW725520 AW725520 GA_Ea0018G22 Gossypium arboreum 7-10 dpa ...	35	0.46
	gb BE052896 BE052896 GA_Ea0025I06f Gossypium arboreum 7-10 dpa ...	35	0.46
	emb AW309936 AW309936 sf26g12.x1 Gm-cl028 Glycine max cDNA clone...	35	0.46
	emb AW310120 AW310120 sf31d06.x1 Gm-cl028 Glycine max cDNA clone...	35	0.46
	emb AW233798 AW233798 sf26g12.y1 Gm-cl028 Glycine max cDNA clone...	35	0.46
40	gb BE053040 BE053040 GA_Ea0015D14f Gossypium arboreum 7-10 dpa ...	35	0.46
	emb AW310598 AW310598 sg21h03.x1 Gm-cl024 Glycine max cDNA clone...	35	0.46
	emb AI731906 AI731906 BNLGHi11249 Six-day Cotton fiber Gossypium...	35	0.46
	gb BE054609 BE054609 GA_Ea0006A14f Gossypium arboreum 7-10 dpa ...	35	0.46
	emb AW278505 AW278505 sf45c08.y1 Gm-cl009 Glycine max cDNA clone...	35	0.46
45	emb AC013353 AC013353 Trypanosoma brucei chromosome VI clone RPC...	34	0.63
	emb AI728996 AI728996 BNLGHi12315 Six-day Cotton fiber Gossypium...	34	0.63
	emb AW691828 AW691828 NF044F04ST1F1000 Developing stem Medicago ...	34	0.63
	emb AI729057 AI729057 BNLGHi12476 Six-day Cotton fiber Gossypium...	34	0.63
	emb AI731500 AI731500 BNLGHi9982 Six-day Cotton fiber Gossypium ...	34	0.63
50	emb AQ660279 AQ660279 Sheared DNA-3L23.TF Sheared DNA Trypanosom...	34	0.63
	emb AI729672 AI729672 BNLGHi13930 Six-day Cotton fiber Gossypium...	34	0.63
	emb AI725456 AI725456 BNLGHi12219 Six-day Cotton fiber Gossypium...	34	0.63
	emb AQ656131 AQ656131 Sheared DNA-27G20.TF Sheared DNA Trypanoso...	34	0.63
	emb AI731231 AI731231 BNLGHi8954 Six-day Cotton fiber Gossypium ...	34	0.87
55	emb AL035477 PFMAL4P4 Plasmodium falciparum chromosome 4 strain ...	34	0.87
	gb BE033791 BE033791 MF06E10 MF Mesembryanthemum crystallinum cD...	34	0.87
	gb BE034803 BE034803 ML04E10 ML Mesembryanthemum crystallinum cD...	34	0.87
	emb AI731464 AI731464 BNLGHi9855 Six-day Cotton fiber Gossypium ...	34	0.87
	emb AI727451 AI727451 BNLGHi8020 Six-day Cotton fiber Gossypium ...	34	0.87
60	emb AW620830 AW620830 sj47b03.y1 Gm-cl033 Glycine max cDNA clone...	28	1.1
	dbj D63449 YSCATF1A Yeast ATF1 gene for alcohol acetyltransferas...	33	1.2

dbj|E08050|E08050 cDNA encoding beer yeast alcohol acetyltransfe... 33 1.2
 dbj|E06817|E06817 DNA encoding alcohol acetyltransferase 1. 33 1.2
 dbj|D26554|YSCATF1 Yeast ATF1 gene for alcohol acetyltransferase... 33 1.2
 dbj|E08049|E08049 cDNA encoding sake yeast alcohol acetyltransfe... 33 1.2
 5 dbj|E06816|E06816 DNA encoding alcohol acetyltransferase 1. 33 1.2
 emb|Z75285|SCYOR377W *S.cerevisiae* chromosome XV reading frame OR... 33 1.2
 emb|AW725476|AW725476 GA__Ea0018C14 *Gossypium arboreum* 7-10 dpa ... 33 1.6
 emb|AI812453|AI812453 11C3 Pine Lambda Zap Xylem library *Pinus t...* 33 1.6
 emb|AW459992|AW459992 si07c04.y1 Gm-c1029 Glycine max cDNA clone... 33 1.6
 10 emb|X01777|HVB3HORD Barley mRNA fragment for B3-hordein. 33 1.6
 emb|AQ449927|AQ449927 500006A04.x1 CplOWAM13mp18gDNA1 *Cryptospor...* 33 1.6
 emb|AE001274|AE001274 *Leishmania major* chromosome 1, complete se... 30 2.2
 emb|AL031261|SPBC3H7 *S.pombe* chromosome II cosmid c3H7. 32 2.2
 emb|AI812374|AI812374 1F12 Pine Lambda Zap Xylem library *Pinus t...* 32 2.2
 15 emb|AI728744|AI728744 BNLGHi11492 Six-day Cotton fiber *Gossypium...* 32 2.2
 gb|BE036189|BE036189 MO20F12 *MO Mesembryanthemum crystallinum* cD... 32 3.1
 emb|AW925749|AW925749 HVSMEg0005G16 *Hordeum vulgare* pre-anthesis... 32 3.1
 emb|AQ411951|AQ411951 CpG0926A CplOWAgDNA1 *Cryptosporidium parvu...* 32 3.1
 emb|AQ935548|AQ935548 CpG2528A CplOWAgDNA1 *Cryptosporidium parvu...* 32 3.1
 20 emb|AQ411952|AQ411952 CpG0926B CplOWAgDNA1 *Cryptosporidium parvu...* 32 3.1
 gb|B67221|B67221 CpG0036A CplOWAgDNA1 *Cryptosporidium parvum* gen... 32 3.1
 emb|AW030301|AW030301 EST273556 tomato callus, TAMU *Lycopersicon...* 31 4.2
 emb|AL160371|LMFLCHR15 *Leishmania major* Friedlin assembled chrom... 31 4.2
 emb|AL122012|LMFL8342 *Leishmania major* Friedlin chromosome 23 co... 31 4.2
 25 emb|X60772|GMOLEOA G.max mRNA for 24 kDa oleosin isoform (partia... 31 4.2

Query= AJ006960.4_s_at 17930_s_at /id_source genbank /description
 emb|caa07352.1| (aj006960) peroxidase [*arabidopsis thaliana*]
 30 /blast_score 1.00e-111 /ec_number /family /chip nova /gb_link /ncgi

(592 letters)

Database: plantfungal
 35 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 40 Sequences producing significant alignments: (bits) Value

emb|X90695|MSRNAPE02 *M.sativa* mRNA for peroxidase 2. 339 1e-92
 emb|AJ011939|TRE011939 *Trifolium repens* mRNA for peroxidase. 335 2e-91
 emb|Y10469|SOPRXR8 *S.oleracea* mRNA for peroxidase, clone PC55. 332 2e-90
 45 emb|AI487510|AI487510 EST245832 tomato ovary, TAMU *Lycopersicon* ... 327 5e-89
 emb|AI486784|AI486784 EST245106 tomato ovary, TAMU *Lycopersicon* ... 327 5e-89
 emb|AI895842|AI895842 EST265285 tomato callus, TAMU *Lycopersicon*... 325 1e-88
 emb|AW032442|AW032442 EST276001 tomato callus, TAMU *Lycopersicon*... 325 2e-88
 gb|L36158|ALFPXDD *Medicago sativa* peroxidase (pxdD) mRNA, 3' end. 320 6e-87
 50 emb|AW216351|AW216351 EST295095 tomato callus, TAMU *Lycopersicon*... 319 1e-86
 emb|AW691003|AW691003 NF040C11ST1F1000 Developing stem *Medicago* ... 319 2e-86
 emb|AW625601|AW625601 EST319508 tomato radicle, 5 d post-imbibit... 318 3e-86
 gb|BE124281|BE124281 EST394406 *DSIL Medicago truncatula* cDNA clo... 314 4e-85
 emb|AI894487|AI894487 EST263930 tomato callus, TAMU *Lycopersicon*... 307 4e-83
 55 emb|AW666274|AW666274 sk34e11.y1 Gm-c1028 Glycine max cDNA clone... 304 4e-82
 emb|AI897419|AI897419 EST266862 tomato ovary, TAMU *Lycopersicon* ... 295 2e-79
 emb|AW329042|AW329042 N200241e rootphos(-) *Medicago truncatula* c... 292 2e-78
 emb|AW666298|AW666298 sk34h04.y1 Gm-c1028 Glycine max cDNA clone... 292 2e-78
 emb|AW030788|AW030788 EST274043 tomato callus, TAMU *Lycopersicon*... 292 2e-78
 60 emb|AW031625|AW031625 EST275079 tomato callus, TAMU *Lycopersicon*... 291 3e-78
 emb|AW278809|AW278809 sf98g02.y1 Gm-c1019 Glycine max cDNA clone... 200 3e-78

	emb AW221693 AW221693 EST298504 tomato fruit red ripe, TAMU Lyco...	290 7e-78
	emb AW216725 AW216725 EST295439 tomato callus, TAMU Lycopersicon...	287 4e-77
	emb AW035689 AW035689 EST281843 tomato callus, TAMU Lycopersicon...	286 1e-76
	emb AW221724 AW221724 EST298535 tomato fruit red ripe, TAMU Lyco...	285 2e-76
5	emb AW030405 AW030405 EST273660 tomato callus, TAMU Lycopersicon...	285 2e-76
	emb AW216626 AW216626 EST295340 tomato callus, TAMU Lycopersicon...	284 5e-76
	emb AA661001 AA661001 00898 MtRHE Medicago truncatula cDNA 5' si...	284 5e-76
	emb AW032463 AW032463 EST276022 tomato callus, TAMU Lycopersicon...	282 2e-75
	emb AW596100 AW596100 si97h09.y1 Gm-cl032 Glycine max cDNA clone...	281 2e-75
10	emb AW035606 AW035606 EST281344 tomato callus, TAMU Lycopersicon...	281 4e-75
	gb BE020228 BE020228 sm42b11.y1 Gm-cl028 Glycine max cDNA clone ...	279 1e-74
	emb AW686501 AW686501 NF038G03NR1F1000 Nodulated root Medicago t...	279 2e-74
	emb AW031359 AW031359 EST274813 tomato callus, TAMU Lycopersicon...	278 2e-74
	emb AW650288 AW650288 EST328742 tomato germinating seedlings, TA...	277 4e-74
15	emb AW705765 AW705765 sk51f01.y1 Gm-cl019 Glycine max cDNA clone...	184 6e-74
	emb AI895322 AI895322 EST264765 tomato callus, TAMU Lycopersicon...	268 2e-71
	emb AW649016 AW649016 EST327470 tomato germinating seedlings, TA...	265 2e-70
	emb AW703879 AW703879 sk25c06.y1 Gm-cl028 Glycine max cDNA clone...	264 5e-70
	emb AW306953 AW306953 sf50h05.y1 Gm-cl009 Glycine max cDNA clone...	263 1e-69
20	emb AW306251 AW306251 se48c03.y1 Gm-cl017 Glycine max cDNA clone...	261 4e-69
	emb AW704671 AW704671 sk39a11.y1 Gm-cl028 Glycine max cDNA clone...	259 1e-68
	emb AI895156 AI895156 EST264599 tomato callus, TAMU Lycopersicon...	257 6e-68
	emb AW686857 AW686857 NF003C01RT1F1000 Developing root Medicago ...	241 8e-68
	emb AV421737 AV421737 AV421737 Lotus japonicus young plants (two...	256 9e-68
25	emb AW029767 AW029767 EST273022 tomato callus, TAMU Lycopersicon...	253 8e-67
	emb AW687854 AW687854 NF014B12RT1F1096 Developing root Medicago ...	214 1e-66
	emb AW704702 AW704702 sk39d10.y1 Gm-cl028 Glycine max cDNA clone...	248 3e-65
	emb AI899344 AI899344 EST268787 tomato ovary, TAMU Lycopersicon ...	248 3e-65
	emb AV420440 AV420440 AV420440 Lotus japonicus young plants (two...	248 3e-65
30	emb AI895840 AI895840 EST265283 tomato callus, TAMU Lycopersicon...	248 4e-65
	emb AI894658 AI894658 EST264101 tomato callus, TAMU Lycopersicon...	246 1e-64
	emb AW030796 AW030796 EST274051 tomato callus, TAMU Lycopersicon...	243 6e-64
	emb AI896743 AI896743 EST266186 tomato callus, TAMU Lycopersicon...	242 2e-63
	emb AW687617 AW687617 NF011E10RT1F1082 Developing root Medicago ...	241 4e-63
35	emb AW029904 AW029904 EST273159 tomato callus, TAMU Lycopersicon...	239 1e-62
	emb AW676864 AW676864 DG1_1_D12.b1_A002 Dark Grown 1 (DG1) Sorgh...	237 4e-62
	emb AI896941 AI896941 EST266384 tomato callus, TAMU Lycopersicon...	236 1e-61
	emb AW622528 AW622528 EST313328 tomato root during/after fruit s...	232 1e-60
	emb AW208032 AW208032 M111060e DSIR Medicago truncatula cDNA clo...	232 1e-60
40	emb AW830948 AW830948 sm30f07.y1 Gm-cl028 Glycine max cDNA clone...	232 2e-60
	emb AI055677 AI055677 coau0004L19 Cotton Boll Abscission Zone cD...	205 4e-58
	emb AW034420 AW034420 EST277991 tomato callus, TAMU Lycopersicon...	149 6e-56
	emb AW032120 AW032120 EST275574 tomato callus, TAMU Lycopersicon...	217 6e-56
	emb AW039340 AW039340 EST281597 tomato mixed elicitor, BTI Lycop...	217 6e-56
45	emb AI896467 AI896467 EST265898 tomato callus, TAMU Lycopersicon...	216 9e-56
	emb AV422712 AV422712 AV422712 Lotus japonicus young plants (two...	216 1e-55
	emb AW651552 AW651552 EST330018 tomato germinating seedlings, TA...	131 1e-54
	emb AW706479 AW706479 sj57a08.y1 Gm-cl033 Glycine max cDNA clone...	204 2e-54
	emb AW234624 AW234624 sf17d08.y1 Gm-cl028 Glycine max cDNA clone...	212 2e-54
50	emb AW832025 AW832025 sm30b11.y1 Gm-cl028 Glycine max cDNA clone...	210 1e-53
	emb AV416661 AV416661 AV416661 Lotus japonicus young plants (two...	209 1e-53
	gb BE053882 BE053882 GA_Ea0034G19f Gossypium arboreum 7-10 dpa ...	123 2e-53
	emb AW033980 AW033980 EST277642 tomato callus, TAMU Lycopersicon...	208 3e-53
	emb AW029821 AW029821 EST273076 tomato callus, TAMU Lycopersicon...	208 4e-53
55	emb AW428756 AW428756 Ljirnp23-845-c9 Ljirnp Lambda HybriZap ...	207 5e-53
	emb AV409794 AV409794 AV409794 Lotus japonicus young plants (two...	205 2e-52
	emb AI895300 AI895300 EST264743 tomato callus, TAMU Lycopersicon...	204 3e-52
	emb AV417685 AV417685 AV417685 Lotus japonicus young plants (two...	204 5e-52
	emb AW033463 AW033463 EST277034 tomato callus, TAMU Lycopersicon...	202 2e-51
60	emb AW030999 AW030999 EST274306 tomato callus, TAMU Lycopersicon...	201 3e-51
	emb AV412313 AV412313 AV412313 Lotus japonicus young plants (two...	201 4e-51

- emb|AV424264|AV424264 AV424264 Lotus japonicus young plants (two... 200 6e-51
 gb|BE021904|BE021904 sm63h11.y1 Gm-c1028 Glycine max cDNA clone ... 198 3e-50
 emb|AW725608|AW725608 GA__Ea0018P10 Gossypium arboreum 7-10 dpa ... 123 7e-50
 emb|AW725586|AW725586 GA__Ea0018N10 Gossypium arboreum 7-10 dpa ... 123 7e-50
 5 emb|AI896550|AI896550 EST265993 tomato callus, TAMU Lycopersicon... 193 7e-49
 emb|AW559285|AW559285 EST306328 DSIR Medicago truncatula cDNA cl... 95 3e-48
 emb|AW684576|AW684576 NF018E05NR1F1000 Nodulated root Medicago t... 93 1e-46
 emb|AW428680|AW428680 Ljirnp22-757-d2 Ljirnp Lambda HybriZap ... 158 1e-46
 emb|AW216534|AW216534 EST295248 tomato callus, TAMU Lycopersicon... 186 2e-46
 10 emb|AW620815|AW620815 sj09h04.y1 Gm-c1032 Glycine max cDNA clone... 109 7e-46
 emb|AI728054|AI728054 BNLGHi9697 Six-day Cotton fiber Gossypium ... 107 1e-45
 emb|AI730473|AI730473 BNLGHi7273 Six-day Cotton fiber Gossypium ... 105 2e-44
 emb|AI729618|AI729618 BNLGHi13779 Six-day Cotton fiber Gossypium... 105 3e-44
 emb|AV422463|AV422463 AV422463 Lotus japonicus young plants (two... 177 9e-44
 15 emb|AW622012|AW622012 EST312810 tomato root during/after fruit s... 106 1e-43
 emb|AW621198|AW621198 EST311996 tomato root during/after fruit s... 106 1e-43
 emb|AW031587|AW031587 EST275041 tomato callus, TAMU Lycopersicon... 176 1e-43
 gb|U51193|GMU51193 Glycine max peroxidase (sEPb1) mRNA, partial ... 95 2e-43
 gb|L13654|TOMTPX1A Lycopersicon esculentum peroxidase (TPX1) mRN... 105 2e-43
 20
 Query= X95573.2_at 18216_at /id_source genbank /description
 gb|aaf24959.1|ac012375_22 (ac012375) t22c5.18 [arabidopsis thaliana]
 /blast_score 1.00e-119 /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 25 post/entrez/query?db=n&form=6&dopt=g&uid=gb|x95573|/ncgi
 http://www.ncgr.org/cgi-bin/ff?x95573
 (940 letters)
 Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters
 Searching.....done
 Score E
 35 Sequences producing significant alignments: (bits) Value
 emb|AF119050|AF119050 Datisca glomerata zinc-finger protein 1 (z... 73 1e-43
 gb|U68763|GMU68763 Glycine max putative transcription factor SCO... 72 2e-39
 dbj|D26083|PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin... 69 4e-38
 40 emb|Y18788|MSY18788 Medicago sativa mRNA for putative TFIIIA (or... 125 7e-38
 dbj|D26086|PETZFP4 Petunia zinc-finger protein gene. 62 3e-36
 emb|AW560934|AW560934 EST315982 DSIR Medicago truncatula cDNA cl... 133 3e-35
 emb|AW729218|AW729218 GA__Ea0024G18 Gossypium arboreum 7-10 dpa ... 70 8e-35
 dbj|D26084|PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro... 70 2e-34
 45 gb|BE095284|BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two-... 70 2e-34
 emb|AW781249|AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone... 67 4e-32
 emb|AI988290|AI988290 sc98f10.y1 Gm-c1020 Glycine max cDNA clone... 69 1e-31
 emb|AI487287|AI487287 EST245609 tomato ovary, TAMU Lycopersicon ... 62 3e-30
 emb|AW775559|AW775559 EST334624 DSIL Medicago truncatula cDNA cl... 66 6e-30
 50 gb|BE123920|BE123920 EST394045 DSIL Medicago truncatula cDNA clo... 66 6e-30
 dbj|D26085|PETZFDB3 Petunia zinc-finger DNA binding protein gene. 59 8e-29
 emb|AW102472|AW102472 sd88f02.y1 Gm-c1009 Glycine max cDNA clone... 70 1e-28
 emb|AI988657|AI988657 sd06b03.y1 Gm-c1020 Glycine max cDNA clone... 70 2e-28
 emb|AF053077|AF053077 Nicotiana tabacum osmotic stress-induced z... 66 5e-27
 55 emb|AW706944|AW706944 sk08e10.y1 Gm-c1023 Glycine max cDNA clone... 64 8e-27
 emb|AI778714|AI778714 EST259593 tomato susceptible, Cornell Lyco... 62 2e-26
 emb|AW279005|AW279005 sg04d04.y1 Gm-c1019 Glycine max cDNA clone... 62 3e-26
 emb|AW164639|AW164639 se74f02.y1 Gm-c1023 Glycine max cDNA clone... 62 3e-26
 emb|Y16131|Y16131 Y16131 young root nodules Medicago sativa subs... 119 3e-26
 60 emb|AW153229|AW153229 se37f05.y1 Gm-c1015 Glycine max cDNA clone... 62 4e-26
 emb|AW616587|AW616587 EST322998 L. hirsutum trichome, Cornell Un... 63 6e-26

	gb BE059872 BE059872 sn38c04.y1 Gm-c1016 Glycine max cDNA clone ...	72 2e-25
	emb AW278572 AW278572 sf46c03.y1 Gm-c1009 Glycine max cDNA clone...	62 5e-25
	emb AW034622 AW034622 EST278306 tomato callus, TAMU Lycopersicon...	62 9e-25
	emb AV426673 AV426673 AV426673 Lotus japonicus young plants (two...	76 1e-24
5	emb AI488218 AI488218 EST246540 tomato ovary, TAMU Lycopersicon ...	62 2e-24
	emb AW037956 AW037956 EST279600 tomato mixed elicitor, BTI Lycop...	62 2e-24
	emb AI966679 AI966679 sc55a11.y1 Gm-c1015 Glycine max cDNA clone...	68 1e-23
	emb AW720367 AW720367 LjNEST21g11r Lotus japonicus nodule librar...	69 5e-23
	emb AI938565 AI938565 sb55e03.y1 Gm-c1018 Glycine max cDNA clone...	70 1e-22
10	gb U76555 BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA...	63 4e-22
	gb U76554 BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR...	63 4e-22
	emb AW625323 AW625323 EST319146 tomato radicle, 5 d post-imbibit...	62 4e-22
	emb AW219736 AW219736 EST302218 tomato root during/after fruit s...	62 2e-21
	emb AW185023 AW185023 se85f12.y1 Gm-c1023 Glycine max cDNA clone...	58 5e-21
15	emb AW277333 AW277333 sf80a11.y1 Gm-c1019 Glycine max cDNA clone...	69 6e-21
	emb AI900061 AI900061 sb98d02.y1 Gm-c1012 Glycine max cDNA clone...	69 6e-21
	emb AW219517 AW219517 EST301915 tomato root during/after fruit s...	62 8e-21
	emb AW032112 AW032112 EST275566 tomato callus, TAMU Lycopersicon...	62 1e-20
	emb AI485651 AI485651 EST243972 tomato ovary, TAMU Lycopersicon ...	62 4e-20
20	dbj D16415 WHTWZF1A Wheat gene for WZF1, complete cds.	62 7e-20
	dbj D16416 WHTWZF1B Wheat mRNA for WZF1, complete cds.	62 7e-20
	emb AV422972 AV422972 AV422972 Lotus japonicus young plants (two...	76 3e-19
	emb AV423707 AV423707 AV423707 Lotus japonicus young plants (two...	76 3e-19
	emb AV424707 AV424707 AV424707 Lotus japonicus young plants (two...	76 3e-19
25	emb AV411009 AV411009 AV411009 Lotus japonicus young plants (two...	76 3e-19
	emb AV413230 AV413230 AV413230 Lotus japonicus young plants (two...	76 3e-19
	emb AV418453 AV418453 AV418453 Lotus japonicus young plants (two...	76 3e-19
	emb AV411580 AV411580 AV411580 Lotus japonicus young plants (two...	76 3e-19
	emb AV412443 AV412443 AV412443 Lotus japonicus young plants (two...	76 3e-19
30	emb AV412455 AV412455 AV412455 Lotus japonicus young plants (two...	76 3e-19
	emb AW033574 AW033574 EST277145 tomato callus, TAMU Lycopersicon...	61 9e-19
	emb AI896031 AI896031 EST265474 tomato callus, TAMU Lycopersicon...	61 1e-18
	emb AW030858 AW030858 EST274148 tomato callus, TAMU Lycopersicon...	61 1e-18
	emb AW033257 AW033257 EST276828 tomato callus, TAMU Lycopersicon...	61 1e-18
35	emb AI771191 AI771191 EST252387 tomato ovary, TAMU Lycopersicon ...	61 1e-18
	emb AV424248 AV424248 AV424248 Lotus japonicus young plants (two...	73 1e-18
	emb AW032357 AW032357 EST275811 tomato callus, TAMU Lycopersicon...	61 1e-18
	emb AW706014 AW706014 sk64g01.y1 Gm-c1016 Glycine max cDNA clone...	66 3e-18
	emb AW648971 AW648971 EST327425 tomato germinating seedlings, TA...	62 4e-18
40	emb AW622660 AW622660 EST313460 tomato root during/after fruit s...	62 5e-18
	emb AV411226 AV411226 AV411226 Lotus japonicus young plants (two...	71 6e-18
	emb AV419929 AV419929 AV419929 Lotus japonicus young plants (two...	71 6e-18
	gb BE058334 BE058334 sn14g01.y1 Gm-c1016 Glycine max cDNA clone ...	72 8e-18
	emb AI894999 AI894999 EST264442 tomato callus, TAMU Lycopersicon...	62 2e-17
45	emb AV423254 AV423254 AV423254 Lotus japonicus young plants (two...	76 3e-17
	emb AW755973 AW755973 sl11h06.y1 Gm-c1036 Glycine max cDNA clone...	70 4e-17
	emb AI960244 AI960244 sc80g07.y1 Gm-c1018 Glycine max cDNA clone...	70 5e-17
	emb AV411565 AV411565 AV411565 Lotus japonicus young plants (two...	68 7e-17
	emb AV424084 AV424084 AV424084 Lotus japonicus young plants (two...	68 7e-17
50	emb AV413163 AV413163 AV413163 Lotus japonicus young plants (two...	68 7e-17
	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon...	54 3e-16
	emb AW684558 AW684558 NF018C10NR1F1000 Nodulated root Medicago t...	70 3e-16
	emb AV422432 AV422432 AV422432 Lotus japonicus young plants (two...	70 3e-16
	gb BE021759 BE021759 sm62a09.y1 Gm-c1028 Glycine max cDNA clone ...	66 3e-16
55	emb AV423639 AV423639 AV423639 Lotus japonicus young plants (two...	70 5e-16
	emb AI736394 AI736394 sb28a06.y1 Gm-c1009 Glycine max cDNA clone...	64 7e-16
	emb AI055219 AI055219 coau0003G03 Cotton Boll Abscission Zone cD...	57 9e-16
	emb AV411832 AV411832 AV411832 Lotus japonicus young plants (two...	64 9e-16
	emb AV408053 AV408053 AV408053 Lotus japonicus young plants (two...	48 1e-15
60	emb AW035987 AW035987 EST282846 tomato callus, TAMU Lycopersicon...	54 2e-15
	emb AV416264 AV416264 AV416264 Lotus japonicus young plants (two...	62 4e-15

emb|AV412367|AV412367 AV412367 Lotus japonicus young plants (two... 62 4e-15
 emb|AV420478|AV420478 AV420478 Lotus japonicus young plants (two... 62 4e-15
 emb|AV412447|AV412447 AV412447 Lotus japonicus young plants (two... 62 4e-15
 emb|AV414463|AV414463 AV414463 Lotus japonicus young plants (two... 62 4e-15
 5 emb|AV419425|AV419425 AV419425 Lotus japonicus young plants (two... 62 4e-15
 emb|AV425774|AV425774 AV425774 Lotus japonicus young plants (two... 46 6e-15
 emb|AW981180|AW981180 EST392374 DSIL Medicago truncatula cDNA cl... 76 1e-14
 emb|AV428712|AV428712 AV428712 Lotus japonicus young plants (two... 42 2e-14
 emb|AV418073|AV418073 AV418073 Lotus japonicus young plants (two... 58 5e-14
 10 emb|AV419180|AV419180 AV419180 Lotus japonicus young plants (two... 58 5e-14
 emb|AV423498|AV423498 AV423498 Lotus japonicus young plants (two... 58 5e-14
 emb|AV428398|AV428398 AV428398 Lotus japonicus young plants (two... 58 5e-14
 emb|AI484099|AI484099 EST249970 tomato ovary, TAMU Lycopersicon ... 62 5e-14
 15 emb|AW738399|AW738399 EST339826 tomato flower buds, anthesis, Co... 62 5e-14

Query= X95573.2_g_at 18217_g_at /id_source genbank /description
 gb|aaf24959.1|ac012375_22 (ac012375) t22c5.18 [arabidopsis thaliana]
 /blast_score 1.00e-119 /ec_number /family /chip nova /gb_link /ncgi
 20 (940 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters
 25 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value
 30

emb|AF119050|AF119050 Datisca glomerata zinc-finger protein 1 (z... 73 1e-43
 gb|U68763|GMU68763 Glycine max putative transcription factor SCO... 72 2e-39
 dbj|D26083|PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin... 69 4e-38
 emb|Y18788|MSY18788 Medicago sativa mRNA for putative TFIIIA (or... 125 7e-38
 35 dbj|D26086|PETZFP4 Petunia zinc-finger protein gene. 62 3e-36
 emb|AW560934|AW560934 EST315982 DSIR Medicago truncatula cDNA cl... 133 3e-35
 emb|AW729218|AW729218 GA__Ea0024G18 Gossypium arboreum 7-10 dpa ... 70 8e-35
 dbj|D26084|PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro... 70 2e-34
 gb|BE095284|BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two-... 70 2e-34
 40 emb|AW781249|AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone... 67 4e-32
 emb|AI988290|AI988290 sc98f10.y1 Gm-c1020 Glycine max cDNA clone... 69 1e-31
 emb|AI487287|AI487287 EST245609 tomato ovary, TAMU Lycopersicon ... 62 3e-30
 emb|AW775559|AW775559 EST334624 DSIL Medicago truncatula cDNA cl... 66 6e-30
 gb|BE123920|BE123920 EST394045 DSIL Medicago truncatula cDNA clo... 66 6e-30
 45 dbj|D26085|PETZFDB3 Petunia zinc-finger DNA binding protein gene. 59 8e-29
 emb|AW102472|AW102472 sd88f02.y1 Gm-c1009 Glycine max cDNA clone... 70 1e-28
 emb|AI988657|AI988657 sd06b03.y1 Gm-c1020 Glycine max cDNA clone... 70 2e-28
 emb|AF053077|AF053077 Nicotiana tabacum osmotic stress-induced z... 66 5e-27
 emb|AW706944|AW706944 sk08e10.y1 Gm-c1023 Glycine max cDNA clone... 64 8e-27
 50 emb|AI778714|AI778714 EST259593 tomato susceptible, Cornell Lyco... 62 2e-26
 emb|AW279005|AW279005 sg04d04.y1 Gm-c1019 Glycine max cDNA clone... 62 3e-26
 emb|AW164639|AW164639 se74f02.y1 Gm-c1023 Glycine max cDNA clone... 62 3e-26
 emb|Y16131|Y16131 Y16131 young root nodules Medicago sativa subs... 119 3e-26
 emb|AW153229|AW153229 se37f05.y1 Gm-c1015 Glycine max cDNA clone... 62 4e-26
 55 emb|AW616587|AW616587 EST322998 L. hirsutum trichome, Cornell Un... 63 6e-26
 gb|BE059872|BE059872 sn38c04.y1 Gm-c1016 Glycine max cDNA clone ... 72 2e-25
 emb|AW278572|AW278572 sf46c03.y1 Gm-c1009 Glycine max cDNA clone... 62 5e-25
 emb|AW034622|AW034622 EST278306 tomato callus, TAMU Lycopersicon... 62 9e-25
 emb|AV426673|AV426673 AV426673 Lotus japonicus young plants (two... 76 1e-24
 60 emb|AI488218|AI488218 EST246540 tomato ovary, TAMU Lycopersicon ... 62 2e-24
 emb|AW037956|AW037956 EST279600 tomato mixed elicitor, BTI Lycop... 62 2e-24

	emb AI966679 AI966679 sc55a11.y1 Gm-cl015 Glycine max cDNA clone...	68	1e-23
	emb AW720367 AW720367 LjNEST21g11r Lotus japonicus nodule librar...	69	5e-23
	emb AI938565 AI938565 sb55e03.y1 Gm-cl018 Glycine max cDNA clone...	70	1e-22
	gb U76555 BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA...	63	4e-22
5	gb U76554 BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR...	63	4e-22
	emb AW625323 AW625323 EST319146 tomato radicle, 5 d post-imbibit...	62	4e-22
	emb AW219736 AW219736 EST302218 tomato root during/after fruit s...	62	2e-21
	emb AW185023 AW185023 se85f12.y1 Gm-cl023 Glycine max cDNA clone...	58	5e-21
	emb AW277333 AW277333 sf80a11.y1 Gm-cl019 Glycine max cDNA clone...	69	6e-21
10	emb AI900061 AI900061 sb98d02.y1 Gm-cl012 Glycine max cDNA clone...	69	6e-21
	emb AW219517 AW219517 EST301915 tomato root during/after fruit s...	62	8e-21
	emb AW032112 AW032112 EST275566 tomato callus, TAMU Lycopersicon...	62	1e-20
	emb AI485651 AI485651 EST243972 tomato ovary, TAMU Lycopersicon ...	62	4e-20
	dbj D16415 WHTWZF1A Wheat gene for WZF1, complete cds.	62	7e-20
15	dbj D16416 WHTWZF1B Wheat mRNA for WZF1, complete cds.	62	7e-20
	emb AV422972 AV422972 AV422972 Lotus japonicus young plants (two...	76	3e-19
	emb AV423707 AV423707 AV423707 Lotus japonicus young plants (two...	76	3e-19
	emb AV424707 AV424707 AV424707 Lotus japonicus young plants (two...	76	3e-19
	emb AV411009 AV411009 AV411009 Lotus japonicus young plants (two...	76	3e-19
20	emb AV413230 AV413230 AV413230 Lotus japonicus young plants (two...	76	3e-19
	emb AV418453 AV418453 AV418453 Lotus japonicus young plants (two...	76	3e-19
	emb AV411580 AV411580 AV411580 Lotus japonicus young plants (two...	76	3e-19
	emb AV412443 AV412443 AV412443 Lotus japonicus young plants (two...	76	3e-19
	emb AV412455 AV412455 AV412455 Lotus japonicus young plants (two...	76	3e-19
25	emb AW033574 AW033574 EST277145 tomato callus, TAMU Lycopersicon...	61	9e-19
	emb AI896031 AI896031 EST265474 tomato callus, TAMU Lycopersicon...	61	1e-18
	emb AW030858 AW030858 EST274148 tomato callus, TAMU Lycopersicon...	61	1e-18
	emb AW033257 AW033257 EST276828 tomato callus, TAMU Lycopersicon...	61	1e-18
	emb AI771191 AI771191 EST252387 tomato ovary, TAMU Lycopersicon ...	61	1e-18
30	emb AV424248 AV424248 AV424248 Lotus japonicus young plants (two...	73	1e-18
	emb AW032357 AW032357 EST275811 tomato callus, TAMU Lycopersicon...	61	1e-18
	emb AW706014 AW706014 sk64g01.y1 Gm-cl016 Glycine max cDNA clone...	66	3e-18
	emb AW648971 AW648971 EST327425 tomato germinating seedlings, TA...	62	4e-18
	emb AW622660 AW622660 EST313460 tomato root during/after fruit s...	62	5e-18
35	emb AV411226 AV411226 AV411226 Lotus japonicus young plants (two...	71	6e-18
	emb AV419929 AV419929 AV419929 Lotus japonicus young plants (two...	71	6e-18
	gb BE058334 BE058334 sn14g01.y1 Gm-cl016 Glycine max cDNA clone ...	72	8e-18
	emb AI894999 AI894999 EST264442 tomato callus, TAMU Lycopersicon...	62	2e-17
	emb AV423254 AV423254 AV423254 Lotus japonicus young plants (two...	76	3e-17
40	emb AW755973 AW755973 sl11h06.y1 Gm-cl036 Glycine max cDNA clone...	70	4e-17
	emb AI960244 AI960244 sc80g07.y1 Gm-cl018 Glycine max cDNA clone...	70	5e-17
	emb AV411565 AV411565 AV411565 Lotus japonicus young plants (two...	68	7e-17
	emb AV424084 AV424084 AV424084 Lotus japonicus young plants (two...	68	7e-17
	emb AV413163 AV413163 AV413163 Lotus japonicus young plants (two...	68	7e-17
45	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon...	54	3e-16
	emb AW684558 AW684558 NF018C10NR1F1000 Nodulated root Medicago t...	70	3e-16
	emb AV422432 AV422432 AV422432 Lotus japonicus young plants (two...	70	3e-16
	gb BE021759 BE021759 sm62a09.y1 Gm-cl028 Glycine max cDNA clone ...	66	3e-16
	emb AV423639 AV423639 AV423639 Lotus japonicus young plants (two...	70	5e-16
50	emb AI736394 AI736394 sb28a06.y1 Gm-cl009 Glycine max cDNA clone...	64	7e-16
	emb AI055219 AI055219 coau0003G03 Cotton Boll Abscission Zone cD...	57	9e-16
	emb AV411832 AV411832 AV411832 Lotus japonicus young plants (two...	64	9e-16
	emb AV408053 AV408053 AV408053 Lotus japonicus young plants (two...	48	1e-15
	emb AW035987 AW035987 EST282846 tomato callus, TAMU Lycopersicon...	54	2e-15
55	emb AV416264 AV416264 AV416264 Lotus japonicus young plants (two...	62	4e-15
	emb AV412367 AV412367 AV412367 Lotus japonicus young plants (two...	62	4e-15
	emb AV420478 AV420478 AV420478 Lotus japonicus young plants (two...	62	4e-15
	emb AV412447 AV412447 AV412447 Lotus japonicus young plants (two...	62	4e-15
	emb AV414463 AV414463 AV414463 Lotus japonicus young plants (two...	62	4e-15
60	emb AV419425 AV419425 AV419425 Lotus japonicus young plants (two...	62	4e-15
	emb AV425774 AV425774 AV425774 Lotus japonicus young plants (two...	46	6e-15

emb|AW981180|AW981180 EST392374 DSIL Medicago truncatula cDNA cl... 76 1e-14
emb|AV428712|AV428712 AV428712 Lotus japonicus young plants (two... 42 2e-14
emb|AV418073|AV418073 AV418073 Lotus japonicus young plants (two... 58 5e-14
emb|AV419180|AV419180 AV419180 Lotus japonicus young plants (two... 58 5e-14
5 emb|AV423498|AV423498 AV423498 Lotus japonicus young plants (two... 58 5e-14
emb|AV428398|AV428398 AV428398 Lotus japonicus young plants (two... 58 5e-14
emb|AI484099|AI484099 EST249970 tomato ovary, TAMU Lycopersicon ... 62 5e-14
emb|AW738399|AW738399 EST339826 tomato flower buds, anthesis, Co... 62 5e-14

10
Query= AL021890.57_s_at 18224_s_at /id_source genbank /description
emb|caa17150.1| (al021890) putative protein [arabidopsis thaliana]
/blast_score 4.00e-81 /ec_number /family /chip nova /gb_link /ncgi
(426 letters)

15
Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

20
Score E
Sequences producing significant alignments: (bits) Value

25
emb|AW667752|AW667752 GA__Ea0010I06 Gossypium arboreum 7-10 dpa ... 247 4e-65
emb|AW224013|AW224013 EST300824 tomato fruit red ripe, TAMU Lyco... 244 3e-64
emb|AW223703|AW223703 EST300514 tomato fruit red ripe, TAMU Lyco... 244 3e-64
emb|AW441269|AW441269 EST310665 tomato fruit red ripe, TAMU Lyco... 244 3e-64
emb|AW034892|AW034892 EST279121 tomato callus, TAMU Lycopersicon... 244 3e-64
gb|BE124622|BE124622 EST393657 GVN Medicago truncatula cDNA clon... 243 5e-64
30 emb|AW747419|AW747419 WS1_68_E10.b1_A002 Water-stressed 1 (WS1) ... 242 1e-63
gb|BE033541|BE033541 MF02E10 MF Mesembryanthemum crystallinum cD... 242 1e-63
emb|AI943438|AI943438 MF02E10 MF Mesembryanthemum crystallinum c... 242 1e-63
emb|AW730496|AW730496 GA__Ea0026O23 Gossypium arboreum 7-10 dpa ... 242 1e-63
emb|AI960575|AI960575 sc86c01.y1 Gm-c1018 Glycine max cDNA clone... 240 4e-63
35 emb|AW706639|AW706639 sj62h07.y1 Gm-c1033 Glycine max cDNA clone... 240 4e-63
emb|AW568285|AW568285 si69gl1.y1 Gm-r1030 Glycine max cDNA clone... 240 5e-63
emb|AW186193|AW186193 se64g04.y1 Gm-c1019 Glycine max cDNA clone... 240 5e-63
gb|BE020351|BE020351 sm43b05.y1 Gm-c1028 Glycine max cDNA clone ... 240 5e-63
emb|AW981480|AW981480 EST392633 DSIL Medicago truncatula cDNA cl... 239 1e-62
40 emb|AW747501|AW747501 WS1_68_E10.g1_A002 Water-stressed 1 (WS1) ... 238 1e-62
emb|AI443884|AI443884 sa44f06.y1 Gm-c1004 Glycine max cDNA clone... 237 5e-62
emb|AI855496|AI855496 sc16h05.y1 Gm-c1013 Glycine max cDNA clone... 232 8e-61
emb|AW132618|AW132618 se06f04.y1 Gm-c1013 Glycine max cDNA clone... 222 9e-58
emb|AW760599|AW760599 sl52d09.y1 Gm-c1027 Glycine max cDNA clone... 217 3e-56
45 emb|AI965929|AI965929 sc79h07.y1 Gm-c1018 Glycine max cDNA clone... 199 1e-50
emb|AV398027|AV398027 AV398027 Chlamydomonas reinhardtii C9 Chla... 127 9e-50
emb|AW907232|AW907232 EST343355 potato stolon, Cornell Universit... 193 4e-49
emb|AW738874|AW738874 gb03e09.y1 Moss EST library PPN Physcomitr... 184 2e-46
emb|AW685341|AW685341 NF026D08NR1F1000 Nodulated root Medicago t... 177 4e-44
50 emb|AW739119|AW739119 gb26a12.y1 Moss EST library PPN Physcomitr... 173 7e-43
emb|AL049558|SPBC216 S.pombe chromosome II cosmid c216. 84 1e-38
emb|AV408412|AV408412 AV408412 Lotus japonicus young plants (two... 157 5e-38
emb|AA948748|AA948748 L0-267M13R Ice plant Lambda Uni-Zap XR exp... 155 1e-37
emb|AW597401|AW597401 si92d06.y1 Gm-c1031 Glycine max cDNA clone... 154 3e-37
55 emb|AI495735|AI495735 sb15f07.y1 Gm-c1004 Glycine max cDNA clone... 154 4e-37
emb|AW351206|AW351206 GM210011A20E12R Gm-r1021 Glycine max cDNA ... 154 4e-37
emb|AI777814|AI777814 EST258693 tomato susceptible, Cornell Lyco... 143 8e-36
emb|AI166395|AI166395 xylem.est.231 Poplar xylem Lambda ZAPII li... 148 3e-35
emb|AW335287|AW335287 S45D10 AGS-1 Pneumocystis carinii f. sp. c... 76 5e-35
60 emb|AI026521|AI026521 TENU0733 T. cruzi epimastigote normalized ... 124 3e-31
emb|AW156084|AW156084 ga24f11.y1 Moss EST library PPU Physcomitr... 130 5e-30

- emb|AA740047|AA740047 812 PtIFG2 Pinus taeda cDNA clone 9275M 3'... 126 1e-28
emb|AI822525|AI822525 L0-1030T3 Ice plant Lambda Uni-Zap XR expr... 92 8e-26
emb|AW933878|AW933878 EST359721 tomato fruit mature green, TAMU ... 89 7e-25
emb|AW222361|AW222361 EST299172 tomato fruit red ripe, TAMU Lyco... 89 7e-25
5 emb|X59720|SCCHRIII S.cerevisiae chromosome III complete DNA seq... 80 8e-25
emb|AW617209|AW617209 EST323620 L. hirsutum trichome, Cornell Un... 89 1e-24
emb|AW775277|AW775277 EST334342 DSIL Medicago truncatula cDNA cl... 85 3e-24
emb|AI730110|AI730110 BNLGHi6160 Six-day Cotton fiber Gossypium ... 90 3e-23
emb|AW933218|AW933218 EST359061 tomato fruit mature green, TAMU ... 89 2e-22
10 emb|AW222638|AW222638 EST299449 tomato fruit red ripe, TAMU Lyco... 89 2e-22
emb|AW094164|AW094164 EST287344 tomato mixed elicitor, BTI Lycop... 89 2e-22
emb|AW145744|AW145744 ga34c05.y1 Moss EST library PPN Physcomitr... 103 9e-22
emb|AV427426|AV427426 AV427426 Lotus japonicus young plants (two... 101 3e-21
gb|BE060018|BE060018 sn39h09.y1 Gm-c1027 Glycine max cDNA clone ... 82 6e-21
15 gb|BE022658|BE022658 sm75g09.y1 Gm-c1015 Glycine max cDNA clone ... 100 1e-20
emb|AI939238|AI939238 sc68h11.y1 Gm-c1016 Glycine max cDNA clone... 82 5e-20
emb|AL160493|LMFLCHR26 Leishmania major Friedlin assembled chrom... 94 5e-19
emb|AW222387|AW222387 EST299198 tomato fruit red ripe, TAMU Lyco... 91 3e-18
emb|AW476911|AW476911 ga38h10.y1 Moss EST library PPU Physcomitr... 91 3e-18
20 emb|AW220746|AW220746 EST297215 tomato fruit mature green, TAMU ... 89 2e-17
emb|AW094112|AW094112 EST287292 tomato mixed elicitor, BTI Lycop... 57 3e-16
emb|AW127596|AW127596 M110327 DSLC Medicago truncatula cDNA clon... 78 5e-14
gb|T36700|T36700 EST101687 S. cerevisiae strain X2180-1A Sacchar... 74 6e-13
emb|AW650769|AW650769 EST329223 tomato germinating seedlings, TA... 72 3e-12
25 emb|AT000681|AT000681 AT000681 Brassica rapa guard cell Brassica... 61 3e-12
gb|BE035973|BE035973 MO22G04 MO Mesembryanthemum crystallinum cD... 68 4e-11
gb|BE036098|BE036098 MO22G05 MO Mesembryanthemum crystallinum cD... 68 4e-11
gb|N81594|N81594 TgESTzy60e01.r1 TgRH Tachyzoite cDNA Toxoplasma... 48 8e-10
emb|AW907238|AW907238 EST343361 potato stolon, Cornell Universit... 63 9e-10
30 emb|AZ215418|AZ215418 Sheared DNA-79B7.TF Sheared DNA Trypanosom... 54 2e-09
emb|AA842826|AA842826 CFB57 Floral bud cDNA library of Hot peppe... 59 2e-08
gb|T37143|T37143 EST102217 S. cerevisiae strain X2180-1A Sacchar... 46 3e-07
emb|AV412908|AV412908 AV412908 Lotus japonicus young plants (two... 54 7e-07
gb|U14566|SCU14566 Saccharomyces cerevisiae formylglycinamide ri... 35 0.23
35 emb|Z72847|SCYGR062C S.cerevisiae chromosome VII reading frame O... 35 0.23
emb|AW156147|AW156147 se20b05.y1 Gm-c1015 Glycine max cDNA clone... 35 0.23
gb|M83672|YSCSPT4A Saccharomyces cerevisiae zinc finger protein ... 35 0.23
gb|U59742|SCU59742 Saccharomyces cerevisiae Cox18p (COX18) gene,... 35 0.23
emb|AI374413|AI374413 T6768 MVAT4 bloodstream form of serodeme W... 26 1.7
40 emb|AQ945483|AQ945483 Sheared DNA-44G3.TR Sheared DNA Trypanosom... 32 2.1
emb|AI374297|AI374297 T6531 MVAT4 bloodstream form of serodeme W... 26 2.3
emb|AW030467|AW030467 EST273722 tomato callus, TAMU Lycopersicon... 31 4.0
emb|AW624450|AW624450 EST322395 tomato flower buds 3-8 mm, Corne... 31 4.0
emb|AW979733|AW979733 EST341357 tomato root deficiency, Cornell ... 31 4.0
45 emb|AW737565|AW737565 EST338992 tomato flower buds, anthesis, Co... 31 4.0
emb|AW679327|AW679327 WS1_23_A02.g1_A002 Water-stressed 1 (WS1) ... 31 5.5
emb|AW282515|AW282515 LG1_312_G03.g1_A002 Light Grown 1 (LG1) So... 31 5.5
emb|AF077352|AF077352 Chlamydomonas reinhardtii myosin heavy cha... 30 7.6
emb|X55012|PSUSP43 Pisum sativum mRNA for an 'unknown seed prote... 30 7.6
50 gb|U73817|CRU73817 Chlamydomonas reinhardtii LRG5 mRNA, complete... 30 7.6
gb|U73818|CRU73818 Chlamydomonas reinhardtii LRG5 gene, complete... 30 7.6

- Query= AC002391.163_at 18551_at /id_source genbank /description
55 gb|aab87112.1| (ac002391) putative cytochrome p450 [arabidopsis
thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002391|/ncgi
http://www.ncgr.org/cgi-bin/ff?ac002391
60 (1632 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments: (bits) Value

	emb AB001379 AB001379 Glycyrrhiza echinata CYP81E1 mRNA for cyto...	337	e-149
10	emb AJ238439 CAR238439 Cicer arietinum mRNA for a cytochrome P45...	338	e-149
	emb AB022732 AB022732 Glycyrrhiza echinata CYP Ge-31 mRNA for cy...	334	e-148
	emb AJ012581 CAR012581 Cicer arietinum mRNA for cytochrome P450.	333	e-147
	emb AB025016 AB025016 Lotus japonicus mRNA for cytochrome P450, ...	309	e-145
	emb AJ000478 HTCYP81L Helianthus tuberosus mRNA for cytochrome P...	227	e-136
15	emb AJ000477 HTCYP81C Helianthus tuberosus mRNA for cytochrome P...	227	e-135
	emb AJ239051 CAR239051 Cicer arietinum mRNA for cytochrome P450 ...	236	7e-85
	emb AJ249800 CAR249800 Cicer arietinum partial mRNA for cytochro...	299	3e-80
	emb AW185361 AW185361 se90e02.y1 Gm-c1027 Glycine max cDNA clone...	272	4e-72
	emb AW234443 AW234443 sf25c03.y1 Gm-c1028 Glycine max cDNA clone...	264	1e-69
20	emb AW307234 AW307234 sf54d12.y1 Gm-c1009 Glycine max cDNA clone...	261	1e-68
	emb AF082028 AF082028 Hemerocallis hybrid cultivar senescence-as...	194	3e-67
	emb AW775904 AW775904 EST334969 DSIL Medicago truncatula cDNA cl...	223	9e-66
	emb AJ249801 CAR249801 Cicer arietinum partial mRNA for cytochro...	250	2e-65
	emb AW733691 AW733691 sk83g07.y1 Gm-c1016 Glycine max cDNA clone...	247	2e-64
25	emb AW171738 AW171738 N100632e rootphos(-) Medicago truncatula c...	245	6e-64
	emb AI495626 AI495626 sb11c08.y1 Gm-c1004 Glycine max cDNA clone...	231	2e-59
	emb AI729126 AI729126 BNLGHi12694 Six-day Cotton fiber Gossypium...	183	4e-58
	emb AI725744 AI725744 BNLGHi12803 Six-day Cotton fiber Gossypium...	182	1e-57
	emb AW257188 AW257188 EST305325 KV2 Medicago truncatula cDNA clo...	189	1e-56
30	emb AW329224 AW329224 N200436e rootphos(-) Medicago truncatula c...	220	2e-56
	emb AF029856 AF029856 Sorghum bicolor cytochrome P450 CYP98A1 (C...	152	9e-55
	emb AI774414 AI774414 EST255514 tomato resistant, Cornell Lycop...	152	4e-54
	emb X95342 NTHSR515 N.tabacum mRNA for HSR515 protein.	84	5e-54
	emb AW932147 AW932147 EST357990 tomato fruit mature green, TAMU ...	212	7e-54
35	emb AW684707 AW684707 NF020A02NR1F1000 Nodulated root Medicago t...	189	7e-53
	emb AW171672 AW171672 N100566e rootphos(-) Medicago truncatula c...	207	2e-52
	emb AW688601 AW688601 NF009D12ST1F1000 Developing stem Medicago ...	185	2e-51
	emb AI731081 AI731081 BNLGHi8648 Six-day Cotton fiber Gossypium ...	203	3e-51
	emb AW100311 AW100311 sd22g12.y2 Gm-c1012 Glycine max cDNA clone...	202	6e-51
40	emb AW299084 AW299084 EST305758 KV2 Medicago truncatula cDNA clo...	182	8e-51
	emb AW616170 AW616170 EST307209 L. hirsutum trichome, Cornell Un...	142	2e-50
	emb AW695923 AW695923 NF100G02ST1F1018 Developing stem Medicago ...	174	1e-49
	emb AI731481 AI731481 BNLGHi9879 Six-day Cotton fiber Gossypium ...	172	9e-49
	emb AW616482 AW616482 EST322893 L. hirsutum trichome, Cornell Un...	142	6e-48
45	emb AW617814 AW617814 EST324213 L. hirsutum trichome, Cornell Un...	142	6e-48
	emb AW034115 AW034115 EST277610 tomato callus, TAMU Lycopersicon...	142	8e-48
	emb AW616075 AW616075 EST296834 L. hirsutum trichome, Cornell Un...	142	1e-47
	emb AI728374 AI728374 BNLGHi10609 Six-day Cotton fiber Gossypium...	167	3e-47
	emb AF156976 AF156976 Gerbera hybrida flavone synthase II (CYP93...	100	5e-47
50	emb AF014802 AF014802 Eschscholzia californica (S)-N-methylcocla...	165	7e-47
	emb AW773754 AW773754 EST332740 KV3 Medicago truncatula cDNA clo...	169	1e-46
	emb AW686025 AW686025 NF037D11NR1F1000 Nodulated root Medicago t...	105	1e-46
	emb AW616066 AW616066 EST296823 L. hirsutum trichome, Cornell Un...	140	2e-46
	emb AV412147 AV412147 AV412147 Lotus japonicus young plants (two...	184	1e-45
55	gb U29333 PSU29333 Pisum sativum novel wound-inducible cytochrom...	161	6e-45
	emb AI776121 AI776121 EST257209 tomato resistant, Cornell Lycop...	106	3e-44
	emb AW687247 AW687247 NF007E11RT1F1086 Developing root Medicago ...	178	8e-44
	emb AW616086 AW616086 EST296847 L. hirsutum trichome, Cornell Un...	142	1e-43
	emb AW617900 AW617900 EST324311 L. hirsutum trichome, Cornell Un...	142	1e-43
60	emb AW031264 AW031264 EST274639 tomato callus, TAMU Lycopersicon...	143	5e-43
	emb AW309826 AW309826 sf25c03.x1 Gm-c1028 Glycine max cDNA clone...	175	8e-43

- dbj|E13663|E13663 cDNA encoding cytochrome P450 which is induced... 103 8e-43
 dbj|D83968|SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)... 103 8e-43
 emb|AW617323|AW617323 EST323734 *L. hirsutum* trichome, Cornell Un... 138 1e-42
 emb|AW617605|AW617605 EST324016 *L. hirsutum* trichome, Cornell Un... 138 1e-42
 5 emb|Y10492|GMC450CP5 *G.max* mRNA for putative cytochrome P450, cl... 105 2e-42
 emb|AF195809|AF195809 *Vigna radiata* isoflavone synthase 4 (ifs4)... 100 3e-42
 emb|AF155332|AF155332 *Petunia x hybrida* flavonoid 3'-hydroxylase... 155 3e-42
 emb|AF135484|AF135484 *Glycine max* cytochrome P450 monooxygenase ... 100 4e-42
 emb|AF195807|AF195807 *Vigna radiata* isoflavone synthase 2 (ifs2)... 100 4e-42
 10 emb|AW616809|AW616809 EST323220 *L. hirsutum* trichome, Cornell Un... 137 4e-42
 emb|AF195811|AF195811 *Trifolium pratense* isoflavone synthase 2 (... 100 5e-42
 emb|AF195810|AF195810 *Trifolium pratense* isoflavone synthase 1 (... 100 5e-42
 emb|AF195808|AF195808 *Vigna radiata* isoflavone synthase 3 (ifs3)... 100 5e-42
 emb|AF195817|AF195817 *Beta vulgaris* isoflavone synthase 2 (ifs2)... 100 5e-42
 15 emb|AF195800|AF195800 *Medicago sativa* isoflavone synthase 1 (ifs... 100 5e-42
 emb|AF195802|AF195802 *Medicago sativa* isoflavone synthase 3 (ifs... 100 5e-42
 emb|AI973839|AI973839 sd11c06.y1 *Gm-c1020* *Glycine max* cDNA clone... 103 5e-42
 emb|AW734404|AW734404 sk19f09.y1 *Gm-c1028* *Glycine max* cDNA clone... 154 6e-42
 emb|AB024931|AB024931 *Lotus japonicus* mRNA for cytochrome P450, ... 98 7e-42
 20 emb|Y10491|GMC450CP4 *G.max* mRNA for putative cytochrome P450, cl... 144 8e-42
 emb|AB015762|AB015762 *Nicotiana tabacum* mRNA for cytochrome P450... 155 8e-42
 emb|AF124372|AF124372 *Nicotiana tabacum* NT7 mRNA, partial cds. 135 8e-42
 emb|AF195798|AF195798 *Glycine max* isoflavone synthase 1 (ifs1) m... 100 1e-41
 emb|AF195799|AF195799 *Glycine max* isoflavone synthase 2 (ifs2) m... 99 1e-41
 25 emb|AF022462|AF022462 *Glycine max* cytochrome P450 monooxygenase ... 99 1e-41
 emb|AF195806|AF195806 *Vigna radiata* isoflavone synthase 1 (ifs1)... 99 1e-41
 emb|AF195812|AF195812 *Pisum sativum* isoflavone synthase 1 (ifs1)... 100 2e-41
 emb|AW728802|AW728802 GA__Ea0028I12 *Gossypium arboreum* 7-10 dpa ... 153 3e-41
 emb|AW617833|AW617833 EST324232 *L. hirsutum* trichome, Cornell Un... 142 3e-41
 30 emb|AW617284|AW617284 EST323695 *L. hirsutum* trichome, Cornell Un... 142 3e-41
 emb|AW616181|AW616181 EST307220 *L. hirsutum* trichome, Cornell Un... 142 3e-41
 emb|AF195813|AF195813 *Lupinus albus* isoflavone synthase 1 (ifs1)... 99 3e-41
 emb|AF195815|AF195815 *Trifolium repens* isoflavone synthase 2 (if... 98 3e-41
 emb|AW616381|AW616381 EST322792 *L. hirsutum* trichome, Cornell Un... 141 5e-41
 35 emb|AF195801|AF195801 *Medicago sativa* isoflavone synthase 2 (ifs... 100 6e-41
 emb|AW278589|AW278589 sf46e01.y1 *Gm-c1009* *Glycine max* cDNA clone... 98 6e-41
 dbj|D86351|D86351 *Glycine max* CYP93A2 mRNA for cytochrome P-450,... 103 9e-41
 emb|AB023636|AB023636 *Glycyrrhiza echinata* CYP Ge-8 mRNA for cyt... 100 1e-40
 emb|AF195814|AF195814 *Trifolium repens* isoflavone synthase 1 (if... 100 1e-40
 40 emb|AF195805|AF195805 *Lens culinaris* isoflavone synthase 2 (ifs2... 100 2e-40
 emb|AW617099|AW617099 EST323510 *L. hirsutum* trichome, Cornell Un... 139 3e-40
 emb|AF195803|AF195803 *Vicia villosa* isoflavone synthase 1 (ifs1)... 97 3e-40
 emb|Y10982|GMP450CP6 *Glycine max* mRNA for cytochrome P450-like p... 150 4e-40
 emb|AW255096|AW255096 ML139 peppermint glandular trichome *Mentha*... 154 5e-40
 45 emb|AF195804|AF195804 *Lens culinaris* isoflavone synthase 1 (ifs1... 96 6e-40
 emb|AF195816|AF195816 *Beta vulgaris* isoflavone synthase 1 (ifs1)... 99 6e-40
 emb|AJ243804|CAR243804 *Cicer arietinum* mRNA for cytochrome P450 ... 96 8e-40

- 50 Query= AC004411.25_at 18567_at /id_source genbank /description
 gb|aac34217.1| (ac004411) putative alcohol dehydrogenase [arabidopsis
 thaliana] /blast_score 1.00e-133 /ec_number /family dehydrogenase
 /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004411|/ncgi)
 55 [post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004411|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004411|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac004411>
 (826 letters)

- Database: plantfungal
 60 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E		(bits)	Value
Sequences producing significant alignments:					
5			emb AJ277945 LES277945 Lycopersicon esculentum mRNA for putative...	125	3e-72
			emb AW234215 AW234215 sf22f01.y1 Gm-cl028 Glycine max cDNA clone...	256	1e-67
			gb U21801 LEU21801 Lycopersicon esculentum alcohol dehydrogenase...	111	1e-64
			emb AW729170 AW729170 GA_Ea0024E17 Gossypium arboreum 7-10 dpa ...	126	3e-59
10			emb AW625848 AW625848 EST319755 tomato radicle, 5 d post-imbibit...	125	2e-54
			emb AW096560 AW096560 EST289740 tomato mixed elicitor, BTI Lycop...	117	5e-52
			emb AI494929 AI494929 sa92g06.y1 Gm-cl004 Glycine max cDNA clone...	203	1e-51
			emb AB018559 AB018559 Citrullus lanatus mRNA for wts2L, complete...	74	1e-50
			emb AF053638 AF053638 Pisum sativum short-chain alcohol dehydrog...	103	3e-50
15			emb AF097651 AF097651 Pisum sativum short-chain alcohol dehydrog...	103	8e-50
			emb AF053639 AF053639 Pisum sativum short-chain alcohol dehydrog...	103	2e-49
			emb AW092874 AW092874 EST286054 tomato mixed elicitor, BTI Lycop...	112	3e-49
			emb AJ223178 NTAJ3178 Nicotiana tabacum SCANT gene.	93	7e-49
			emb AJ223177 NTAJ3177 Nicotiana tabacum mRNA for short chain alc...	93	7e-49
20			emb AW350415 AW350415 GM210008B10E12R Gm-r1021 Glycine max cDNA ...	155	2e-47
			gb U53828 SLU53828 Silene latifolia ssp. alba STA1-12 (STA1-12) ...	140	8e-47
			emb AW682978 AW682978 NF005G04LF1F1035 Developing leaf Medicago ...	107	8e-47
			emb AW093147 AW093147 EST286327 tomato mixed elicitor, BTI Lycop...	118	8e-47
			gb U53827 SLU53827 Silene latifolia ssp. alba STA1-2 (STA1-2) mR...	140	2e-46
25			gb U53829 SLU53829 Silene latifolia ssp. alba STA1-18 (STA1-18) ...	140	2e-46
			emb AI773378 AI773378 EST254478 tomato resistant, Cornell Lycope...	117	2e-45
			emb AF072447 AF072447 Ipomoea trifida short-chain alcohol dehydr...	97	5e-45
			emb AF072449 AF072449 Ipomoea trifida short-chain alcohol dehydr...	96	9e-45
			emb AF072450 AF072450 Ipomoea trifida short-chain alcohol dehydr...	94	4e-44
30			emb AF072448 AF072448 Ipomoea trifida short-chain alcohol dehydr...	94	4e-44
			emb AW349377 AW349377 GM210007A20C11R Gm-r1021 Glycine max cDNA ...	78	2e-43
			emb AI778245 AI778245 EST259124 tomato susceptible, Cornell Lyco...	117	3e-41
			emb AW776982 AW776982 EST336047 DSIL Medicago truncatula cDNA cl...	105	5e-41
			dbj D88121 D88121 Vigna unguiculata mRNA for CPRD12 protein, com...	79	8e-41
35			emb AW945039 AW945039 EST337089 tomato flower buds 3-8 mm, Corne...	107	3e-38
			emb AI486382 AI486382 EST244703 tomato ovary, TAMU Lycopersicon ...	101	1e-35
			emb AW032711 AW032711 EST276270 tomato callus, TAMU Lycopersicon...	98	9e-35
			emb AI483613 AI483613 EST249463 tomato ovary, TAMU Lycopersicon ...	98	9e-35
			emb AW441202 AW441202 EST310598 tomato fruit red ripe, TAMU Lyco...	98	2e-34
40			emb AI486640 AI486640 EST244961 tomato ovary, TAMU Lycopersicon ...	95	4e-34
			emb AW185846 AW185846 se60d03.y1 Gm-cl019 Glycine max cDNA clone...	83	3e-33
			emb AW255499 AW255499 ML524 peppermint glandular trichome Mentha...	100	1e-32
			emb AW185845 AW185845 se60d02.y1 Gm-cl019 Glycine max cDNA clone...	86	2e-32
			emb AW692543 AW692543 NF056F02ST1F1000 Developing stem Medicago ...	103	2e-31
45			emb AW202061 AW202061 sf10f02.y1 Gm-cl027 Glycine max cDNA clone...	98	5e-30
			dbj D29976 TOBT FHP1 Tobacco mRNA for TFHP-1 protein, complete cds.	87	9e-30
			emb AW254739 AW254739 ML1026 peppermint glandular trichome Menth...	92	1e-29
			gb U89270 TDU89270 Tripsacum dactyloides short-chain alcohol deh...	84	2e-29
			gb U89271 TDU89271 Tripsacum dactyloides short-chain alcohol deh...	84	2e-29
50			emb AI443505 AI443505 sa32f06.x1 Gm-cl004 Glycine max cDNA clone...	80	6e-28
			emb AW278238 AW278238 sf41e03.y1 Gm-cl009 Glycine max cDNA clone...	98	7e-28
			emb AW039180 AW039180 EST281415 tomato mixed elicitor, BTI Lycop...	75	1e-27
			emb AW031743 AW031743 EST275197 tomato callus, TAMU Lycopersicon...	71	9e-27
			emb AW203395 AW203395 sf29g01.y1 Gm-cl028 Glycine max cDNA clone...	50	8e-25
55			emb AW031891 AW031891 EST275345 tomato callus, TAMU Lycopersicon...	60	2e-24
			emb AL115211 CNS01C8J Botrytis cinerea strain T4 cDNA library un...	111	1e-23
			emb AW221824 AW221824 EST298635 tomato fruit red ripe, TAMU Lyco...	60	1e-23
			emb AW093827 AW093827 EST287007 tomato mixed elicitor, BTI Lycop...	60	1e-23
			emb AI488267 AI488267 EST246589 tomato ovary, TAMU Lycopersicon ...	60	3e-23
60			emb AW679848 AW679848 WS1_32_F10.g1_A002 Water-stressed 1 (WS1) ...	78	5e-23
			emb AW040207 AW040207 EST282706 tomato mixed elicitor, BTI Lycop...	58	5e-23

emb|AW040198|AW040198 EST282697 tomato mixed elicitor, BTI Lycop... 58 5e-23
emb|AI897246|AI897246 EST266605 tomato ovary, TAMU Lycopersicon ... 57 9e-23
emb|AW757208|AW757208 sl30e10.y1 Gm-cl027 Glycine max cDNA clone... 94 2e-22
emb|AW698458|AW698458 g412 glandular-haired subtracted cDNA libr... 75 3e-22
5 emb|AW686040|AW686040 NF037F07NR1F1000 Nodulated root Medicago t... 104 1e-21
emb|AW689744|AW689744 NF023H04ST1F1000 Developing stem Medicago ... 104 1e-21
emb|AW559784|AW559784 EST314832 DSIR Medicago truncatula cDNA cl... 101 6e-21
emb|AW862634|AW862634 00093 leafy spurge Lambda HybriZAP 2.1 two... 75 1e-20
emb|AW821919|AW821919 00010 leafy spurge Lambda HybriZAP 2.1 two... 75 1e-20
10 emb|AW277819|AW277819 sf87a01.y1 Gm-cl019 Glycine max cDNA clone... 65 2e-20
emb|AW032875|AW032875 EST276434 tomato callus, TAMU Lycopersicon... 53 2e-20
gb|BE020693|BE020693 sm45g06.y1 Gm-cl028 Glycine max cDNA clone ... 82 3e-20
emb|AW094463|AW094463 EST287643 tomato mixed elicitor, BTI Lycop... 98 7e-20
emb|AI442526|AI442526 sa32f06.y1 Gm-cl004 Glycine max cDNA clone... 98 7e-20
15 emb|AI900071|AI900071 sb98e02.y1 Gm-cl012 Glycine max cDNA clone... 98 7e-20
emb|AW931981|AW931981 EST357824 tomato fruit mature green, TAMU ... 98 7e-20
emb|AW759370|AW759370 sl41e03.y1 Gm-cl027 Glycine max cDNA clone... 98 1e-19
emb|AI813131|AI813131 23C8 Pine Lambda Zap Xylem library Pinus t... 49 2e-19
emb|AW222302|AW222302 EST299113 tomato fruit red ripe, TAMU Lyco... 55 2e-19
20 emb|AW092588|AW092588 EST285768 tomato mixed elicitor, BTI Lycop... 62 6e-19
emb|AI495898|AI495898 sb17e12.y1 Gm-cl004 Glycine max cDNA clone... 95 7e-19
emb|AW034003|AW034003 EST277665 tomato callus, TAMU Lycopersicon... 55 1e-18
emb|AI486457|AI486457 EST244778 tomato ovary, TAMU Lycopersicon ... 55 1e-18
emb|AI441861|AI441861 sa53c11.y1 Gm-cl004 Glycine max cDNA clone... 91 8e-18
25 emb|AW932087|AW932087 EST357930 tomato fruit mature green, TAMU ... 55 4e-17
emb|AW277586|AW277586 sf84a04.y1 Gm-cl019 Glycine max cDNA clone... 61 6e-17
emb|AW290533|AW290533 NXNV025G01F Nsf Xylem Normal wood Vertical... 60 1e-16
emb|AW928544|AW928544 EST337332 tomato flower buds 8 mm to pre-a... 85 5e-16
emb|AI494694|AI494694 sb14a12.y1 Gm-cl004 Glycine max cDNA clone... 84 1e-15
30 emb|AW923985|AW923985 WS1_32_F10.b1_A002 Water-stressed 1 (WS1) ... 57 1e-15
emb|AW432507|AW432507 sh75b08.y1 Gm-cl015 Glycine max cDNA clone... 64 1e-15
emb|AW030102|AW030102 EST273357 tomato callus, TAMU Lycopersicon... 55 2e-15
emb|AA825003|AA825003 CT286.SK Tomato Leaf cDNA from cv. VFNT ch... 55 3e-15
emb|AW309265|AW309265 sf29f03.x1 Gm-cl028 Glycine max cDNA clone... 60 9e-15
35 emb|AW728352|AW728352 GA_Ea0016G23 Gossypium arboreum 7-10 dpa ... 81 9e-15
emb|AW676767|AW676767 DG1_14_E09.g1_A002 Dark Grown 1 (DG1) Sorg... 61 6e-14
emb|AW648661|AW648661 EST327031 tomato germinating seedlings, TA... 53 6e-14
emb|AW309650|AW309650 sf22f01.x1 Gm-cl028 Glycine max cDNA clone... 56 1e-13
emb|AQ162057|AQ162057 mgxb0010H24r CUGI Rice Blast BAC Library P... 66 9e-13
40 emb|AV408902|AV408902 AV408902 Lotus japonicus young plants (two... 52 9e-12
emb|AW727400|AW727400 GA_Ea0011O17 Gossypium arboreum 7-10 dpa ... 69 3e-11
emb|AW442057|AW442057 EST311453 tomato fruit red ripe, TAMU Lyco... 49 3e-11
emb|AW037838|AW037838 EST279467 tomato mixed elicitor, BTI Lycop... 68 7e-11
emb|X72730|LEERT10 L.esculentum (ERT 10) ripening-related mRNA. 47 1e-10
45

Query= AJ222713.4_at 18590_at /id_source genbank /description
emb|caa10955.1| (aj222713) unnamed protein product [arabidopsis
thaliana] /blast_score 1.00e-151 /ec_number /family /chip nova
50 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|aj222713| /ncgi
http://www.ncgr.org/cgi-bin/ff?aj222713
(1056 letters)

55 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

60 Score E
Sequences producing significant alignments: (bits) Value

	emb AI488099 AI488099 EST246421 tomato ovary, TAMU Lycopersicon ...	341	5e-93
	emb AI487552 AI487552 EST245874 tomato ovary, TAMU Lycopersicon ...	337	9e-92
	emb AI487693 AI487693 EST246015 tomato ovary, TAMU Lycopersicon ...	336	1e-91
5	emb AI898890 AI898890 EST268333 tomato ovary, TAMU Lycopersicon ...	336	2e-91
	emb AI490551 AI490551 EST249105 tomato ovary, TAMU Lycopersicon ...	336	2e-91
	emb AI898058 AI898058 EST267501 tomato ovary, TAMU Lycopersicon ...	336	2e-91
	emb AI488773 AI488773 EST247112 tomato ovary, TAMU Lycopersicon ...	336	2e-91
	emb AW032532 AW032532 EST276091 tomato callus, TAMU Lycopersicon...	334	6e-91
10	emb AI488959 AI488959 EST247298 tomato ovary, TAMU Lycopersicon ...	334	6e-91
	emb AW035679 AW035679 EST281698 tomato callus, TAMU Lycopersicon...	331	4e-90
	emb AI488673 AI488673 EST247012 tomato ovary, TAMU Lycopersicon ...	330	2e-89
	emb AW220879 AW220879 EST297348 tomato fruit mature green, TAMU ...	329	3e-89
	emb AW650556 AW650556 EST329010 tomato germinating seedlings, TA...	328	5e-89
15	emb AI484813 AI484813 EST243074 tomato ovary, TAMU Lycopersicon ...	325	5e-88
	gb BE020071 BE020071 sm38f07.y1 Gm-cl028 Glycine max cDNA clone ...	314	5e-85
	emb AI488758 AI488758 EST247097 tomato ovary, TAMU Lycopersicon ...	308	5e-83
	emb AI898567 AI898567 EST268010 tomato ovary, TAMU Lycopersicon ...	287	3e-82
	emb AI897442 AI897442 EST266885 tomato ovary, TAMU Lycopersicon ...	304	8e-82
20	emb AI486892 AI486892 EST245214 tomato ovary, TAMU Lycopersicon ...	284	3e-81
	emb AW032194 AW032194 EST275648 tomato callus, TAMU Lycopersicon...	302	4e-81
	emb AI489402 AI489402 EST247741 tomato ovary, TAMU Lycopersicon ...	282	6e-81
	emb AW035194 AW035194 EST280456 tomato callus, TAMU Lycopersicon...	299	2e-80
	emb AI485389 AI485389 EST243710 tomato ovary, TAMU Lycopersicon ...	297	1e-79
25	emb AI487373 AI487373 EST245695 tomato ovary, TAMU Lycopersicon ...	284	4e-79
	emb AI897257 AI897257 EST266616 tomato ovary, TAMU Lycopersicon ...	292	4e-78
	emb AI771859 AI771859 EST252959 tomato ovary, TAMU Lycopersicon ...	292	4e-78
	emb AI487093 AI487093 EST245415 tomato ovary, TAMU Lycopersicon ...	292	4e-78
	emb AI898263 AI898263 EST267706 tomato ovary, TAMU Lycopersicon ...	291	8e-78
30	emb AI899016 AI899016 EST268459 tomato ovary, TAMU Lycopersicon ...	288	5e-77
	emb AI490061 AI490061 EST248400 tomato ovary, TAMU Lycopersicon ...	286	2e-76
	emb AW650475 AW650475 EST328929 tomato germinating seedlings, TA...	281	5e-75
	emb AW036798 AW036798 EST252187 tomato ovary, TAMU Lycopersicon ...	185	2e-72
	emb AI894523 AI894523 EST263966 tomato callus, TAMU Lycopersicon...	185	2e-72
35	emb AI897596 AI897596 EST267039 tomato ovary, TAMU Lycopersicon ...	270	1e-71
	emb AW034429 AW034429 EST278000 tomato callus, TAMU Lycopersicon...	193	6e-70
	emb AW442290 AW442290 EST311686 tomato fruit red ripe, TAMU Lyco...	186	3e-68
	emb AF011555 AF011555 Lycopersicon esculentum jasmonic acid 2 (L...	233	5e-68
	emb AW931430 AW931430 EST357273 tomato fruit mature green, TAMU ...	233	5e-68
40	emb AW934046 AW934046 EST359889 tomato fruit mature green, TAMU ...	233	5e-68
	emb AW032396 AW032396 EST275935 tomato callus, TAMU Lycopersicon...	233	5e-68
	emb AJ010829 TSP010829 Triticum sp. mRNA for GRAB1 protein.	258	7e-68
	emb A82384 A82384 Sequence 9 from Patent WO9856811.	258	7e-68
	emb A82380 A82380 Sequence 5 from Patent WO9856811.	255	5e-67
45	emb AI896316 AI896316 EST265759 tomato callus, TAMU Lycopersicon...	185	2e-66
	emb AI895235 AI895235 EST264678 tomato callus, TAMU Lycopersicon...	169	2e-66
	emb AW932278 AW932278 EST358121 tomato fruit mature green, TAMU ...	169	2e-66
	emb AI489104 AI489104 EST247443 tomato ovary, TAMU Lycopersicon ...	215	5e-66
	emb AI771112 AI771112 EST252212 tomato ovary, TAMU Lycopersicon ...	215	5e-66
50	emb AW035978 AW035978 EST282837 tomato callus, TAMU Lycopersicon...	193	9e-66
	emb AW560823 AW560823 EST315871 DSIR Medicago truncatula cDNA cl...	193	1e-65
	emb AW775926 AW775926 EST334991 DSIL Medicago truncatula cDNA cl...	229	1e-65
	emb AW442348 AW442348 EST311744 tomato fruit red ripe, TAMU Lyco...	169	1e-65
	emb AW775866 AW775866 EST334931 DSIL Medicago truncatula cDNA cl...	166	5e-65
55	emb AI896441 AI896441 EST265872 tomato callus, TAMU Lycopersicon...	233	5e-65
	emb AI487186 AI487186 EST245508 tomato ovary, TAMU Lycopersicon ...	229	7e-65
	emb AW625882 AW625882 EST319789 tomato radicle, 5 d post-imbibit...	169	2e-64
	emb AI485002 AI485002 EST243265 tomato ovary, TAMU Lycopersicon ...	143	2e-64
	emb AW932996 AW932996 EST358839 tomato fruit mature green, TAMU ...	193	3e-64
60	gb BE034140 BE034140 MG05E02 MG Mesembryanthemum crystallinum cD...	224	5e-64
	emb AW443857 AW443857 EST308787 tomato mixed elicitor, BTI Lycop...	224	6e-64

emb|AI487893|AI487893 EST246215 tomato ovary, TAMU Lycopersicon ... 229 9e-64
 emb|AI488078|AI488078 EST246400 tomato ovary, TAMU Lycopersicon ... 241 6e-63
 emb|AW164307|AW164307 se70g05.y1 Gm-c1023 Glycine max cDNA clone... 190 1e-62
 emb|AW216517|AW216517 EST295231 tomato callus, TAMU Lycopersicon... 213 1e-62
 5 emb|AW668121|AW668121 GA_Ea0012N05 Gossypium arboreum 7-10 dpa ... 167 3e-62
 emb|AW442068|AW442068 EST311464 tomato fruit red ripe, TAMU Lyco... 160 7e-62
 emb|AI773092|AI773092 EST254192 tomato resistant, Cornell Lycop... 160 7e-62
 emb|AI488314|AI488314 EST246636 tomato ovary, TAMU Lycopersicon ... 160 1e-61
 emb|AI489361|AI489361 EST247700 tomato ovary, TAMU Lycopersicon ... 160 1e-61
 10 emb|AW680754|AW680754 WS1_7_A09.b1_A002 Water-stressed 1 (WS1) S... 170 3e-61
 emb|AI856667|AI856667 sb42d09.y1 Gm-c1014 Glycine max cDNA clone... 169 3e-61
 emb|AW099384|AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone... 144 5e-61
 emb|AW100389|AW100389 sd27a08.y2 Gm-c1012 Glycine max cDNA clone... 180 6e-61
 emb|AW737167|AW737167 EST338594 tomato flower buds, anthesis, Co... 160 9e-61
 15 emb|AW030017|AW030017 EST273272 tomato callus, TAMU Lycopersicon... 193 2e-60
 emb|AW223963|AW223963 EST300774 tomato fruit red ripe, TAMU Lyco... 186 4e-60
 emb|AW033350|AW033350 EST276921 tomato callus, TAMU Lycopersicon... 230 1e-59
 emb|AI896351|AI896351 EST265794 tomato callus, TAMU Lycopersicon... 230 2e-59
 emb|AI897423|AI897423 EST266866 tomato ovary, TAMU Lycopersicon ... 230 2e-59
 20 emb|AI484784|AI484784 EST243045 tomato ovary, TAMU Lycopersicon ... 230 2e-59
 emb|AI771893|AI771893 EST252993 tomato ovary, TAMU Lycopersicon ... 229 2e-59
 emb|AW560904|AW560904 EST315952 DSIR Medicago truncatula cDNA cl... 168 3e-59
 emb|AW040320|AW040320 EST283184 tomato mixed elicitor, BTI Lycop... 229 3e-59
 emb|AW736371|AW736371 EST332290 KV3 Medicago truncatula cDNA clo... 160 5e-59
 25 emb|AI484577|AI484577 EST242807 tomato ovary, TAMU Lycopersicon ... 228 5e-59
 emb|AI488159|AI488159 EST246481 tomato ovary, TAMU Lycopersicon ... 228 6e-59
 gb|BE124309|BE124309 EST394434 DSIL Medicago truncatula cDNA clo... 161 1e-58
 emb|AW775409|AW775409 EST334474 DSIL Medicago truncatula cDNA cl... 161 1e-58
 emb|AW092910|AW092910 EST286090 tomato mixed elicitor, BTI Lycop... 160 1e-58
 30 emb|AW559397|AW559397 EST314445 DSIR Medicago truncatula cDNA cl... 159 4e-58
 emb|AI487779|AI487779 EST246101 tomato ovary, TAMU Lycopersicon ... 160 7e-58
 emb|AV410710|AV410710 AV410710 Lotus japonicus young plants (two... 224 1e-57
 emb|AI773440|AI773440 EST254540 tomato resistant, Cornell Lycop... 169 3e-57
 emb|AW041100|AW041100 EST283964 tomato mixed elicitor, BTI Lycop... 222 4e-57
 35 emb|AW930743|AW930743 EST356586 tomato fruit mature green, TAMU ... 221 5e-57
 emb|AW775964|AW775964 EST335029 DSIL Medicago truncatula cDNA cl... 161 1e-56
 emb|AI490656|AI490656 EST249210 tomato ovary, TAMU Lycopersicon... 220 1e-56
 emb|AI490318|AI490318 EST248644 tomato ovary, TAMU Lycopersicon ... 220 2e-56
 emb|AI490458|AI490458 EST248784 tomato ovary, TAMU Lycopersicon ... 199 4e-56
 40 emb|AI486445|AI486445 EST244766 tomato ovary, TAMU Lycopersicon ... 199 4e-56

Query= X74756.2_at 18591_at /id_source genbank /description
 emb|caa52772.1| (x74756) ataf2 [arabidopsis thaliana] /blast_score
 45 2.00e-99 /ec_number /family /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x74756|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|x74756|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x74756|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?x74756>
 (1216 letters)

50 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

55
 Score E
 Sequences producing significant alignments: (bits) Value

emb|AW775866|AW775866 EST334931 DSIL Medicago truncatula cDNA cl... 317 1e-97
 60 emb|AW668121|AW668121 GA_Ea0012N05 Gossypium arboreum 7-10 dpa ... 304 6e-94
 gb|BE124309|BE124309 EST394434 DSIL Medicago truncatula cDNA clo... 304 9e-94

- emb|AW775409|AW775409 EST334474 DSIL *Medicago truncatula* cDNA cl... 304 9e-94
emb|AW559397|AW559397 EST314445 DSIR *Medicago truncatula* cDNA cl... 301 6e-93
emb|AI856667|AI856667 sb42d09.y1 Gm-cl014 Glycine max cDNA clone... 293 2e-92
emb|AW442068|AW442068 EST311464 tomato fruit red ripe, TAMU Lyco... 300 5e-92
5 emb|AI773092|AI773092 EST254192 tomato resistant, Cornell Lycope... 300 5e-92
emb|AW442348|AW442348 EST311744 tomato fruit red ripe, TAMU Lyco... 306 7e-91
emb|AW737167|AW737167 EST338594 tomato flower buds, anthesis, Co... 297 7e-91
emb|AI489361|AI489361 EST247700 tomato ovary, TAMU Lycopersicon ... 296 9e-91
emb|AW696936|AW696936 NF110E07ST1F1054 Developing stem *Medicago* ... 301 2e-90
10 emb|AI895235|AI895235 EST264678 tomato callus, TAMU Lycopersicon... 302 2e-90
emb|AW932278|AW932278 EST358121 tomato fruit mature green, TAMU ... 302 2e-90
emb|AI488314|AI488314 EST246636 tomato ovary, TAMU Lycopersicon ... 300 1e-89
emb|AW775964|AW775964 EST335029 DSIL *Medicago truncatula* cDNA cl... 304 6e-89
emb|AW690801|AW690801 NF035B09ST1F1000 Developing stem *Medicago* ... 304 2e-88
15 emb|AW687506|AW687506 NF010C12RT1F1097 Developing root *Medicago* ... 302 3e-88
emb|AW680754|AW680754 WS1_7_A09.b1_A002 Water-stressed 1 (WS1) S... 292 5e-88
emb|AW625882|AW625882 EST319789 tomato radicle, 5 d post-imbibit... 306 7e-88
emb|AW560904|AW560904 EST315952 DSIR *Medicago truncatula* cDNA cl... 282 1e-87
emb|AW686733|AW686733 NF041H04NR1F1000 Nodulated root *Medicago* t... 304 2e-87
20 emb|AW736371|AW736371 EST332290 KV3 *Medicago truncatula* cDNA clo... 280 5e-87
emb|AW203537|AW203537 sf35d02.y1 Gm-cl028 Glycine max cDNA clone... 287 5e-87
emb|AW092910|AW092910 EST286090 tomato mixed elicitor, BTI Lycop... 300 3e-85
emb|AW278088|AW278088 sf39e10.y1 Gm-cl009 Glycine max cDNA clone... 314 6e-85
emb|AI487779|AI487779 EST246101 tomato ovary, TAMU Lycopersicon ... 300 1e-84
25 emb|AI896058|AI896058 EST265501 tomato callus, TAMU Lycopersicon... 306 3e-82
emb|AI773440|AI773440 EST254540 tomato resistant, Cornell Lycope... 305 5e-82
emb|AI486492|AI486492 EST244813 tomato ovary, TAMU Lycopersicon ... 297 8e-80
emb|AW220707|AW220707 EST297176 tomato fruit mature green, TAMU ... 297 2e-79
emb|AI486833|AI486833 EST245155 tomato ovary, TAMU Lycopersicon ... 295 5e-79
30 emb|AW030038|AW030038 EST273293 tomato callus, TAMU Lycopersicon... 293 2e-78
emb|AW931009|AW931009 EST356852 tomato fruit mature green, TAMU ... 291 7e-78
emb|AW306698|AW306698 sf47c01.y1 Gm-cl009 Glycine max cDNA clone... 275 4e-77
gb|BE126167|BE126167 DG1_66_F07.b1_A002 Dark Grown 1 (DG1) Sorgh... 281 8e-75
emb|AJ010829|TSP010829 Triticum sp. mRNA for GRAB1 protein. 195 2e-69
35 emb|A82384|A82384 Sequence 9 from Patent WO9856811. 195 2e-69
emb|AW776648|AW776648 EST335713 DSIL *Medicago truncatula* cDNA cl... 262 5e-69
emb|AI488057|AI488057 EST246379 tomato ovary, TAMU Lycopersicon ... 261 6e-69
emb|AI900247|AI900247 sc03a01.y1 Gm-cl012 Glycine max cDNA clone... 251 1e-65
emb|AW617735|AW617735 EST324146 *L. hirsutum* trichome, Cornell Un... 250 1e-65
40 emb|AI777446|AI777446 EST258325 tomato susceptible, Cornell Lyco... 248 6e-65
emb|AW775926|AW775926 EST334991 DSIL *Medicago truncatula* cDNA cl... 179 3e-64
emb|AW442290|AW442290 EST311686 tomato fruit red ripe, TAMU Lyco... 175 3e-64
emb|AW034429|AW034429 EST278000 tomato callus, TAMU Lycopersicon... 176 4e-64
gb|BE034140|BE034140 MG05E02 MG *Mesembryanthemum crystallinum* cD... 182 5e-64
45 emb|AI487038|AI487038 EST245360 tomato ovary, TAMU Lycopersicon ... 206 7e-64
emb|A82380|A82380 Sequence 5 from Patent WO9856811. 183 9e-64
emb|AI352742|AI352742 MB56-5B PZ204.BNlib *Brassica napus* cDNA cl... 211 1e-63
emb|AW560823|AW560823 EST315871 DSIR *Medicago truncatula* cDNA cl... 179 1e-63
emb|AW443857|AW443857 EST308787 tomato mixed elicitor, BTI Lycop... 182 8e-63
50 emb|AW727788|AW727788 GA_Ea0028C07 *Gossypium arboreum* 7-10 dpa ... 200 2e-62
emb|AI896316|AI896316 EST265759 tomato callus, TAMU Lycopersicon... 171 2e-61
emb|AW035978|AW035978 EST282837 tomato callus, TAMU Lycopersicon... 176 9e-61
emb|AI484102|AI484102 EST249973 tomato ovary, TAMU Lycopersicon ... 234 1e-60
emb|AI488099|AI488099 EST246421 tomato ovary, TAMU Lycopersicon ... 167 6e-60
55 emb|AV410710|AV410710 AV410710 *Lotus japonicus* young plants (two... 185 2e-59
emb|AI487693|AI487693 EST246015 tomato ovary, TAMU Lycopersicon ... 167 4e-59
emb|AW755370|AW755370 sl03b07.y1 Gm-cl036 Glycine max cDNA clone... 159 3e-58
emb|AW932996|AW932996 EST358839 tomato fruit mature green, TAMU ... 176 4e-58
emb|AI487552|AI487552 EST245874 tomato ovary, TAMU Lycopersicon ... 160 5e-58
60 emb|AI488773|AI488773 EST247112 tomato ovary, TAMU Lycopersicon ... 160 5e-58
emb|AI490551|AI490551 EST249105 tomato ovary, TAMU Lycopersicon ... 160 5e-58

emb|AI898058|AI898058 EST267501 tomato ovary, TAMU Lycopersicon ... 160 5e-58
 emb|AI898890|AI898890 EST268333 tomato ovary, TAMU Lycopersicon ... 160 5e-58
 emb|AW032532|AW032532 EST276091 tomato callus, TAMU Lycopersicon... 160 2e-57
 emb|AI488959|AI488959 EST247298 tomato ovary, TAMU Lycopersicon ... 160 2e-57
 5 emb|AW041100|AW041100 EST283964 tomato mixed elicitor, BTI Lycop... 182 3e-57
 emb|AF011555|AF011555 Lycopersicon esculentum jasmonic acid 2 (L... 174 4e-57
 emb|AW931430|AW931430 EST357273 tomato fruit mature green, TAMU ... 174 4e-57
 emb|AW934046|AW934046 EST359889 tomato fruit mature green, TAMU ... 174 4e-57
 emb|AW032396|AW032396 EST275935 tomato callus, TAMU Lycopersicon... 174 4e-57
 10 emb|AI896441|AI896441 EST265872 tomato callus, TAMU Lycopersicon... 174 4e-57
 emb|AI488673|AI488673 EST247012 tomato ovary, TAMU Lycopersicon ... 160 1e-56
 emb|AW164307|AW164307 se70g05.y1 Gm-cl023 Glycine max cDNA clone... 174 1e-56
 emb|AW040320|AW040320 EST283184 tomato mixed elicitor, BTI Lycop... 174 1e-56
 emb|AW035679|AW035679 EST281698 tomato callus, TAMU Lycopersicon... 160 2e-56
 15 emb|AW220879|AW220879 EST297348 tomato fruit mature green, TAMU ... 167 2e-56
 emb|AW223963|AW223963 EST300774 tomato fruit red ripe, TAMU Lyco... 177 3e-56
 emb|AW776779|AW776779 EST335844 DSIL Medicago truncatula cDNA cl... 219 4e-56
 emb|AW650556|AW650556 EST329010 tomato germinating seedlings, TA... 160 3e-55
 emb|AI773941|AI773941 EST255041 tomato resistant, Cornell Lycope... 215 4e-55
 20 emb|AI484813|AI484813 EST243074 tomato ovary, TAMU Lycopersicon ... 150 2e-54
 emb|AW733637|AW733637 sk83b05.y1 Gm-cl016 Glycine max cDNA clone... 213 3e-54
 emb|AI488758|AI488758 EST247097 tomato ovary, TAMU Lycopersicon ... 167 3e-54
 emb|AW100389|AW100389 sd27a08.y2 Gm-cl012 Glycine max cDNA clone... 169 4e-54
 emb|AW030017|AW030017 EST273272 tomato callus, TAMU Lycopersicon... 176 7e-54
 25 gb|BE020071|BE020071 sm38f07.y1 Gm-cl028 Glycine max cDNA clone ... 171 2e-53
 emb|AI899016|AI899016 EST268459 tomato ovary, TAMU Lycopersicon ... 163 1e-52
 emb|AI897442|AI897442 EST266885 tomato ovary, TAMU Lycopersicon ... 160 4e-52
 emb|AW032194|AW032194 EST275648 tomato callus, TAMU Lycopersicon... 160 4e-52
 emb|AW035194|AW035194 EST280456 tomato callus, TAMU Lycopersicon... 160 4e-52
 30 emb|AI897257|AI897257 EST266616 tomato ovary, TAMU Lycopersicon ... 160 4e-52
 emb|AI771859|AI771859 EST252959 tomato ovary, TAMU Lycopersicon ... 160 4e-52
 emb|AI487093|AI487093 EST245415 tomato ovary, TAMU Lycopersicon ... 160 4e-52
 emb|AI490061|AI490061 EST248400 tomato ovary, TAMU Lycopersicon ... 160 8e-52
 emb|AW678664|AW678664 WS1_1_H04.b1_A002 Water-stressed 1 (WS1) S... 120 3e-51
 35 emb|AW099384|AW099384 sd39f03.y1 Gm-cl016 Glycine max cDNA clone... 137 4e-51
 emb|AI898263|AI898263 EST267706 tomato ovary, TAMU Lycopersicon ... 160 5e-50

40 Query= AC005278.22_at 18625_at /id_source genbank /description
 "gb|aac72125.1| (ac005278) ests gb|h36966, gb|r65511, gb|t42324 and
 gb|t20569 come from this gene. [arabidopsis thaliana]" /blast_score 0
 /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005278|/ncgi
 45 http://www.ncgr.org/cgi-bin/ff?ac005278
 (1716 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

50 Searching.....done

	Score	E	(bits)	Value
Sequences producing significant alignments:				
55 emb AI780241 AI780241 EST261120 tomato susceptible, Cornell Lyco...	156	2e-49		
emb AW626380 AW626380 EST320287 tomato radicle, 5 d post-imbibit...	122	5e-43		
emb AW703985 AW703985 sk26b05.y1 Gm-cl028 Glycine max cDNA clone...	132	6e-30		
emb AW289599 AW289599 NXNV002D08F Nsf Xylem Normal wood Vertical...	115	1e-24		
60 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago ...	88	2e-16		
emb AW685613 AW685613 NF032C12NR1F1000 Nodulated root Medicago t...	88	2e-16		

emb|AW736154|AW736154 EST332140 KV3 Medicago truncatula cDNA clo... 88 2e-16
 emb|AW736412|AW736412 EST332426 KV3 Medicago truncatula cDNA clo... 88 2e-16
 emb|AW929060|AW929060 EST337764 tomato flower buds 8 mm to pre-a... 76 9e-13
 gb|C95256|C95256 C95256 Citrus unshiu Miyagawa-wase maturation s... 59 1e-07
 5 emb|AW981624|AW981624 PC14G07 Pine TriplEx pollen cone library P... 58 2e-07
 emb|Z72807|SCYGR022C S.cerevisiae chromosome VII reading frame O... 29 1.3
 emb|AW726115|AW726115 GA_Ea0020L02 Gossypium arboreum 7-10 dpa ... 35 1.7
 emb|AW690315|AW690315 NF029D02ST1F1000 Developing stem Medicago ... 34 3.1
 emb|AQ852328|AQ852328 LMAJFV1_lm68c02.y1 Leishmania major FV1 ra... 34 3.1
 10 emb|AW695266|AW695266 NF092H10ST1F1091 Developing stem Medicago ... 34 3.1
 emb|AW691641|AW691641 NF047D12ST1F1000 Developing stem Medicago ... 34 3.1
 emb|AE001413|AE001413 Plasmodium falciparum chromosome 2, sectio... 34 3.1
 emb|AL136326|LMFL377 Leishmania major Friedlin chromosome 23 cos... 34 3.1
 emb|AW683188|AW683188 NF008F07LF1F1062 Developing leaf Medicago ... 34 3.1
 15 emb|AJ001925|PAAJ1925 Picea abies cad7 gene. 33 4.3
 emb|AV395482|AV395482 AV395482 Chlamydomonas reinhardtii C9 Chla... 33 4.3
 emb|AW981387|AW981387 EST392540 DSIL Medicago truncatula cDNA cl... 33 5.6
 emb|AW759380|AW759380 sl41f02.y1 Gm-cl027 Glycine max cDNA clone... 33 5.9
 emb|AQ641451|AQ641451 RPCI93-EcoRI-4I17.TV RPCI93-EcoRI Trypanos... 33 5.9
 20 emb|AC006281|AC006281 Plasmodium falciparum chromosome 12 clone ... 33 7.7
 gb|C96380|C96380 C96380 Marchantia polymorpha immature sex organ... 33 7.7
 emb|AW735863|AW735863 EST336631 tomato flower buds 0-3 mm, Corne... 32 8.1
 emb|AW184933|AW184933 se83h06.y1 Gm-cl023 Glycine max cDNA clone... 32 8.1
 emb|AW030335|AW030335 EST273590 tomato callus, TAMU Lycopersicon... 32 8.1
 25 emb|AW221805|AW221805 EST298616 tomato fruit red ripe, TAMU Lyco... 32 8.1
 gb|U33007|SCD9461 Saccharomyces cerevisiae chromosome IV lambda ... 32 8.1
 emb|AW311676|AW311676 NXNV055A06F Nsf Xylem Normal wood Vertical... 32 8.1
 emb|AI895127|AI895127 EST264570 tomato callus, TAMU Lycopersicon... 32 8.1
 gb|S69101|S69101 HKR1=Hansenula mrakii killer toxin-resistant ge... 32 8.1
 30

Query= AF055848.2_i_at 18908_i_at /id_source genbank /description
 gb|aac62611.1| (af055848) subtilisin-like protease [arabidopsis
 thaliana] /blast_score 0 /ec_number /family protease /chip nova
 35 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|af055848| /ncgi
 http://www.ncgr.org/cgi-bin/ff?af055848
 (2403 letters)

40 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

45 Score E
 Sequences producing significant alignments: (bits) Value

emb|AJ006378|LES6378 Lycopersicon esculentum sbt1 gene. 240 e-157
 emb|X98929|LESBT1 L.esculentum mRNA for serine protease, SBT1. 240 e-157
 50 emb|Y18932|LES18932 Lycopersicon esculentum p69F gene. 142 e-152
 emb|Y17278|LES17278 Lycopersicon esculentum p69d gene, complete ... 141 e-146
 emb|AJ005173|LEAJ5173 Lycopersicon esculentum p69f gene, complet... 141 e-146
 emb|AJ005172|LEAJ5172 Lycopersicon esculentum p69e gene, complet... 142 e-146
 emb|Y18931|LES18931 Lycopersicon esculentum p69E gene. 144 e-144
 55 emb|AJ006379|LES6379 Lycopersicon esculentum sbt2 gene. 163 e-142
 emb|X98930|LESBT2 L.esculentum mRNA for serine protease, SBT2. 163 e-142
 emb|AJ006786|LES6786 Lycopersicon esculentum p69d gene. 141 e-136
 emb|AJ005171|LEAJ517 Lycopersicon esculentum p69c gene, complete... 142 e-136
 emb|Y17276|LES17276 Lycopersicon esculentum p69b gene, complete ... 138 e-130
 60 emb|Y10149|LESUBTILI L.esculentum mRNA for subtilisin-like protein. 138 e-130
 emb|Y17275|LES17275 Lycopersicon esculentum p69a gene, complete ... 138 e-126

- emb|X95270|LESUBENDO *L. esculentum* mRNA for subtilisin-like endop... 138 e-126
 dbj|D32206|CUSSP Melon mRNA for cucumisin (serine protease), com... 92 e-120
 emb|Y17277|LES17277 *Lycopersicon esculentum* p69c gene, complete ... 148 2e-97
 emb|AI960990|AI960990 sc93f09.y1 Gm-cl019 Glycine max cDNA clone... 338 9e-92
 5 emb|AW218382|AW218382 EST303565 tomato radicle, 5 d post-imbibit... 322 6e-87
 dbj|D86598|D86598 Norway spruce mRNA for antifreeze-like protein... 135 6e-77
 emb|X85975|AGAG12 *A. glutinosa* mRNA for subtilisin-like protein. 139 1e-73
 gb|BE124129|BE124129 EST394254 *DSIL Medicago truncatula* cDNA clo... 263 5e-69
 emb|AJ006380|LES6380 *Lycopersicon esculentum* sbt3 gene. 102 3e-68
 10 emb|AJ006376|LES6376 *Lycopersicon esculentum* mRNA for serine pro... 102 3e-68
 emb|AJ006480|LES6480 *Lycopersicon esculentum* sbt4b gene. 146 2e-66
 emb|AJ006481|LES6481 *Lycopersicon esculentum* sbt4c gene. 138 2e-66
 emb|AW267784|AW267784 EST305912 *DSIR Medicago truncatula* cDNA cl... 128 3e-65
 emb|AJ006483|LES6483 *Lycopersicon esculentum* sbt4e gene. 140 5e-65
 15 emb|AJ006377|LES6377 *Lycopersicon esculentum* mRNA for serine pro... 138 5e-65
 emb|AW459354|AW459354 sh41a03.y1 Gm-cl017 Glycine max cDNA clone... 192 6e-64
 emb|AW349252|AW349252 GM210004B21G12R Gm-r1021 Glycine max cDNA ... 144 1e-63
 emb|AJ276710|GMA276710 Glycine max mRNA for putative subtilisin ... 124 8e-63
 20 emb|AJ012164|CGL012164 *Casuarina glauca* mRNA for cg12 gene fragm... 114 4e-62
 emb|AI730592|AI730592 BNLGHi7352 Six-day Cotton fiber *Gossypium* ... 216 2e-61
 emb|AW728806|AW728806 GA__Ea0028I22 *Gossypium arboreum* 7-10 dpa ... 125 5e-60
 emb|AI794673|AI794673 sb67d01.y1 Gm-cl019 Glycine max cDNA clone... 171 1e-59
 emb|AW773858|AW773858 EST332844 KV3 *Medicago truncatula* cDNA clo... 87 2e-58
 25 emb|AW695319|AW695319 NF093H12ST1F1103 Developing stem *Medicago* ... 105 2e-57
 emb|AW299160|AW299160 EST305970 KV2 *Medicago truncatula* cDNA clo... 135 3e-57
 emb|AF201883|AF201883 *Gossypoides kirkii* subtilisin-like protea... 108 7e-57
 emb|AW720622|AW720622 LjNEST22e12rc *Lotus japonicus* nodule libra... 137 2e-56
 emb|AW925917|AW925917 HVSMEg0005N16 *Hordeum vulgare* pre-anthesis... 157 4e-56
 30 emb|AW668484|AW668484 GA__Ea0014C06 *Gossypium arboreum* 7-10 dpa ... 188 4e-56
 emb|AF139438|AF139438 *Gossypium hirsutum* (A-subgenome) locus A17... 106 5e-55
 emb|AF139437|AF139437 *Gossypium herbaceum* locus A1751, sequence ... 106 5e-55
 emb|AF139441|AF139441 *Gossypium robinsonii* locus A1751, sequence... 106 7e-55
 emb|AF139440|AF139440 *Gossypium hirsutum* (D-subgenome) locus A17... 106 7e-55
 35 emb|AF139439|AF139439 *Gossypium raimondii* locus A1751, sequence ... 106 7e-55
 emb|AW687885|AW687885 NF014E10RT1F1082 Developing root *Medicago* ... 91 5e-54
 emb|AW563397|AW563397 LG1_214_C02.b1_A002 Light Grown 1 (LG1) So... 210 4e-53
 emb|AW730974|AW730974 GA__Ea0029F08 *Gossypium arboreum* 7-10 dpa ... 163 8e-53
 emb|AW257362|AW257362 EST305499 KV2 *Medicago truncatula* cDNA clo... 138 4e-52
 40 emb|AW221342|AW221342 EST297811 tomato fruit mature green, TAMU ... 154 7e-52
 emb|AW221343|AW221343 EST297812 tomato fruit mature green, TAMU ... 154 7e-52
 emb|AI441432|AI441432 sa59h01.y1 Gm-cl1004 Glycine max cDNA clone... 189 1e-51
 emb|AW279412|AW279412 sf79c02.y1 Gm-cl019 Glycine max cDNA clone... 204 3e-51
 emb|AI730369|AI730369 BNLGHi6751 Six-day Cotton fiber *Gossypium* ... 166 3e-51
 45 emb|AW221789|AW221789 EST298600 tomato fruit red ripe, TAMU Lyco... 95 3e-51
 emb|AW030462|AW030462 EST273717 tomato callus, TAMU *Lycopersicon*... 173 4e-51
 emb|AQ917453|AQ917453 T233488b *Medicago truncatula* BAC library M... 134 5e-51
 emb|AW559414|AW559414 EST314462 *DSIR Medicago truncatula* cDNA cl... 152 1e-50
 emb|AW697284|AW697284 NF117B12ST1F1096 Developing stem *Medicago* ... 128 2e-50
 50 emb|AW666485|AW666485 GA__Ea0005E24 *Gossypium arboreum* 7-10 dpa ... 137 3e-50
 emb|AQ917126|AQ917126 T233155b *Medicago truncatula* BAC library M... 148 3e-50
 emb|AW780798|AW780798 sl76c06.y1 Gm-cl027 Glycine max cDNA clone... 161 1e-49
 emb|AW221341|AW221341 EST297810 tomato fruit mature green, TAMU ... 154 2e-49
 emb|AI727340|AI727340 BNLGHi7810 Six-day Cotton fiber *Gossypium* ... 194 2e-48
 55 emb|AW704701|AW704701 sk39d09.y1 Gm-cl028 Glycine max cDNA clone... 124 2e-47
 emb|AW101793|AW101793 sd70e04.y1 Gm-cl008 Glycine max cDNA clone... 190 3e-47
 emb|AW730930|AW730930 GA__Ea0029M05 *Gossypium arboreum* 7-10 dpa ... 122 6e-47
 emb|AW219463|AW219463 EST301861 tomato root during/after fruit s... 141 8e-47
 emb|AW688392|AW688392 NF006H03ST1F1000 Developing stem *Medicago* ... 78 1e-46
 60 gb|BE053648|BE053648 GA__Ea0001B22f *Gossypium arboreum* 7-10 dpa ... 81 9e-46
 emb|AW108783|AW108783 gate0001B22f *Gossypium arboreum* 7-10 dpa f... 81 5e-45

- emb|AI727162|AI727162 BNLGHi7467 Six-day Cotton fiber Gossypium ... 167 2e-44
 emb|AW725183|AW725183 GA__Ea0015F02 Gossypium arboreum 7-10 dpa ... 158 2e-44
 emb|AJ006482|LES6482 Lycopersicon esculentum sbt4d gene. 101 4e-44
 emb|AA660563|AA660563 00449 MtRHE Medicago truncatula cDNA 5' si... 138 4e-44
 5 emb|AW597797|AW597797 sj86c05.y1 Gm-c1034 Glycine max cDNA clone... 157 2e-43
 emb|AW220186|AW220186 EST302669 tomato root during/after fruit s... 104 2e-43
 emb|AW720560|AW720560 LjNEST10e10rc Lotus japonicus nodule libra... 84 4e-43
 emb|AI729604|AI729604 BNLGHi13761 Six-day Cotton fiber Gossypium... 84 8e-43
 emb|AF036960|AF036960 Glycine max subtilisin-like protease mRNA,... 145 2e-42
 10 emb|AW774365|AW774365 EST333516 KV3 Medicago truncatula cDNA clo... 94 3e-42
 emb|AW278983|AW278983 sg04b02.y1 Gm-c1019 Glycine max cDNA clone... 174 3e-42
 emb|AW775672|AW775672 EST334737 DSIL Medicago truncatula cDNA cl... 135 7e-42
 emb|AW441244|AW441244 EST310640 tomato fruit red ripe, TAMU Lyco... 95 3e-41
 emb|AW220925|AW220925 EST297394 tomato fruit mature green, TAMU... 138 5e-41
 15 emb|AW278806|AW278806 sf98f09.y1 Gm-c1019 Glycine max cDNA clone... 74 8e-41
 emb|AI728612|AI728612 BNLGHi11202 Six-day Cotton fiber Gossypium... 123 1e-40
 emb|AW234933|AW234933 sf20h03.y1 Gm-c1028 Glycine max cDNA clone... 134 2e-40
 gb|BE021322|BE021322 sm57b06.y1 Gm-c1028 Glycine max cDNA clone ... 134 2e-40
 emb|AW032762|AW032762 EST276321 tomato callus, TAMU Lycopersicon... 167 4e-40
 20 emb|AW691170|AW691170 NF041H07ST1F1000 Developing stem Medicago ... 122 5e-40
 emb|AW186434|AW186434 se67g06.y1 Gm-c1019 Glycine max cDNA clone... 122 5e-39
 emb|AI778546|AI778546 EST259425 tomato susceptible, Cornell Lyco... 133 5e-39
 emb|AI900421|AI900421 sc05e05.y1 Gm-c1012 Glycine max cDNA clone... 98 5e-39
 emb|AW287918|AW287918 N100762e rootphos(-) Medicago truncatula c... 93 1e-38
 25 emb|AW692289|AW692289 NF054B05ST1F1000 Developing stem Medicago ... 128 2e-38
 emb|AW185724|AW185724 se58g11.y1 Gm-c1019 Glycine max cDNA clone... 122 2e-38

30 Query= AF055848.2_s_at 18909_s_at /id_source genbank /description
 gb|aac62611.1| (af055848) subtilisin-like protease [arabidopsis
 thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
 /ncgi
 (2403 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

40 Score E
 Sequences producing significant alignments: (bits) Value

- emb|AJ006378|LES6378 Lycopersicon esculentum sbt1 gene. 240 e-157
 emb|X98929|LESBT1 L.esculentum mRNA for serine protease, SBT1. 240 e-157
 45 emb|Y18932|LES18932 Lycopersicon esculentum p69F gene. 142 e-152
 emb|Y17278|LES17278 Lycopersicon esculentum p69d gene, complete ... 141 e-146
 emb|AJ005173|LEAJ5173 Lycopersicon esculentum p69f gene, complet... 141 e-146
 emb|AJ005172|LEAJ5172 Lycopersicon esculentum p69e gene, complet... 142 e-146
 emb|Y18931|LES18931 Lycopersicon esculentum p69E gene. 144 e-144
 50 emb|AJ006379|LES6379 Lycopersicon esculentum sbt2 gene. 163 e-142
 emb|X98930|LESBT2 L.esculentum mRNA for serine protease, SBT2. 163 e-142
 emb|AJ006786|LES6786 Lycopersicon esculentum p69d gene. 141 e-136
 emb|AJ005171|LEAJ517 Lycopersicon esculentum p69c gene, complete... 142 e-136
 emb|Y17276|LES17276 Lycopersicon esculentum p69b gene, complete ... 138 e-130
 55 emb|Y10149|LESUBTILI L.esculentum mRNA for subtilisin-like protein. 138 e-130
 emb|Y17275|LES17275 Lycopersicon esculentum p69a gene, complete ... 138 e-126
 emb|X95270|LESUBENDO L.esculentum mRNA for subtilisin-like endop... 138 e-126
 dbj|D32206|CUSSP Melon mRNA for cucumisin (serine protease), com... 92 e-120
 emb|Y17277|LES17277 Lycopersicon esculentum p69c gene, complete ... 148 2e-97
 60 emb|AJ960990|AJ960990 sc93f09.y1 Gm-c1019 Glycine max cDNA clone... 338 9e-92
 emb|AW218382|AW218382 EST303565 tomato radicle, 5 d post-imbibit... 322 6e-87

- dbj|D86598|D86598 Norway spruce mRNA for antifreeze-like protein... 135 6e-77
 emb|X85975|AGAG12 A. glutinosa mRNA for subtilisin-like protein. 139 1e-73
 gb|BE124129|BE124129 EST394254 DSIL Medicago truncatula cDNA clo... 263 5e-69
 emb|AJ006380|LES6380 Lycopersicon esculentum sbt3 gene. 102 3e-68
 5 emb|AJ006376|LES6376 Lycopersicon esculentum mRNA for serine pro... 102 3e-68
 emb|AJ006480|LES6480 Lycopersicon esculentum sbt4b gene. 146 2e-66
 emb|AJ006481|LES6481 Lycopersicon esculentum sbt4c gene. 138 2e-66
 emb|AW267784|AW267784 EST305912 DSIR Medicago truncatula cDNA cl... 128 3e-65
 emb|AJ006483|LES6483 Lycopersicon esculentum sbt4e gene. 140 5e-65
 10 emb|AJ006377|LES6377 Lycopersicon esculentum mRNA for serine pro... 138 5e-65
 emb|AW459354|AW459354 sh41a03.y1 Gm-cl017 Glycine max cDNA clone... 192 6e-64
 emb|AW349252|AW349252 GM210004B21G12R Gm-r1021 Glycine max cDNA ... 144 1e-63
 emb|AJ276710|GMA276710 Glycine max mRNA for putative subtilisin ... 124 8e-63
 15 emb|AJ012164|CGL012164 Casuarina glauca mRNA for cg12 gene fragm... 114 4e-62
 emb|AI730592|AI730592 BNLGHi7352 Six-day Cotton fiber Gossypium ... 216 2e-61
 emb|AW728806|AW728806 GA__Ea0028I22 Gossypium arboreum 7-10 dpa ... 125 5e-60
 emb|AI794673|AI794673 sb67d01.y1 Gm-cl019 Glycine max cDNA clone... 171 1e-59
 emb|AW773858|AW773858 EST332844 KV3 Medicago truncatula cDNA clo... 87 2e-58
 20 emb|AW695319|AW695319 NF093H12ST1F1103 Developing stem Medicago ... 105 2e-57
 emb|AW299160|AW299160 EST305970 KV2 Medicago truncatula cDNA clo... 135 3e-57
 emb|AF201883|AF201883 Gossypioides kirkii subtilisin-like protea... 108 7e-57
 emb|AW720622|AW720622 LjNEST22e12rc Lotus japonicus nodule libra... 137 2e-56
 emb|AW925917|AW925917 HVSMEg0005N16 Hordeum vulgare pre-anthesis... 157 4e-56
 25 emb|AW668484|AW668484 GA__Ea0014C06 Gossypium arboreum 7-10 dpa ... 188 4e-56
 emb|AF139438|AF139438 Gossypium hirsutum (A-subgenome) locus A17... 106 5e-55
 emb|AF139437|AF139437 Gossypium herbaceum locus A1751, sequence ... 106 5e-55
 emb|AF139441|AF139441 Gossypium robinsonii locus A1751, sequence... 106 7e-55
 emb|AF139440|AF139440 Gossypium hirsutum (D-subgenome) locus A17... 106 7e-55
 30 emb|AF139439|AF139439 Gossypium raimondii locus A1751, sequence ... 106 7e-55
 emb|AW687885|AW687885 NF014E10RT1F1082 Developing root Medicago ... 91 5e-54
 emb|AW563397|AW563397 LG1_214_C02.b1_A002 Light Grown 1 (LG1) So... 210 4e-53
 emb|AW730974|AW730974 GA__Ea0029F08 Gossypium arboreum 7-10 dpa ... 163 8e-53
 emb|AW257362|AW257362 EST305499 KV2 Medicago truncatula cDNA clo... 138 4e-52
 35 emb|AW221342|AW221342 EST297811 tomato fruit mature green, TAMU ... 154 7e-52
 emb|AW221343|AW221343 EST297812 tomato fruit mature green, TAMU ... 154 7e-52
 emb|AI441432|AI441432 sa59h01.y1 Gm-cl004 Glycine max cDNA clone... 189 1e-51
 emb|AW279412|AW279412 sf79c02.y1 Gm-cl019 Glycine max cDNA clone... 204 3e-51
 emb|AI730369|AI730369 BNLGHi6751 Six-day Cotton fiber Gossypium ... 166 3e-51
 40 emb|AW221789|AW221789 EST298600 tomato fruit red ripe, TAMU Lyco... 95 3e-51
 emb|AW030462|AW030462 EST273717 tomato callus, TAMU Lycopersicon... 173 4e-51
 emb|AQ917453|AQ917453 T233488b Medicago truncatula BAC library M... 134 5e-51
 emb|AW559414|AW559414 EST314462 DSIR Medicago truncatula cDNA cl... 152 1e-50
 emb|AW697284|AW697284 NF117B12ST1F1096 Developing stem Medicago ... 128 2e-50
 45 emb|AW666485|AW666485 GA__Ea0005E24 Gossypium arboreum 7-10 dpa ... 137 3e-50
 emb|AQ917126|AQ917126 T233155b Medicago truncatula BAC library M... 148 3e-50
 emb|AW780798|AW780798 sl76c06.y1 Gm-cl027 Glycine max cDNA clone... 161 1e-49
 emb|AW221341|AW221341 EST297810 tomato fruit mature green, TAMU ... 154 2e-49
 emb|AI727340|AI727340 BNLGHi7810 Six-day Cotton fiber Gossypium ... 194 2e-48
 50 emb|AW704701|AW704701 sk39d09.y1 Gm-cl028 Glycine max cDNA clone... 124 2e-47
 emb|AW101793|AW101793 sd70e04.y1 Gm-cl008 Glycine max cDNA clone... 190 3e-47
 emb|AW730930|AW730930 GA__Ea0029M05 Gossypium arboreum 7-10 dpa ... 122 6e-47
 emb|AW219463|AW219463 EST301861 tomato root during/after fruit s... 141 8e-47
 emb|AW688392|AW688392 NF006H03ST1F1000 Developing stem Medicago ... 78 1e-46
 55 gb|BE053648|BE053648 GA__Ea0001B22f Gossypium arboreum 7-10 dpa ... 81 9e-46
 emb|AW108783|AW108783 gate0001B22f Gossypium arboreum 7-10 dpa f... 81 5e-45
 emb|AI727162|AI727162 BNLGHi7467 Six-day Cotton fiber Gossypium ... 167 2e-44
 emb|AW725183|AW725183 GA__Ea0015F02 Gossypium arboreum 7-10 dpa ... 158 2e-44
 emb|AJ006482|LES6482 Lycopersicon esculentum sbt4d gene. 101 4e-44
 60 emb|AA660563|AA660563 00449 MtRHE Medicago truncatula cDNA 5' si... 138 4e-44
 emb|AW597797|AW597797 sj86c05.y1 Gm-cl034 Glycine max cDNA clone... 157 2e-43

emb|AW220186|AW220186 EST302669 tomato root during/after fruit s... 104 2e-43
 emb|AW720560|AW720560 LjNEST10e10rc Lotus japonicus nodule libra... 84 4e-43
 emb|AI729604|AI729604 BNLGHi13761 Six-day Cotton fiber Gossypium... 84 8e-43
 emb|AF036960|AF036960 Glycine max subtilisin-like protease mRNA,... 145 2e-42
 5 emb|AW774365|AW774365 EST333516 KV3 Medicago truncatula cDNA clo... 94 3e-42
 emb|AW278983|AW278983 sg04b02.y1 Gm-c1019 Glycine max cDNA clone... 174 3e-42
 emb|AW775672|AW775672 EST334737 DSIL Medicago truncatula cDNA cl... 135 7e-42
 emb|AW441244|AW441244 EST310640 tomato fruit red ripe, TAMU Lyco... 95 3e-41
 emb|AW220925|AW220925 EST297394 tomato fruit mature green, TAMU ... 138 5e-41
 10 emb|AW278806|AW278806 sf98f09.y1 Gm-c1019 Glycine max cDNA clone... 74 8e-41
 emb|AI728612|AI728612 BNLGHi11202 Six-day Cotton fiber Gossypium... 123 1e-40
 emb|AW234933|AW234933 sf20h03.y1 Gm-c1028 Glycine max cDNA clone... 134 2e-40
 gb|BE021322|BE021322 sm57b06.y1 Gm-c1028 Glycine max cDNA clone ... 134 2e-40
 emb|AW032762|AW032762 EST276321 tomato callus, TAMU Lycopersicon... 167 4e-40
 15 emb|AW691170|AW691170 NF041H07ST1F1000 Developing stem Medicago ... 122 5e-40
 emb|AW186434|AW186434 se67g06.y1 Gm-c1019 Glycine max cDNA clone... 122 5e-39
 emb|AI778546|AI778546 EST259425 tomato susceptible, Cornell Lyco... 133 5e-39
 emb|AI900421|AI900421 sc05e05.y1 Gm-c1012 Glycine max cDNA clone... 98 5e-39
 emb|AW287918|AW287918 N100762e rootphos(-) Medicago truncatula c... 93 1e-38
 20 emb|AW692289|AW692289 NF054B05ST1F1000 Developing stem Medicago ... 128 2e-38
 emb|AW185724|AW185724 se58g11.y1 Gm-c1019 Glycine max cDNA clone... 122 2e-38

Query= AC002338.11_at 18920_at /id_source genbank /description
 25 gb|aac16927.1| (ac002338) putative laccase [arabidopsis thaliana]
 /blast_score 0 /ec_number /family oxidase /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002338|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002338|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002338|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac002338>
 30 (2002 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

35 Searching.....done

	Score	E
Sequences producing significant alignments:	(bits)	Value
40 emb Y13772 PTY13772 Populus trichocarpa mRNA for laccase, lac90 ...	314	0.0
gb U73106 LTU73106 Liriodendron tulipifera high-pl laccase (LAC2...	356	e-179
gb U73105 LTU73105 Liriodendron tulipifera high-pl laccase (LAC2...	355	e-178
gb U45243 NTU45243 Nicotiana tabacum diphenol oxidase mRNA, part...	232	e-124
emb Y13769 PTY13769 Populus trichocarpa mRNA for laccase, lac1 g...	237	e-121
45 emb AW774748 AW774748 EST333899 KV3 Medicago truncatula cDNA clo...	419	e-116
gb BE033690 BE033690 MF07A08 MF Mesembryanthemum crystallinum cD...	408	e-113
gb U43542 NTU43542 Nicotiana tabacum diphenol oxidase mRNA, comp...	379	e-104
gb U73103 LTU73103 Liriodendron tulipifera high-pl laccase (LAC2...	363	e-103
gb U12757 APU12757 Acer pseudoplatanus laccase mRNA, complete cds.	368	e-100
50 gb U73104 LTU73104 Liriodendron tulipifera high-pl laccase (LAC2...	353	3e-99
emb Y13773 PTY13773 Populus trichocarpa mRNA for laccase, lac110...	355	4e-99
emb AW688902 AW688902 NF013A07ST1F1000 Developing stem Medicago ...	360	2e-98
gb BE033689 BE033689 MF07A07 MF Mesembryanthemum crystallinum cD...	349	4e-95
emb AW559612 AW559612 EST314660 DSIR Medicago truncatula cDNA cl...	328	2e-93
55 emb Y13771 PTY13771 Populus trichocarpa mRNA for laccase, lac3 g...	257	1e-88
emb AW696424 AW696424 NF103G08ST1F1067 Developing stem Medicago ...	323	3e-87
emb AW649943 AW649943 EST328397 tomato germinating seedlings, TA...	268	9e-84
emb AW706547 AW706547 sj57h07.y1 Gm-c1033 Glycine max cDNA clone...	297	1e-79
emb AW693679 AW693679 NF067A06ST1F1040 Developing stem Medicago ...	279	1e-75
60 emb AW696234 AW696234 NF104B07ST1F1060 Developing stem Medicago ...	258	4e-75
emb AV406815 AV406815 AV406815 Lotus japonicus young plants (two...	270	3e-71

- emb|Y13770|PTY13770 *Populus trichocarpa* mRNA for laccase, lac2 g... 256 3e-70
emb|AI896093|AI896093 EST265536 tomato callus, TAMU Lycopersicon... 238 9e-70
emb|AW056468|AW056468 ST52C01 Pine TriplEx shoot tip library Pin... 261 2e-68
emb|AW689490|AW689490 NF019H02ST1F1000 Developing stem Medicago ... 248 1e-64
5 emb|AW625159|AW625159 EST319066 tomato radicle, 5 d post-imbibit... 247 3e-64
emb|AW625489|AW625489 EST319396 tomato radicle, 5 d post-imbibit... 245 1e-63
emb|AW691876|AW691876 NF045B04ST1F1000 Developing stem Medicago ... 243 4e-63
emb|AW693746|AW693746 NF068F07ST1F1062 Developing stem Medicago ... 243 4e-63
emb|AW869960|AW869960 NXNV_120_D07_F Nsf Xylem Normal wood Verti... 158 1e-62
10 emb|AI166538|AI166538 xylem.est.360 Poplar xylem Lambda ZAPII li... 240 2e-62
emb|AW688017|AW688017 NF003D03ST1F1000 Developing stem Medicago ... 231 1e-59
emb|AI166411|AI166411 xylem.est.246 Poplar xylem Lambda ZAPII li... 227 2e-58
emb|AW290117|AW290117 NXNV010D09F Nsf Xylem Normal wood Vertical... 226 5e-58
emb|AW693528|AW693528 NF067B10ST1F1080 Developing stem Medicago ... 223 4e-57
15 emb|AW869847|AW869847 NXNV_122_B11_F Nsf Xylem Normal wood Verti... 223 4e-57
emb|AW698095|AW698095 NXNV_066_B07_F Nsf Xylem Normal wood Verti... 160 2e-56
emb|AW306602|AW306602 se52h11.y1 Gm-cl017 Glycine max cDNA clone... 202 1e-54
emb|AW694378|AW694378 NF075F01ST1F1013 Developing stem Medicago ... 138 3e-54
emb|AW688967|AW688967 NF013G11ST1F1000 Developing stem Medicago ... 197 3e-53
20 emb|AW692427|AW692427 NF055E11ST1F1000 Developing stem Medicago ... 209 6e-53
emb|AI166601|AI166601 xylem.est.417 Poplar xylem Lambda ZAPII li... 207 3e-52
emb|AI167062|AI167062 xylem.est.832 Poplar xylem Lambda ZAPII li... 207 3e-52
emb|AI166632|AI166632 xylem.est.445 Poplar xylem Lambda ZAPII li... 207 3e-52
emb|AI166389|AI166389 xylem.est.226 Poplar xylem Lambda ZAPII li... 207 3e-52
25 emb|AI166520|AI166520 xylem.est.344 Poplar xylem Lambda ZAPII li... 207 3e-52
emb|AI166460|AI166460 xylem.est.290 Poplar xylem Lambda ZAPII li... 207 3e-52
emb|AI166300|AI166300 xylem.est.146 Poplar xylem Lambda ZAPII li... 207 3e-52
emb|AI166804|AI166804 xylem.est.60 Poplar xylem Lambda ZAPII lib... 207 3e-52
emb|AI167056|AI167056 xylem.est.827 Poplar xylem Lambda ZAPII li... 207 3e-52
30 emb|AW694997|AW694997 NF082C04ST1F1033 Developing stem Medicago ... 180 2e-51
emb|AI895135|AI895135 EST264578 tomato callus, TAMU Lycopersicon... 203 2e-51
emb|AW032528|AW032528 EST276087 tomato callus, TAMU Lycopersicon... 196 2e-51
emb|AW126324|AW126324 NI00431e rootphos(-) Medicago truncatula c... 204 3e-51
emb|AB029124|AB029124 AB029124 Cucumis sativus library (Chono M)... 204 3e-51
35 emb|AI167003|AI167003 xylem.est.78 Poplar xylem Lambda ZAPII lib... 204 3e-51
emb|AW035109|AW035109 EST280371 tomato callus, TAMU Lycopersicon... 196 1e-50
emb|AW289657|AW289657 NXNV003D03F Nsf Xylem Normal wood Vertical... 198 1e-49
emb|AW455342|AW455342 EST311880 tomato root during/after fruit s... 196 6e-49
emb|AW432566|AW432566 sh76a01.y1 Gm-cl015 Glycine max cDNA clone... 195 8e-49
40 emb|AW695232|AW695232 NF092F05ST1F1046 Developing stem Medicago ... 195 1e-48
emb|AW694631|AW694631 NF078E04ST1F1034 Developing stem Medicago ... 190 3e-48
emb|AW691613|AW691613 NF047A09ST1F1000 Developing stem Medicago ... 193 5e-48
emb|AW736716|AW736716 EST333208 KV3 Medicago truncatula cDNA clo... 187 2e-46
emb|AW736717|AW736717 EST333209 KV3 Medicago truncatula cDNA clo... 187 2e-46
45 emb|AA556518|AA556518 373 Loblolly pine C Pinus taeda cDNA clone... 164 1e-45
emb|AW985001|AW985001 NXNV_118_H12_F Nsf Xylem Normal wood Verti... 122 2e-45
emb|AI812943|AI812943 22G11 Pine Lambda Zap Xylem library Pinus ... 173 4e-45
emb|AI812863|AI812863 20H3 Pine Lambda Zap Xylem library Pinus t... 183 4e-45
emb|AW307139|AW307139 sf53c04.y1 Gm-cl009 Glycine max cDNA clone... 157 9e-44
50 emb|AW985217|AW985217 NXNV_132_E12_F Nsf Xylem Normal wood Verti... 178 1e-43
emb|AW689013|AW689013 NF014D06ST1F1000 Developing stem Medicago ... 177 3e-43
gb|BE022993|BE022993 sm69b10.y1 Gm-cl028 Glycine max cDNA clone ... 177 3e-43
emb|AA556786|AA556786 628 Loblolly pine NA Pinus taeda cDNA clon... 133 3e-43
emb|AW350964|AW350964 GM210010A10B4R Gm-r1021 Glycine max cDNA 3... 177 4e-43
55 43
emb|AW887962|AW887962 NXNV_127_D08_F Nsf Xylem Normal wood Verti... 176 7e-43
emb|AW690520|AW690520 NF035E02ST1F1000 Developing stem Medicago ... 174 2e-42
emb|AW626092|AW626092 EST319999 tomato radicle, 5 d post-imbibit... 119 5e-42
emb|AW698220|AW698220 NXNV_070_B05_F Nsf Xylem Normal wood Verti... 172 9e-42
60 emb|AW289555|AW289555 NXNV002H11F Nsf Xylem Normal wood Vertical... 170 3e-41
emb|AW698218|AW698218 NXNV_070_B03_F Nsf Xylem Normal wood Verti... 107 4e-41

emb|AW693471|AW693471 NF065C09ST1F1000 Developing stem Medicago ... 169 8e-41
emb|AJ234679|HVVU234679 Hordeum vulgare genomic DNA fragment; clo... 88 9e-41
emb|AI166348|AI166348 xylem.est.19 Poplar xylem Lambda ZAPII lib... 168 1e-40
emb|AW032099|AW032099 EST275553 tomato callus, TAMU Lycopersicon... 163 3e-40
5 emb|AW691027|AW691027 NF036H01ST1F1000 Developing stem Medicago ... 115 5e-40
emb|AW290667|AW290667 NXNV044G05F Nsf Xylem Normal wood Vertical... 166 8e-40
gb|BE123599|BE123599 NXNV_146_A10_F Nsf Xylem Normal wood Vertic... 163 5e-39
gb|U43543|NTU43543 Nicotiana tabacum diphenol oxidase mRNA, part... 163 5e-39
emb|AW979587|AW979587 EST341186 tomato root deficiency, Cornell ... 159 9e-38
10 emb|AW695246|AW695246 NF092G11ST1F1087 Developing stem Medicago ... 92 5e-37
gb|BE020582|BE020582 sm51a03.y1 Gm-cl028 Glycine max cDNA clone ... 133 7e-37
emb|AI794703|AI794703 sb67h06.y1 Gm-cl019 Glycine max cDNA clone... 136 6e-36
emb|AW597115|AW597115 sj71g06.y1 Gm-cl034 Glycine max cDNA clone... 150 4e-35
emb|AI920039|AI920039 1569 Pine Lambda Zap Xylem library Pinus t... 85 7e-35
15 emb|AW626664|AW626664 NXNV068B04 Nsf Xylem Normal wood Vertical ... 146 6e-34
emb|AV412458|AV412458 AV412458 Lotus japonicus young plants (two... 124 1e-33
emb|AI726707|AI726707 BNLGHi6374 Six-day Cotton fiber Gossypium ... 145 1e-33
emb|AW626589|AW626589 NXNV067B05 Nsf Xylem Normal wood Vertical ... 84 2e-33
20
Query= Y11788.1_at 18946_at /id_source genbank /description
emb|caa72484.1| (y11788) peroxidase atp24a [arabidopsis thaliana]
/blast_score 1.00e-148 /ec_number /family peroxidase /chip nova
/gb_link http://www3.ncbi.nlm.nih.gov/htbin-
25 post/entrez/query?db=n&form=6&dopt=g&uid=gb|y11788| /ncgi
http://www.ncgr.org/cgi-bin/ff?y11788
(965 letters)
Database: plantfungal
30 661,018 sequences; 426,114,510 total letters
Searching.....done
Score E
35 Sequences producing significant alignments: (bits) Value
gb|M37637|ARCPNC2 A.hypogaea cationic peroxidase mRNA, complete ... 230 e-105
emb|X94943|LECEVI16G L.esculentum mRNA for peroxidase. 212 e-100
emb|AB027753|AB027753 Nicotiana tabacum mRNA for peroxidase, com... 191 1e-94
40 emb|AF149279|AF149279 Phaseolus vulgaris peroxidase 4 precursor ... 220 2e-94
gb|L36112|SSNPEROXIC Stylosanthes humilis peroxidase mRNA. 157 2e-86
emb|AW033820|AW033820 EST277391 tomato callus, TAMU Lycopersicon... 170 2e-79
emb|Y10468|SOPR XR7 S.oleracea mRNA for peroxidase, clone PC36. 196 6e-78
emb|AW759829|AW759829 sl54f01.y1 Gm-cl027 Glycine max cDNA clone... 213 1e-77
45 emb|AW216873|AW216873 EST295587 tomato callus, TAMU Lycopersicon... 212 3e-73
emb|AW224632|AW224632 EST303075 tomato root, plants pre-anthesis... 193 2e-66
emb|AF145349|AF145349 Glycine max peroxidase (Prx3) mRNA, partia... 131 4e-66
emb|AW219312|AW219312 EST301794 tomato root during/after fruit s... 193 2e-65
emb|AW219112|AW219112 EST301594 tomato root during/after fruit s... 193 2e-65
50 emb|AW032353|AW032353 EST275807 tomato callus, TAMU Lycopersicon... 137 1e-61
emb|AW031362|AW031362 EST274816 tomato callus, TAMU Lycopersicon... 180 9e-60
emb|AW035239|AW035239 EST280501 tomato callus, TAMU Lycopersicon... 212 1e-58
emb|AW035958|AW035958 EST282817 tomato callus, TAMU Lycopersicon... 212 1e-58
emb|AW035446|AW035446 EST281184 tomato callus, TAMU Lycopersicon... 212 1e-58
55 emb|AW029850|AW029850 EST273105 tomato callus, TAMU Lycopersicon... 170 5e-58
emb|AW030052|AW030052 EST273307 tomato callus, TAMU Lycopersicon... 165 7e-58
emb|AW569733|AW569733 si79g02.y1 Gm-cl031 Glycine max cDNA clone... 153 1e-57
emb|AW224631|AW224631 EST303074 tomato root, plants pre-anthesis... 193 3e-57
emb|AW348753|AW348753 GM210003A22D6R Gm-r1021 Glycine max cDNA 3... 144 6e-
60 57
emb|AW033082|AW033082 EST276641 tomato callus, TAMU Lycopersicon... 129 4e-56

- emb|AV414872|AV414872 AV414872 Lotus japonicus young plants (two... 182 2e-55
dbj|D30653|POPPB Populus kitakamiensis mRNA for peroxidase, part... 94 3e-55
emb|AV414074|AV414074 AV414074 Lotus japonicus young plants (two... 215 4e-55
emb|AW032485|AW032485 EST276044 tomato callus, TAMU Lycopersicon... 212 3e-54
5 emb|AW216562|AW216562 EST295276 tomato callus, TAMU Lycopersicon... 210 2e-53
emb|X57564|ARNEUPERO A.rusticana mRNA for neutral peroxidase. 118 2e-53
emb|AI777064|AI777064 EST252031 tomato callus, TAMU Lycopersicon... 206 2e-52
emb|AF155124|AF155124 Gossypium hirsutum bacterial-induced perox... 93 6e-52
emb|AW219314|AW219314 EST301796 tomato root during/after fruit s... 193 4e-51
10 emb|AB042103|AB042103 Asparagus officinalis AspPOX1 mRNA for per... 84 5e-51
emb|AW219926|AW219926 EST302409 tomato root during/after fruit s... 193 8e-51
emb|AW224630|AW224630 EST303073 tomato root, plants pre-anthesis... 193 8e-51
emb|AF149280|AF149280 Phaseolus vulgaris peroxidase 5 precursor ... 81 8e-51
gb|L13654|TOMTPX1A Lycopersicon esculentum peroxidase (TPX1) mRN... 104 3e-50
15 emb|AJ242742|IBA242742 Ipomoea batatas mRNA for peroxidase (pod ... 82 5e-50
emb|Y10470|SOPR XR9 S.oleracea mRNA for peroxidase, clone PC56. 132 3e-49
emb|AV422753|AV422753 AV422753 Lotus japonicus young plants (two... 195 4e-49
emb|AI773788|AI773788 EST254888 tomato resistant, Cornell Lycope... 194 7e-49
emb|X90692|MSRNAPE1A M.sativa mRNA for peroxidase 1A. 76 1e-48
20 emb|X56011|TAPERO Wheat mRNA for peroxidase. 102 2e-48
emb|X97351|PTPXP4PER P.trichocarpa mRNA for anionic peroxidase P... 90 8e-48
emb|AW666030|AW666030 sk31c04.y1 Gm-c1028 Glycine max cDNA clone... 191 9e-48
gb|M37636|ARCPNC1 Arachis hypogaea cationic peroxidase (PNC1) mR... 89 1e-47
emb|AB024437|AB024437 Scutellaria baicalensis mRNA for peroxidase... 122 1e-47
25 gb|M74103|TOBANPER Nicotiana sylvestris anionic peroxidase mRNA,... 100 2e-47
gb|M60729|HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge... 78 3e-47
emb|AW621675|AW621675 EST312473 tomato root during/after fruit s... 189 3e-47
emb|Y17192|CPY17192 Cucurbita pepo mRNA for peroxidase. 109 5e-47
emb|AI895427|AI895427 EST264870 tomato callus, TAMU Lycopersicon... 121 7e-47
30 emb|AW035207|AW035207 EST280469 tomato callus, TAMU Lycopersicon... 188 8e-47
gb|L13653|TOMTPX2A Lycopersicon esculentum peroxidase (TPX2) mRN... 101 1e-46
emb|Y10463|SOPR XR2 S.oleracea mRNA for peroxidase, clone PB22. 140 4e-46
emb|AW224633|AW224633 EST303076 tomato root, plants pre-anthesis... 185 4e-46
gb|L36157|ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple... 73 9e-46
35 gb|M91372|CUSPREPERB Cucumis sativus peroxidase mRNA, complete cds. 89 2e-45
emb|X91232|MARNAPRX M.annua mRNA for peroxidase. 90 2e-45
emb|AF244924|AF244924 Spinacia oleracea peroxidase prx15 precurs... 92 2e-45
emb|Z22920|SPPEROXDS S.polyrrhiza mRNA for peroxidase. 96 2e-45
emb|X90694|MSRNAPE1C M.sativa mRNA for peroxidase 1C. 75 3e-45
40 gb|M91374|CUSPREPERA Cucumis sativus peroxidase mRNA, complete cds. 109 4e-45
emb|AW035872|AW035872 EST282181 tomato callus, TAMU Lycopersicon... 182 5e-45
emb|Y16776|SOY16776 Spinacia oleracea mRNA for peroxidase, prx10... 95 5e-45
dbj|D42065|TOBCPI40KB Tobacco mRNA for cationic peroxidase isozy... 77 7e-45
dbj|D42064|TOBCPI38KA Tobacco mRNA for cationic peroxidase isozy... 77 1e-44
45 emb|AI772237|AI772237 EST253337 tomato resistant, Cornell Lycope... 180 2e-44
emb|AF149278|AF149278 Phaseolus vulgaris peroxidase 3 precursor ... 84 2e-44
emb|AW035660|AW035660 EST281492 tomato callus, TAMU Lycopersicon... 178 5e-44
emb|AF244922|AF244922 Spinacia oleracea peroxidase prx13 precurs... 83 1e-43
emb|X97350|PTPXP3PER P.trichocarpa mRNA for anionic peroxidase P... 83 2e-43
50 gb|L36111|SSNPEROXIB Stylosanthes humilis peroxidase mRNA. 77 3e-43
emb|X58396|HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7). 90 3e-43
emb|X97348|PTPXP1PER P.trichocarpa mRNA for anionic peroxidase P... 85 4e-43
gb|L36093|BLYPRX Barley peroxidase mRNA, complete cds. 89 4e-43
emb|AF043234|AF043234 Striga asiatica ferriprotein porphyrin-con... 83 7e-43
55 emb|X90693|MSRNAPE1B M.sativa mRNA for peroxidase 1B. 74 7e-43
emb|X97349|PTPXP2PER P.trichocarpa mRNA for anionic peroxidase P... 83 2e-42
gb|L24120|LINFLXP Linum usitatissimum peroxidase precursor (FLXP... 88 2e-42
emb|AW705192|AW705192 sk42h02.y1 Gm-c1019 Glycine max cDNA clone... 111 2e-42
emb|AW705312|AW705312 sk59d04.y1 Gm-c1019 Glycine max cDNA clone... 128 2e-42
60 gb|L07554|LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA... 92 3e-42
gb|L77080|SSNCAPEA Stylosanthes humilis cationic peroxidase gene... 122 1e-41

emb|AI778513|AI778513 EST259392 tomato susceptible, Cornell Lyco... 170 1e-41
 emb|AB027752|AB027752 Nicotiana tabacum mRNA for peroxidase, com... 87 2e-41
 emb|AF007211|AF007211 Glycine max peroxidase precursor (GMIPER1)... 72 2e-41
 emb|A00741|A00741 A.rusticana synthetic gene (reverse complement... 76 2e-41
 5 emb|A00740|A00740 A.rusticana synthetic gene for peroxidase. 76 2e-41
 dbj|E01651|E01651 cDNA encoding horseradish peroxidase. 76 2e-41
 emb|AF244923|AF244923 Spinacia oleracea peroxidase prx14 precurs... 84 3e-41
 emb|AF149277|AF149277 Phaseolus vulgaris peroxidase 1 precursor ... 71 3e-41
 dbj|D30652|POPPA Populus kitakamiensis mRNA for peroxidase, part... 80 4e-41
 10 emb|Y10469|SOPR XR8 S.oleracea mRNA for peroxidase, clone PC55. 111 4e-41
 emb|AJ011939|TRE011939 Trifolium repens mRNA for peroxidase. 105 6e-41
 emb|Y10465|SOPR XR4 S.oleracea mRNA for peroxidase, clone PC44. 86 6e-41
 gb|U12315|CCU12315 Cenchrus ciliaris clone PX18 peroxidase mRNA,... 106 9e-41
 dbj|D11337|VIRPRX Vigna angularis mRNA for peroxidase basic isoz... 77 1e-40
 15 gb|M91373|CUSPREPER Cucumis sativus peroxidase mRNA, complete cds. 107 1e-40

Query= AF163823.4_at 18968_at /id_source genbank /description
 gb|aad45127.1|af163823_1 (af163823) endoxyloglucan transferase
 [arabidopsis thaliana] /blast_score 1.00e-161 /ec_number /family
 20 /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|af163823|/ncgi
 http://www.ncgr.org/cgi-bin/ff?af163823
 (1025 letters)

25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

30 Searching.....done

	Score	E	(bits)	Value
Sequences producing significant alignments:				
emb AJ130885 FSY130885 Fagus sylvatica mRNA for xyloglucan endot...	424	e-134		
35 emb X93174 HVXETXEA H.vulgare mRNA for xyloglucan endotransglyco...	418	e-130		
gb L22162 SOYMER5HOM Glycine max brassinosteroid-regulated prote...	384	e-118		
emb AW220372 AW220372 EST302855 tomato root during/after fruit s...	416	e-115		
emb AW030111 AW030111 EST273366 tomato callus, TAMU Lycopersicon...	416	e-115		
emb AW032346 AW032346 EST275800 tomato callus, TAMU Lycopersicon...	415	e-115		
40 emb AW218856 AW218856 EST301338 tomato root during/after fruit s...	413	e-115		
emb AW031139 AW031139 EST274446 tomato callus, TAMU Lycopersicon...	380	e-115		
emb AI725820 AI725820 BNLGHi13219 Six-day Cotton fiber Gossypium...	413	e-114		
emb AI938507 AI938507 sb46e06.y1 Gm-c1015 Glycine max cDNA clone...	407	e-112		
emb AW776635 AW776635 EST335700 DSIL Medicago truncatula cDNA cl...	407	e-112		
45 emb AI488729 AI488729 EST247068 tomato ovary, TAMU Lycopersicon ...	406	e-112		
emb AI485531 AI485531 EST243852 tomato ovary, TAMU Lycopersicon ...	402	e-111		
emb AW033905 AW033905 EST277476 tomato callus, TAMU Lycopersicon...	401	e-111		
emb AW216717 AW216717 EST295431 tomato callus, TAMU Lycopersicon...	397	e-110		
gb BE035552 BE035552 MO09A12 MO Mesembryanthemum crystallinum cD...	353	e-109		
50 emb AW729695 AW729695 GA__Ea0025M09 Gossypium arboreum 7-10 dpa ...	394	e-109		
emb X93175 HVXETXEB H.vulgare mRNA for xyloglucan endotransglyco...	387	e-109		
emb AW651314 AW651314 EST329768 tomato germinating seedlings, TA...	390	e-108		
emb AW218734 AW218734 EST301214 tomato root during/after fruit s...	388	e-107		
emb AI460643 AI460643 sa71e04.y1 Gm-c1004 Glycine max cDNA clone...	387	e-107		
55 emb AI898515 AI898515 EST267958 tomato ovary, TAMU Lycopersicon ...	386	e-106		
emb AI488903 AI488903 EST247242 tomato ovary, TAMU Lycopersicon ...	386	e-106		
emb AW218894 AW218894 EST301376 tomato root during/after fruit s...	386	e-106		
emb AI487536 AI487536 EST245858 tomato ovary, TAMU Lycopersicon ...	379	e-104		
emb AW981262 AW981262 EST392415 DSIL Medicago truncatula cDNA cl...	315	e-104		
60 emb AW033629 AW033629 EST277200 tomato callus, TAMU Lycopersicon...	378	e-104		
emb AW033699 AW033699 EST277270 tomato callus, TAMU Lycopersicon...	376	e-103		

- gb|BE036915|BE036915 MP09A12 MP Mesembryanthemum crystallinum cD... 368 e-101
emb|AI495154|AI495154 sa88f09.y1 Gm-cl004 Glycine max cDNA clone... 367 e-101
emb|AW096328|AW096328 EST289508 tomato mixed elicitor, BTI Lycop... 366 e-100
emb|AI487279|AI487279 EST245601 tomato ovary, TAMU Lycopersicon ... 365 e-100
5 emb|AI485293|AI485293 EST243597 tomato ovary, TAMU Lycopersicon ... 364 e-100
emb|AW649744|AW649744 EST328198 tomato germinating seedlings, TA... 293 8e-99
emb|AW031478|AW031478 EST274932 tomato callus, TAMU Lycopersicon... 360 1e-98
emb|X82684|LETXETB2 L.esculentum tXET-B2 mRNA for xyloglucan end... 355 3e-97
emb|AW093001|AW093001 EST286181 tomato mixed elicitor, BTI Lycop... 354 5e-97
10 emb|AW218862|AW218862 EST301344 tomato root during/after fruit s... 354 5e-97
emb|AI725839|AI725839 BNLGHi13291 Six-day Cotton fiber Gossypium... 354 7e-97
emb|AW033371|AW033371 EST276942 tomato callus, TAMU Lycopersicon... 354 7e-97
emb|X82685|LETXETB1 L.esculentum tXET-B1 mRNA for xyloglucan end... 354 7e-97
emb|AI490390|AI490390 EST248728 tomato ovary, TAMU Lycopersicon ... 352 2e-96
15 emb|AI773291|AI773291 EST254391 tomato resistant, Cornell Lycope... 293 1e-95
emb|AI486834|AI486834 EST245156 tomato ovary, TAMU Lycopersicon ... 350 1e-95
emb|AW930090|AW930090 EST340547 tomato fruit mature green, TAMU ... 348 4e-95
emb|AI485404|AI485404 EST243725 tomato ovary, TAMU Lycopersicon ... 348 4e-95
emb|AW691431|AW691431 NF041B05ST1F1000 Developing stem Medicago ... 334 8e-95
20 emb|AW685669|AW685669 NF030A11NR1F1000 Nodulated root Medicago t... 276 1e-94
gb|BE124065|BE124065 EST394190 DSIL Medicago truncatula cDNA clo... 346 2e-94
emb|AW307509|AW307509 sf57h02.y1 Gm-cl009 Glycine max cDNA clone... 346 2e-94
emb|AI487162|AI487162 EST245484 tomato ovary, TAMU Lycopersicon ... 344 6e-94
emb|AI489159|AI489159 EST247498 tomato ovary, TAMU Lycopersicon ... 291 1e-93
25 emb|AI485855|AI485855 EST244176 tomato ovary, TAMU Lycopersicon ... 343 1e-93
emb|AW432541|AW432541 sh75f05.y1 Gm-cl015 Glycine max cDNA clone... 342 3e-93
dbj|D16455|SOYEXT2 Soybean mRNA for endo-xyloglucan transferase,... 310 4e-93
dbj|E06969|E06969 DNA encoding xyloglucan endotransferase. 310 4e-93
dbj|E06964|E06964 Anti-sense RNA of xyloglucan endotransferase g... 310 4e-93
30 emb|AI489962|AI489962 EST248301 tomato ovary, TAMU Lycopersicon ... 341 4e-93
emb|AI898758|AI898758 EST268201 tomato ovary, TAMU Lycopersicon ... 286 7e-93
emb|AW394832|AW394832 sh35h09.y1 Gm-cl017 Glycine max cDNA clone... 341 7e-93
dbj|E06959|E06959 Anti-sense DNA of xyloglucan endotransferase g... 306 6e-92
gb|L46792|ACTXET Actinidia deliciosa clone AdXET-5 xyloglucan en... 320 8e-92
35 dbj|D16458|VIREXT5 V.angularis mRNA for endo-xyloglucan transfer... 314 1e-90
gb|L43094|TRUXET1G Tropaeolum majus xyloglucan endotransglycosyl... 324 1e-90
dbj|E06968|E06968 DNA encoding xyloglucan endotransferase. 314 1e-90
dbj|E06963|E06963 Anti-sense RNA of xyloglucan endotransferase g... 314 1e-90
dbj|E06958|E06958 Anti-sense DNA of xyloglucan endotransferase g... 314 1e-90
40 emb|AJ004917|CAAJ4917 Cicer arietinum mRNA for endoxyloglucan tr... 310 1e-89
emb|X91659|HVEXTGENE H.vulgare mRNA for endoxyloglucan transferase. 318 1e-89
dbj|D16457|WHTEXT4 Wheat mRNA for endo-xyloglucan transferase, c... 319 2e-89
dbj|E06972|E06972 DNA encoding xyloglucan endotransferase. 319 6e-89
dbj|E06967|E06967 Anti-sense RNA of xyloglucan endotransferase g... 319 6e-89
45 dbj|E06962|E06962 Anti-sense DNA of xyloglucan endotransferase g... 319 6e-89
emb|AW687253|AW687253 NF007F05RT1F1046 Developing root Medicago ... 292 1e-88
emb|AI488724|AI488724 EST247063 tomato ovary, TAMU Lycopersicon ... 273 2e-88
dbj|D86730|D86730 Nicotiana tabacum mRNA for endoxyloglucan tran... 303 3e-88
emb|AB017025|AB017025 Nicotiana tabacum mRNA for endo-xyloglucan... 303 3e-88
50 emb|AB015428|AB015428 Pisum sativum mRNA for EXGT1, complete cds. 309 3e-88
emb|AW038999|AW038999 EST280972 tomato mixed elicitor, BTI Lycop... 303 3e-88
emb|AW184781|AW184781 se82c12.y1 Gm-cl023 Glycine max cDNA clone... 274 8e-88
emb|AI487551|AI487551 EST245873 tomato ovary, TAMU Lycopersicon ... 268 1e-87
emb|AW980364|AW980364 EST391517 GVN Medicago truncatula cDNA clo... 322 2e-87
55 emb|AI487338|AI487338 EST245660 tomato ovary, TAMU Lycopersicon ... 265 3e-87
emb|AI496348|AI496348 sb05e11.y1 Gm-cl004 Glycine max cDNA clone... 320 8e-87
emb|AF052194|AF052194 Actinidia deliciosa xyloglucan endotransgl... 320 1e-86
emb|AW598083|AW598083 sj88g10.y1 Gm-cl034 Glycine max cDNA clone... 319 2e-86
emb|AI898560|AI898560 EST268003 tomato ovary, TAMU Lycopersicon ... 319 2e-86
60 emb|AW184871|AW184871 se69f08.y1 Gm-cl019 Glycine max cDNA clone... 300 7e-86
emb|AI489200|AI489200 EST247539 tomato ovary, TAMU Lycopersicon ... 274 2e-85

	emb AJ726805 AJ726805 BNLGHi6594 Six-day Cotton fiber Gossypium ...	315	3e-85
	emb AJ729066 AJ729066 BNLGHi12528 Six-day Cotton fiber Gossypium...	315	4e-85
	dbj D16456 TOMEXT3 Tomato mRNA for endo-xyloglucan transferase, ...	295	4e-85
	dbj E06971 E06971 DNA encoding xyloglucan endotransferase.	295	4e-85
5	dbj E06966 E06966 Anti-sense RNA of xyloglucan endotransferase g...	295	4e-85
	dbj E06961 E06961 Anti-sense DNA of xyloglucan endotransferase g...	295	4e-85
	emb AW934469 AW934469 EST353373 tomato flower buds 0-3 mm, Corne...	314	7e-85
	emb AW185234 AW185234 se88f12.y1 Gm-cl023 Glycine max cDNA clone...	314	1e-84
	emb AI487776 AI487776 EST246098 tomato ovary, TAMU Lycopersicon ...	266	2e-84
10	emb AW216790 AW216790 EST295504 tomato callus, TAMU Lycopersicon...	312	3e-84
	emb AI895031 AI895031 EST264474 tomato callus, TAMU Lycopersicon...	312	4e-84
15	Query= AF163823.4_g_at 18969_g_at /id_source genbank /description gb aad45127.1 af163823_1 (af163823) endoxyloglucan transferase [arabidopsis thaliana] /blast_score 1.00e-161 /ec_number /family /chip nova /gb_link /ncgi (1025 letters)		
20	Database: plantfungal 661,018 sequences; 426,114,510 total letters		
	Searching.....done		
25	Score E Sequences producing significant alignments: (bits) Value		
	emb AJ130885 FSY130885 Fagus sylvatica mRNA for xyloglucan endot...	424	e-134
	emb X93174 HVXETXEA H.vulgare mRNA for xyloglucan endotransglyco...	418	e-130
30	gb L22162 SOYMER5HOM Glycine max brassinosteroid-regulated prote...	384	e-118
	emb AW220372 AW220372 EST302855 tomato root during/after fruit s...	416	e-115
	emb AW030111 AW030111 EST273366 tomato callus, TAMU Lycopersicon...	416	e-115
	emb AW032346 AW032346 EST275800 tomato callus, TAMU Lycopersicon...	415	e-115
	emb AW218856 AW218856 EST301338 tomato root during/after fruit s...	413	e-115
35	emb AW031139 AW031139 EST274446 tomato callus, TAMU Lycopersicon...	380	e-115
	emb AI725820 AI725820 BNLGHi13219 Six-day Cotton fiber Gossypium...	413	e-114
	emb AI938507 AI938507 sb46e06.y1 Gm-cl015 Glycine max cDNA clone...	407	e-112
	emb AW776635 AW776635 EST335700 DSIL Medicago truncatula cDNA cl...	407	e-112
	emb AI488729 AI488729 EST247068 tomato ovary, TAMU Lycopersicon ...	406	e-112
40	emb AI485531 AI485531 EST243852 tomato ovary, TAMU Lycopersicon ...	402	e-111
	emb AW033905 AW033905 EST277476 tomato callus, TAMU Lycopersicon...	401	e-111
	emb AW216717 AW216717 EST295431 tomato callus, TAMU Lycopersicon...	397	e-110
	gb BE035552 BE035552 MO09A12 MO Mesembryanthemum crystallinum cD...	353	e-109
	emb AW729695 AW729695 GA__Ea0025M09 Gossypium arboreum 7-10 dpa ...	394	e-109
45	emb X93175 HVXETXEB H.vulgare mRNA for xyloglucan endotransglyco...	387	e-109
	emb AW651314 AW651314 EST329768 tomato germinating seedlings, TA...	390	e-108
	emb AW218734 AW218734 EST301214 tomato root during/after fruit s...	388	e-107
	emb AI460643 AI460643 sa71e04.y1 Gm-cl1004 Glycine max cDNA clone...	387	e-107
	emb AI898515 AI898515 EST267958 tomato ovary, TAMU Lycopersicon ...	386	e-106
50	emb AI488903 AI488903 EST247242 tomato ovary, TAMU Lycopersicon ...	386	e-106
	emb AW218894 AW218894 EST301376 tomato root during/after fruit s...	386	e-106
	emb AI487536 AI487536 EST245858 tomato ovary, TAMU Lycopersicon ...	379	e-104
	emb AW981262 AW981262 EST392415 DSIL Medicago truncatula cDNA cl...	315	e-104
	emb AW033629 AW033629 EST277200 tomato callus, TAMU Lycopersicon...	378	e-104
55	emb AW033699 AW033699 EST277270 tomato callus, TAMU Lycopersicon...	376	e-103
	gb BE036915 BE036915 MP09A12 MP Mesembryanthemum crystallinum cD...	368	e-101
	emb AI495154 AI495154 sa88f09.y1 Gm-cl1004 Glycine max cDNA clone...	367	e-101
	emb AW096328 AW096328 EST289508 tomato mixed elicitor, BTI Lycop...	366	e-100
	emb AI487279 AI487279 EST245601 tomato ovary, TAMU Lycopersicon ...	365	e-100
60	emb AI485293 AI485293 EST243597 tomato ovary, TAMU Lycopersicon ...	364	e-100
	emb AW649744 AW649744 EST328198 tomato germinating seedlings, TA...	293	8e-99

- emb|AW031478|AW031478 EST274932 tomato callus, TAMU Lycopersicon... 360 1e-98
 emb|X82684|LETXETB2 L.esculentum tXET-B2 mRNA for xyloglucan end... 355 3e-97
 emb|AW093001|AW093001 EST286181 tomato mixed elicitor, BTI Lycop... 354 5e-97
 emb|AW218862|AW218862 EST301344 tomato root during/after fruit s... 354 5e-97
 5 emb|AI725839|AI725839 BNLGHi13291 Six-day Cotton fiber Gossypium... 354 7e-97
 emb|AW033371|AW033371 EST276942 tomato callus, TAMU Lycopersicon... 354 7e-97
 emb|X82685|LETXETB1 L.esculentum tXET-B1 mRNA for xyloglucan end... 354 7e-97
 emb|AI490390|AI490390 EST248728 tomato ovary, TAMU Lycopersicon ... 352 2e-96
 emb|AI773291|AI773291 EST254391 tomato resistant, Cornell Lycop... 293 1e-95
 10 emb|AI486834|AI486834 EST245156 tomato ovary, TAMU Lycopersicon ... 350 1e-95
 emb|AW930090|AW930090 EST340547 tomato fruit mature green, TAMU ... 348 4e-95
 emb|AI485404|AI485404 EST243725 tomato ovary, TAMU Lycopersicon ... 348 4e-95
 emb|AW691431|AW691431 NF041B05ST1F1000 Developing stem Medicago ... 334 8e-95
 emb|AW685669|AW685669 NF030A11NR1F1000 Nodulated root Medicago t... 276 1e-94
 15 gb|BE124065|BE124065 EST394190 DSIL Medicago truncatula cDNA clo... 346 2e-94
 emb|AW307509|AW307509 sf57h02.y1 Gm-cl009 Glycine max cDNA clone... 346 2e-94
 emb|AI487162|AI487162 EST245484 tomato ovary, TAMU Lycopersicon ... 344 6e-94
 emb|AI489159|AI489159 EST247498 tomato ovary, TAMU Lycopersicon ... 291 1e-93
 emb|AI485855|AI485855 EST244176 tomato ovary, TAMU Lycopersicon ... 343 1e-93
 20 emb|AW432541|AW432541 sh75f05.y1 Gm-cl015 Glycine max cDNA clone... 342 3e-93
 dbj|D16455|SOYEXT2 Soybean mRNA for endo-xyloglucan transferase,... 310 4e-93
 dbj|E06969|E06969 DNA encoding xyloglucan endotransferase. 310 4e-93
 dbj|E06964|E06964 Anti-sense RNA of xyloglucan endotransferase g... 310 4e-93
 emb|AI489962|AI489962 EST248301 tomato ovary, TAMU Lycopersicon ... 341 4e-93
 25 emb|AI898758|AI898758 EST268201 tomato ovary, TAMU Lycopersicon ... 286 7e-93
 emb|AW394832|AW394832 sh35h09.y1 Gm-cl017 Glycine max cDNA clone... 341 7e-93
 dbj|E06959|E06959 Anti-sense DNA of xyloglucan endotransferase g... 306 6e-92
 gb|L46792|ACTXET Actinidia deliciosa clone AdXET-5 xyloglucan en... 320 8e-92
 dbj|D16458|VIREXT5 V.angularis mRNA for endo-xyloglucan transfer... 314 1e-90
 30 gb|L43094|TRUXET1G Tropaeolum majus xyloglucan endotransglycosyl... 324 1e-90
 dbj|E06968|E06968 DNA encoding xyloglucan endotransferase. 314 1e-90
 dbj|E06963|E06963 Anti-sense RNA of xyloglucan endotransferase g... 314 1e-90
 dbj|E06958|E06958 Anti-sense DNA of xyloglucan endotransferase g... 314 1e-90
 emb|AJ004917|CAAJ4917 Cicer arietinum mRNA for endoxyloglucan tr... 310 1e-89
 35 emb|X91659|HVEXTGENE H.vulgare mRNA for endoxyloglucan transferase. 318 1e-89
 dbj|D16457|WHTEXT4 Wheat mRNA for endo-xyloglucan transferase, c... 319 2e-89
 dbj|E06972|E06972 DNA encoding xyloglucan endotransferase. 319 6e-89
 dbj|E06967|E06967 Anti-sense RNA of xyloglucan endotransferase g... 319 6e-89
 dbj|E06962|E06962 Anti-sense DNA of xyloglucan endotransferase g... 319 6e-89
 40 emb|AW687253|AW687253 NF007F05RT1F1046 Developing root Medicago ... 292 1e-88
 emb|AI488724|AI488724 EST247063 tomato ovary, TAMU Lycopersicon ... 273 2e-88
 dbj|D86730|D86730 Nicotiana tabacum mRNA for endoxyloglucan tran... 303 3e-88
 emb|AB017025|AB017025 Nicotiana tabacum mRNA for endo-xyloglucan... 303 3e-88
 emb|AB015428|AB015428 Pisum sativum mRNA for EXGT1, complete cds. 309 3e-88
 45 emb|AW038999|AW038999 EST280972 tomato mixed elicitor, BTI Lycop... 303 3e-88
 emb|AW184781|AW184781 se82c12.y1 Gm-cl023 Glycine max cDNA clone... 274 8e-88
 emb|AI487551|AI487551 EST245873 tomato ovary, TAMU Lycopersicon ... 268 1e-87
 emb|AW980364|AW980364 EST391517 GVN Medicago truncatula cDNA clo... 322 2e-87
 emb|AI487338|AI487338 EST245660 tomato ovary, TAMU Lycopersicon ... 265 3e-87
 50 emb|AI496348|AI496348 sb05e11.y1 Gm-cl004 Glycine max cDNA clone... 320 8e-87
 emb|AF052194|AF052194 Actinidia deliciosa xyloglucan endotransgl... 320 1e-86
 emb|AW598083|AW598083 sj88g10.y1 Gm-cl034 Glycine max cDNA clone... 319 2e-86
 emb|AI898560|AI898560 EST268003 tomato ovary, TAMU Lycopersicon ... 319 2e-86
 emb|AW184871|AW184871 se69f08.y1 Gm-cl019 Glycine max cDNA clone... 300 7e-86
 55 emb|AI489200|AI489200 EST247539 tomato ovary, TAMU Lycopersicon ... 274 2e-85
 emb|AI726805|AI726805 BNLGHi6594 Six-day Cotton fiber Gossypium ... 315 3e-85
 emb|AI729066|AI729066 BNLGHi12528 Six-day Cotton.fiber Gossypium... 315 4e-85
 dbj|D16456|TOMEXT3 Tomato mRNA for endo-xyloglucan transferase, ... 295 4e-85
 dbj|E06971|E06971 DNA encoding xyloglucan endotransferase. 295 4e-85
 60 dbj|E06966|E06966 Anti-sense RNA of xyloglucan endotransferase g... 295 4e-85
 dbj|E06961|E06961 Anti-sense DNA of xyloglucan endotransferase g... 295 4e-85

emb|AW934469|AW934469 EST353373 tomato flower buds 0-3 mm, Corne... 314 7e-85
 emb|AW185234|AW185234 se88f12.y1 Gm-c1023 Glycine max cDNA clone... 314 1e-84
 emb|AI487776|AI487776 EST246098 tomato ovary, TAMU Lycopersicon ... 266 2e-84
 emb|AW216790|AW216790 EST295504 tomato callus, TAMU Lycopersicon... 312 3e-84
 5 emb|AI895031|AI895031 EST264474 tomato callus, TAMU Lycopersicon... 312 4e-84

Query= AL049730.104_s_at 18983_s_at /id_source genbank /description
 emb|cab41722.1| (al049730) pearli 1-like protein [arabidopsis
 thaliana] /blast_score 4.00e-25 /ec_number /family /chip nova
 10 /gb_link /ncgi
 (390 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

15 Searching.....done

		Score	E	
	Sequences producing significant alignments:			(bits) Value
20	emb AW980687 AW980687 EST391840 GVN Medicago truncatula cDNA clo...	95	2e-22	
	emb AW980826 AW980826 EST391979 GVN Medicago truncatula cDNA clo...	95	2e-22	
	emb AW980547 AW980547 EST391700 GVN Medicago truncatula cDNA clo...	95	2e-22	
	emb AW685869 AW685869 NF031B09NR1F1000 Nodulated root Medicago t...	95	2e-22	
25	gb BE124445 BE124445 EST393480 GVN Medicago truncatula cDNA clon...	95	2e-22	
	gb BE124752 BE124752 EST393787 GVN Medicago truncatula cDNA clon...	95	2e-22	
	emb AW684629 AW684629 NF019B05NR1F1000 Nodulated root Medicago t...	95	2e-22	
	emb AW329233 AW329233 N200445e rootphos(-) Medicago truncatula c...	95	2e-22	
	gb BE124520 BE124520 EST393555 GVN Medicago truncatula cDNA clon...	95	4e-22	
30	emb AW125962 AW125962 N100157e rootphos(-) Medicago truncatula c...	92	2e-21	
	emb AW622601 AW622601 EST313401 tomato root during/after fruit s...	101	2e-21	
	emb AW624937 AW624937 EST313766 tomato radicle, 5 d post-imbibit...	101	2e-21	
	emb AW560894 AW560894 EST315942 DSIR Medicago truncatula cDNA cl...	95	3e-21	
	emb AW621250 AW621250 EST312048 tomato root during/after fruit s...	98	9e-21	
35	emb AW626221 AW626221 EST320128 tomato radicle, 5 d post-imbibit...	98	9e-21	
	emb AW035571 AW035571 EST281309 tomato callus, TAMU Lycopersicon...	98	1e-20	
	emb AW217082 AW217082 EST295796 tomato callus, TAMU Lycopersicon...	98	1e-20	
	emb AW032764 AW032764 EST276323 tomato callus, TAMU Lycopersicon...	98	1e-20	
	emb AW443140 AW443140 EST308070 tomato mixed elicitor, BTI Lycop...	98	1e-20	
40	emb AW622645 AW622645 EST313445 tomato root during/after fruit s...	96	1e-20	
	emb AW907202 AW907202 EST343325 potato stolon, Cornell Universit...	99	2e-20	
	emb AI776056 AI776056 EST257156 tomato resistant, Cornell Lycop...	98	3e-20	
	emb AI779211 AI779211 EST260090 tomato susceptible, Cornell Lyco...	98	3e-20	
	emb AW034083 AW034083 EST277578 tomato callus, TAMU Lycopersicon...	98	3e-20	
45	emb AW094444 AW094444 EST287624 tomato mixed elicitor, BTI Lycop...	98	3e-20	
	emb AW685279 AW685279 NF025G02NR1F1000 Nodulated root Medicago t...	90	4e-20	
	emb AF109654 AF109654 AF109654 Capsicum annuum root susceptible ...	97	5e-20	
	emb AW625740 AW625740 EST319647 tomato radicle, 5 d post-imbibit...	96	9e-20	
	dbj D83227 POPELPG Populus nigra gene for extensin like protein,...	92	2e-19	
50	dbj D83226 POPELP Populus nigra mRNA for extensin like protein, ...	92	2e-19	
	emb AW287846 AW287846 N100689e rootphos(-) Medicago truncatula c...	95	2e-19	
	gb BE124789 BE124789 EST393824 GVN Medicago truncatula cDNA clon...	95	2e-19	
	gb BE124744 BE124744 EST393779 GVN Medicago truncatula cDNA clon...	95	2e-19	
	emb AW217088 AW217088 EST295802 tomato callus, TAMU Lycopersicon...	95	3e-19	
55	emb AW725519 AW725519 GA_Ea0018G20 Gossypium arboreum 7-10 dpa ...	94	4e-19	
	gb S68113 S68113 proline-rich SAC51 [Brassica napus=oilseed rape...	94	4e-19	
	emb X71618 BNPRPPDA B.napus proline-rich mRNA accumulating durin...	94	4e-19	
	emb AF026382 AF026382 Fragaria x ananassa HyPRP mRNA, complete cds.	94	4e-19	
	emb AI779212 AI779212 EST260091 tomato susceptible, Cornell Lyco...	94	6e-19	
60	emb AV413531 AV413531 AV413531 Lotus japonicus young plants (two...	93	1e-18	
	emb AW685624 AW685624 NF032E01NR1F1000 Nodulated root Medicago t...	81	2e-18	

- emb|AW287985|AW287985 N100829e rootphos(-) Medicago truncatula c... 89 1e-17
emb|AW257148|AW257148 EST305285 KV2 Medicago truncatula cDNA clo... 89 1e-17
emb|AW349572|AW349572 GM210005A21F12R Gm-r1021 Glycine max cDNA ... 88 3e-17
emb|X85206|CRRNAHPRP C.roseus mRNA for hybrid proline-rich protein. 86 1e-16
5 emb|Z26880|CR14KDPP C.roseus mRNA for 14 kDa polypeptide. 86 1e-16
emb|AW278328|AW278328 sf42f09.y1 Gm-c1009 Glycine max cDNA clone... 78 1e-16
emb|AW703723|AW703723 sk23f03.y1 Gm-c1028 Glycine max cDNA clone... 78 1e-16
emb|AI352845|AI352845 MB69-3F PZ204.BNlib Brassica napus cDNA cl... 68 1e-16
gb|BE021488|BE021488 sm59b04.y1 Gm-c1028 Glycine max cDNA clone ... 85 3e-16
10 emb|AW234182|AW234182 sf22b12.y1 Gm-c1028 Glycine max cDNA clone... 65 3e-16
gb|BE022318|BE022318 sm73d03.y1 Gm-c1028 Glycine max cDNA clone ... 65 5e-16
emb|AW625137|AW625137 EST313954 tomato radicle, 5 d post-imbibit... 83 9e-16
emb|AV422321|AV422321 AV422321 Lotus japonicus young plants (two... 70 2e-15
emb|AW597680|AW597680 sj49e04.y1 Gm-c1033 Glycine max cDNA clone... 62 2e-15
15 emb|AW306872|AW306872 sf49g05.y1 Gm-c1009 Glycine max cDNA clone... 62 3e-15
emb|AW163963|AW163963 Ljirmp17-382-g10 Ljirmp Lambda HybriZap... 78 3e-15
dbj|D86629|D86629 Nicotiana tabacum mRNA for NT16 polypeptide, c... 81 3e-15
emb|AW666281|AW666281 sk34f10.y1 Gm-c1028 Glycine max cDNA clone... 62 4e-15
emb|AV413898|AV413898 AV413898 Lotus japonicus young plants (two... 70 4e-15
20 gb|BE022257|BE022257 sm72g11.y1 Gm-c1028 Glycine max cDNA clone ... 62 5e-15
dbj|D86721|D86721 Nicotiana tabacum DNA for glycine-rich polypep... 80 8e-15
emb|AI166167|AI166167 _A013P67U Hybrid aspen plasmid library Pop... 72 9e-15
emb|AJ389048|AJ389048 AJ389048 Medicago truncatula R108 Medicago... 65 1e-14
emb|AW719418|AW719418 LjNEST4c12r Lotus japonicus nodule library... 68 1e-14
25 emb|AW031617|AW031617 EST275071 tomato callus, TAMU Lycopersicon... 79 2e-14
emb|AV424931|AV424931 AV424931 Lotus japonicus young plants (two... 71 2e-14
emb|AW625399|AW625399 EST319222 tomato radicle, 5 d post-imbibit... 78 2e-14
emb|AW621368|AW621368 EST312166 tomato root during/after fruit s... 78 2e-14
emb|AV423170|AV423170 AV423170 Lotus japonicus young plants (two... 71 2e-14
30 emb|AI736342|AI736342 sb27c03.y1 Gm-c1009 Glycine max cDNA clone... 64 3e-14
emb|AB035125|AB035125 Nicotiana tabacum mRNA for glycine-rich pr... 78 3e-14
dbj|D26454|TOBTID23 Nicotiana glauca X Nicotiana langsdorffii mR... 78 3e-14
emb|AV415427|AV415427 AV415427 Lotus japonicus young plants (two... 70 4e-14
emb|AV416097|AV416097 AV416097 Lotus japonicus young plants (two... 70 4e-14
35 emb|AV415022|AV415022 AV415022 Lotus japonicus young plants (two... 78 4e-14
emb|AV413103|AV413103 AV413103 Lotus japonicus young plants (two... 78 4e-14
emb|AV411456|AV411456 AV411456 Lotus japonicus young plants (two... 78 4e-14
emb|AV411686|AV411686 AV411686 Lotus japonicus young plants (two... 78 4e-14
emb|AV425640|AV425640 AV425640 Lotus japonicus young plants (two... 78 4e-14
40 emb|AV411414|AV411414 AV411414 Lotus japonicus young plants (two... 78 4e-14
emb|AW163953|AW163953 Ljirmp17-369-f9 Ljirmp Lambda HybriZap ... 78 4e-14
emb|AV424226|AV424226 AV424226 Lotus japonicus young plants (two... 78 4e-14
emb|AV423183|AV423183 AV423183 Lotus japonicus young plants (two... 78 4e-14
emb|AV411071|AV411071 AV411071 Lotus japonicus young plants (two... 78 4e-14
45 emb|AV411588|AV411588 AV411588 Lotus japonicus young plants (two... 78 4e-14
emb|AI496419|AI496419 sb04e01.y1 Gm-c1004 Glycine max cDNA clone... 69 1e-13
emb|AI507807|AI507807 sb12h09.y1 Gm-c1004 Glycine max cDNA clone... 69 1e-13
emb|AI772831|AI772831 EST253931 tomato resistant, Cornell Lycopersicon... 65 2e-13
emb|AI776903|AI776903 EST258003 tomato resistant, Cornell Lycopersicon... 65 2e-13
50 emb|AW650068|AW650068 EST328522 tomato germinating seedlings, TA... 75 2e-13
emb|AW650542|AW650542 EST328996 tomato germinating seedlings, TA... 65 2e-13
emb|AI967649|AI967649 Ljirmp08-651-c10 Ljirmp Lambda HybriZap... 65 2e-13
emb|AW092951|AW092951 EST286131 tomato mixed elicitor, BTI Lycopersicon... 65 2e-13
emb|AI442516|AI442516 sa32e08.y1 Gm-c1004 Glycine max cDNA clone... 69 2e-13
55 emb|AI736269|AI736269 sb26b02.y1 Gm-c1008 Glycine max cDNA clone... 69 3e-13
emb|AW830131|AW830131 sm23c07.y1 Gm-c1028 Glycine max cDNA clone... 69 3e-13
emb|AW152920|AW152920 se32g01.y1 Gm-c1015 Glycine max cDNA clone... 69 3e-13
gb|BE020655|BE020655 sm51h06.y1 Gm-c1028 Glycine max cDNA clone ... 69 3e-13
emb|AW570545|AW570545 sj63d10.y1 Gm-c1033 Glycine max cDNA clone... 69 3e-13
60

Query= X95738.2_at 19158_at /id_source genbank /description

emb|caa65053.1| (x95738) proline transporter 2 [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|x95738|/ncgi
 5 http://www.ncgr.org/cgi-bin/ff?x95738
 (1579 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

10

Searching.....done

	Score	E	(bits)	Value
15	Sequences producing significant alignments:			
	emb AF014809 AF014809	Lycopersicon esculentum proline transporte...	677	0.0
	emb AF014810 AF014810	Lycopersicon esculentum proline transporte...	676	0.0
	emb AF014808 AF014808	Lycopersicon esculentum proline transporte...	668	0.0
	emb AW563318 AW563318	LG1_228_A07.g1_A002 Light Grown 1 (LG1) So...	173	9e-66
20	emb AI054471 AI054471	coau0001B09 Cotton Boll Abscission Zone cD...	168	3e-53
	emb AI895644 AI895644	EST265087 tomato callus, TAMU Lycopersicon...	206	3e-52
	emb AW691556 AW691556	NF046C09ST1F1000 Developing stem Medicago ...	178	8e-52
	emb AW287445 AW287445	LG1_228_A07.b1_A002 Light Grown 1 (LG1) So...	201	1e-50
	emb AW428965 AW428965	EST306505 tomato flower buds 0-3 mm, Corne...	198	9e-50
25	emb AW672225 AW672225	LG1_358_C11.b1_A002 Light Grown 1 (LG1) So...	192	6e-48
	emb AW102341 AW102341	sd86d12.y1 Gm-c1009 Glycine max cDNA clone...	186	4e-46
	emb AW063020 AW063020	SBcD66 Sugar beet leaf cDNA library Beta v...	133	3e-44
	emb AW686923 AW686923	NF004A10RT1F1072 Developing root Medicago ...	91	2e-40
	emb AW773932 AW773932	EST332918 KV3 Medicago truncatula cDNA clo...	91	6e-35
30	emb AW011298 AW011298	ST19B09 Pine TriplEx shoot tip library Pin...	83	2e-32
	emb AW694902 AW694902	NF081C08ST1F1065 Developing stem Medicago ...	88	1e-24
	emb AW754669 AW754669	PC04H09 Pine TriplEx pollen cone library P...	113	4e-24
	emb AW034884 AW034884	EST279113 tomato callus, TAMU Lycopersicon...	82	1e-14
	emb AW279551 AW279551	sf95a10.y1 Gm-c1019 Glycine max cDNA clone...	58	7e-14
35	gb U31932 NSU31932	Nicotiana sylvestris amino acid permease 1 (N...	58	6e-11
	emb AW690084 AW690084	NF028B08ST1F1000 Developing stem Medicago ...	48	6e-09
	emb AI776947 AI776947	EST258047 tomato resistant, Cornell Lycope...	58	2e-07
	emb AJ007574 RCO7574	Ricinus communis mRNA for amino acid carrier.	49	3e-06
	emb AW306512 AW306512	se51h04.y1 Gm-c1017 Glycine max cDNA clone...	54	4e-06
40	emb AJ132228 RCO132228	Ricinus communis mRNA for amino acid carr...	48	5e-06
	emb Y09825 STAAP1	S.tuberosum mRNA for amino acid transporter AA...	48	7e-06
	emb AJ004959 CAA004959	Cicer arietinum mRNA for hypothetical pro...	52	9e-06
	emb AF080542 AF080542	Nepenthes alata amino acid transporter (AA...	47	2e-05
	emb AW164093 AW164093	Ljirnp19-543-g11 Ljirnp Lambda HybriZap...	50	5e-05
45	emb AW309945 AW309945	sf27a03.x1 Gm-c1028 Glycine max cDNA clone...	50	5e-05
	emb AF080544 AF080544	Nepenthes alata amino acid transporter (AA...	45	6e-05
	gb U64823 NSU64823	Nicotiana sylvestris amino acid permease (nsa...	50	6e-05
	emb AJ238635 CPR238635	Chlorella protothecoides partial mRNA for...	49	1e-04
	emb AI974813 AI974813	T113295e KV2 Medicago truncatula cDNA clon...	49	1e-04
50	emb AI773761 AI773761	EST254861 tomato resistant, Cornell Lycope...	48	2e-04
	emb AW736648 AW736648	EST333140 KV3 Medicago truncatula cDNA clo...	47	3e-04
	emb AW255060 AW255060	ML1355 peppermint glandular trichome Menth...	40	4e-04
	emb Y09591 VFAMACTRA	V.faba mRNA for amino acid transporter.	46	6e-04
	emb AI441371 AI441371	sa64f02.y1 Gm-c1004 Glycine max cDNA clone...	46	6e-04
55	emb AW396191 AW396191	sh02e09.y1 Gm-c1026 Glycine max cDNA clone...	46	6e-04
	emb AW395873 AW395873	sh01d01.y1 Gm-c1026 Glycine max cDNA clone...	37	0.003
	emb AI166826 AI166826	xylem.est.62 Poplar xylem Lambda ZAPII lib...	44	0.003
	emb AW830239 AW830239	sm24g01.y1 Gm-c1028 Glycine max cDNA clone...	44	0.004
	emb AF074703 AF074703	Glycine max pA381 marker, sequence tagged ...	43	0.005
60	emb AQ842052 AQ842052	T134338 Soybean RFLP probe Glycine max gen...	43	0.005
	gb BE022301 BE022301	sm73b09.y1 Gm-c1028 Glycine max cDNA clone ...	43	0.007

emb|AW102174|AW102174 sd84c08.y1 Gm-c1009 Glycine max cDNA clone... 42 0.010
 emb|AI166882|AI166882 xylem.est.670 Poplar xylem Lambda ZAPII li... 41 0.019
 emb|Y09826|STAAP2 S.tuberosum mRNA for amino acid transporter AA... 36 0.020
 emb|AW307208|AW307208 sf54b08.y1 Gm-c1009 Glycine max cDNA clone... 41 0.026
 5 emb|AF080543|AF080543 Nepenthes alata amino acid transporter (AA... 40 0.049
 emb|AW096758|AW096758 EST289938 tomato mixed elicitor, BTI Lycop... 40 0.068
 emb|AI727855|AI727855 BNLGHi9274 Six-day Cotton fiber Gossypium ... 29 0.17
 emb|AI487167|AI487167 EST245489 tomato ovary, TAMU Lycopersicon ... 38 0.18
 emb|AW649763|AW649763 EST328217 tomato germinating seedlings, TA... 38 0.18
 10 emb|AW310916|AW310916 sg29h08.x1 Gm-c1024 Glycine max cDNA clone... 38 0.24
 emb|AJ400848|SOL400848 Spinacia oleracea complete chloroplast ge... 37 0.46
 emb|AW203255|AW203255 sf27a03.y1 Gm-c1028 Glycine max cDNA clone... 36 0.63
 emb|AI778004|AI778004 EST258883 tomato susceptible, Cornell Lyco... 36 0.86
 emb|AW649841|AW649841 EST328295 tomato germinating seedlings, TA... 36 0.86
 15 emb|AF061435|AF061435 Vicia faba amino acid transporter b (AAPB)... 35 1.2
 emb|AQ492251|AQ492251 V109G12 mTn-3xHA/lacZ Insertion Library Sa... 35 1.2
 emb|AI779305|AI779305 EST260184 tomato susceptible, Cornell Lyco... 35 1.2
 emb|AI779304|AI779304 EST260183 tomato susceptible, Cornell Lyco... 35 1.2
 emb|AW982545|AW982545 HVSMEg0003I22f Hordeum vulgare pre-anthesi... 29 1.4
 20 emb|AQ874703|AQ874703 V113C6 mTn-3xHA/lacZ Insertion Library, st... 35 1.6
 emb|AV428014|AV428014 AV428014 Lotus japonicus young plants (two... 35 1.6
 emb|AI856198|AI856198 sb39a11.x1 Gm-c1014 Glycine max cDNA clone... 35 1.6
 gb|L28920|YSCCHR1RAA Saccharomyces cerevisiae chromosome I right... 35 2.2
 emb|AQ874913|AQ874913 V118E8 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 25 emb|AF061434|AF061434 Vicia faba amino acid transporter a (AAPA)... 35 2.2
 emb|AQ876251|AQ876251 V153B8 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 emb|AQ874228|AQ874228 V105B1 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 emb|X74552|SCSWH1 S.cerevisiae SWH1 gene. 35 2.2
 emb|AQ876104|AQ876104 V133C7 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 30 emb|AQ876111|AQ876111 V133D2 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 emb|AQ875710|AQ875710 V128E8 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 emb|AW092708|AW092708 EST285888 tomato mixed elicitor, BTI Lycop... 34 3.1
 emb|AI938816|AI938816 sc60f01.y1 Gm-c1016 Glycine max cDNA clone... 34 4.2
 emb|AW704460|AW704460 sk53c11.y1 Gm-c1019 Glycine max cDNA clone... 34 4.2
 35 emb|AI965655|AI965655 sc75b03.y1 Gm-c1018 Glycine max cDNA clone... 34 4.2
 emb|AW010573|AW010573 ST08D02 Pine TriplEx shoot tip library Pin... 34 4.2
 emb|AJ277985|NTA277985 Nicotiana tabacum drepp1 gene, exons 1-4. 33 5.8
 emb|AL049559|SPCC1450 S.pombe chromosome III cosmid c1450. 33 8.0
 emb|Z72791|SCYGR006W S.cerevisiae chromosome VII reading frame O... 33 8.0
 40 emb|Z34930|TV18SRRN T.violaceum (var. violaceum) gene for 18S rRNA. 33 8.0
 gb|U42663|TGU42663 Tuber gibbosum 18S small subunit ribosomal RN... 33 8.0
 emb|AQ940191|AQ940191 Sheared DNA-42C20.TF Sheared DNA Trypanoso... 33 8.0
 emb|AA274279|AA274279 TgESTzz24b06.s1 TgME49 invivo Bradyzoite c... 33 8.0
 emb|AU006886|AU006886 AU006886 Schizosaccharomyces pombe late lo... 33 8.0
 45 emb|AW926892|AW926892 HVSMEg0008N19 Hordeum vulgare pre-anthesis... 33 8.0
 dbj|D64123|D64123 Fibulobasidium inconspicuum DNA for small subu... 33 8.0

50 Query= AC002335.160_at 19171_at /id_source genbank /description
 gb|aab64325.1| (ac002335) putative trypsin inhibitor [arabidopsis
 thaliana] /blast_score 7.00e-40 /ec_number /family /chip nova
 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002335| /ncgi
 http://www.ncgr.org/cgi-bin/ff?ac002335
 55 (449 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

60 Searching.....done

	Score	E		(bits)	Value
	Sequences producing significant alignments:				
	emb Y16190 SAMTI2	Sinapsis alba mRNA for trypsin inhibitor 2.	161	2e-39	
5	emb X84208 SSAMTI2	Sinapsis alba mti-2 gene for trypsin inhibitor 2.	161	3e-39	
	emb AT002119 AT002119	AT002119 Flower bud cDNA Brassica rapa sub...	72	5e-14	
	gb L33539 L33539	BNAESTF178 Mustard flower buds Brassica rapa cD...	72	6e-14	
	emb AF025857 AF025857	Aegilops caudata RAPD marker generated by ...	36	0.18	
	emb AI065316 AI065316	TENU2203 T. cruzi epimastigote normalized ...	31	0.42	
10	emb AF066077 AF066077	Helianthus annuus RPL5A-related protein (R...	34	0.89	
	emb AL356173 NCB14D6	Neurospora crassa DNA linkage group II BAC ...	34	0.89	
	emb AF242188 AF242188	Plasmodium falciparum membrane protein Pfl...	34	0.89	
	gb M28889 PFAMEM12A	P.falciparum membrane protein Pfl2 gene, com...	34	0.89	
	emb AL160371 LMFLCHR15	Leishmania major Friedlin assembled chrom...	33	1.2	
15	gb U47092 U47092	DCU47092 Carrot somatic embryos Daucus carota c...	33	1.2	
	emb AL354533 LMFL6294	Leishmania major Friedlin chromosome 21 co...	33	1.2	
	emb AW278233 AW278233	sf41d09.y1 Gm-c1009 Glycine max cDNA clone...	33	1.2	
	emb AQ849793 AQ849793	LMAJFV1_lm49f04.x1 Leishmania major FV1 ra...	33	1.2	
	gb U91982 SHU91982	Stylosanthes hamata EREBP-3 homolog mRNA, com...	33	1.7	
20	emb AW727560 AW727560	GA_Ea0012P04 Gossypium arboreum 7-10 dpa ...	33	1.7	
	emb AQ848503 AQ848503	LMAJFV1_lm10a08.x1 Leishmania major FV1 ra...	33	1.7	
	emb AW668496 AW668496	GA_Ea0014C23 Gossypium arboreum 7-10 dpa ...	33	1.7	
	emb AL136236 SPAPJ696	S.pombe chromosome I PCR product p696.	32	2.3	
	emb AL133359 SPAP696	S.pombe chromosome I PCR product p696.	32	2.3	
25	emb AW728870 AW728870	GA_Ea0028O24 Gossypium arboreum 7-10 dpa ...	32	2.3	
	emb AW099428 AW099428	sd40c12.y1 Gm-c1016 Glycine max cDNA clone...	32	2.3	
	emb AV389315 AV389315	AV389315 Chlamydomonas reinhardtii C9 Chla...	32	2.3	
	emb AW707869 AW707869	832013D08.y1 C. reinhardtii CC-125 nutrien...	32	2.3	
	emb AC068564 AC068564	Filobasidiella neoformans var. neoformans,...	32	3.2	
30	emb Z38058 LMCLPB	L.major (MHOM/SU/5ASKH) DNA for 100 kDa heat s...	32	3.2	
	emb AW932211 AW932211	EST358054 tomato fruit mature green, TAMU ...	32	3.2	
	emb AL356172 NCB23L21	Neurospora crassa DNA linkage group II BAC...	32	3.2	
	emb AQ445563 AQ445563	GSSTc0014 Trypanosoma cruzi random genomic...	32	3.2	
	emb AF263283 AF263283	Filobasidiella neoformans var. neoformans ...	32	3.2	
35	emb X95256 HVXYLISOG	H.vulgare xylose isomerase gene.	32	3.2	
	emb AW217087 AW217087	EST295801 tomato callus, TAMU Lycopersicon...	32	3.2	
	emb X62675 TRMINEX5S	T.rangeli DNA for mini-exon and 5S rRNA.	29	3.5	
	emb AW745480 AW745480	WS1_35_H03.b1_A002 Water-stressed 1 (WS1) ...	31	4.4	
	emb AW705201 AW705201	sk43a03.y1 Gm-c1019 Glycine max cDNA clone...	31	4.4	
40	emb AI496396 AI496396	sb04b11.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4	
	emb AW694532 AW694532	NF077E02ST1F1017 Developing stem Medicago ...	31	4.4	
	emb AW598155 AW598155	sj89b07.y1 Gm-c1034 Glycine max cDNA clone...	31	4.4	
	emb AW508121 AW508121	si51a09.y1 Gm-r1030 Glycine max cDNA clone...	31	4.4	
	emb AW317929 AW317929	sg59a02.y1 Gm-c1007 Glycine max cDNA clone...	31	4.4	
45	emb AW185756 AW185756	se59c04.y1 Gm-c1019 Glycine max cDNA clone...	31	4.4	
	emb AW119645 AW119645	sd50d05.y1 Gm-c1016 Glycine max cDNA clone...	31	4.4	
	emb AI522947 AI522947	sa92d09.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4	
	gb L38627 GYNRGNA	Gymnodinium catenatum 24S ribosomal RNA (24S r...	31	4.4	
	emb AW926726 AW926726	HVSMEg0007P17 Hordeum vulgare pre-anthesis...	31	4.4	
50	emb AW307483 AW307483	sf57e09.y1 Gm-c1009 Glycine max cDNA clone...	31	4.4	
	emb AW307220 AW307220	sf54c09.y1 Gm-c1009 Glycine max cDNA clone...	31	4.4	
	emb AI437852 AI437852	sa40e07.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4	
	emb AW733531 AW733531	sk74g09.y1 Gm-c1016 Glycine max cDNA clone...	31	4.4	
	emb AW186505 AW186505	se68f10.y1 Gm-c1019 Glycine max cDNA clone...	31	4.4	
55	emb AW099682 AW099682	sd29g03.y2 Gm-c1012 Glycine max cDNA clone...	31	4.4	
	emb AW761228 AW761228	sl64h04.y1 Gm-c1027 Glycine max cDNA clone...	31	4.4	
	emb AI900314 AI900314	sc03h10.y1 Gm-c1012 Glycine max cDNA clone...	31	4.4	
	emb AF031065 AF031065	Dipsacomyces acuminosporus 28S ribosomal R...	31	4.4	
	emb AW099689 AW099689	sd29h03.y2 Gm-c1012 Glycine max cDNA clone...	31	4.4	
60	emb AI494951 AI494951	sa93a10.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4	
	emb AI988406 AI988406	sd01f04.y1 Gm-c1020 Glycine max cDNA clone...	31	4.4	

emb|AW782121|AW782121 sm01g01.y1 Gm-c1027 Glycine max cDNA clone... 31 4.4
 emb|AW100084|AW100084 sd20b03.y2 Gm-c1012 Glycine max cDNA clone... 31 4.4
 emb|AI939026|AI939026 sc64f02.y1 Gm-c1016 Glycine max cDNA clone... 31 4.4
 emb|AI736322|AI736322 sb27a03.y1 Gm-c1009 Glycine max cDNA clone... 31 4.4
 5 emb|AI965890|AI965890 sc79c09.y1 Gm-c1018 Glycine max cDNA clone... 31 4.4
 emb|AI901200|AI901200 sc22a07.y1 Gm-c1013 Glycine max cDNA clone... 31 4.4
 emb|AI736604|AI736604 sb31b04.y1 Gm-c1012 Glycine max cDNA clone... 31 4.4
 emb|AW666300|AW666300 sk34h06.y1 Gm-c1028 Glycine max cDNA clone... 31 6.0
 emb|AW831353|AW831353 sm32e10.y1 Gm-c1028 Glycine max cDNA clone... 31 6.0
 10 gb|L37877|CPCRPL27P *Cryptococcus neoformans* ribosomal protein L2... 31 6.0
 emb|Z75290|SCYOR382W *S.cerevisiae* chromosome XV reading frame OR... 31 6.0
 emb|AQ850290|AQ850290 LMAJFV1_lm28c06.x1 *Leishmania major* FV1 ra... 31 6.0
 gb|L26508|CPCAAA *Filobasidiella neoformans* CAP59 gene, complete ... 31 6.0
 emb|AQ847349|AQ847349 LMAJFV1_lm30a04.x1 *Leishmania major* FV1 ra... 31 6.0
 15 emb|AC008241|AC008241 *Leishmania major* clone L952b strain Friedl... 31 6.0
 emb|AW667667|AW667667 GA__Ea0010C24 *Gossypium arboreum* 7-10 dpa ... 31 6.0
 emb|AF031066|AF031066 *Martensiomycetes pterosporus* 28S ribosomal R... 31 6.0
 emb|AQ398504|AQ398504 mgxb0019M20f CUGI Rice Blast BAC Library P... 31 6.0
 emb|AZ215468|AZ215468 Sheared DNA-79C4.TF Sheared DNA Trypanosom... 25 7.1
 20 dbj|D50617|YSCCHRVIN *Saccharomyces cerevisiae* chromosome VI comp... 30 8.3
 dbj|D44598|YSCF4121F *Saccharomyces cerevisiae* chromosome VI phag... 30 8.3
 dbj|D87895|D87895 *Aspergillus nidulans* chiA gene for chitinase, ... 30 8.3
 emb|AQ162420|AQ162420 mgxb0012N11r CUGI Rice Blast BAC Library P... 30 8.3
 gb|BE036961|BE036961 MP09G07 MP *Mesembryanthemum crystallinum* cD... 30 8.3
 25 emb|AW101721|AW101721 sd69c10.y1 Gm-c1008 Glycine max cDNA clone... 30 8.3
 emb|AW980894|AW980894 EST392047 GVN *Medicago truncatula* cDNA clo... 30 8.3
 emb|AQ447068|AQ447068 mgxb0004O05f CUGI Rice Blast BAC Library P... 30 8.3
 emb|AW727134|AW727134 GA__Ea0023J07 *Gossypium arboreum* 7-10 dpa ... 26 8.7
 gb|BE053868|BE053868 GA__Ea0013O20f *Gossypium arboreum* 7-10 dpa ... 27 8.9
 30

 Query= X99923.1_at 19177_at /id_source genbank /description
 emb|caa68191.1| (x99923) male sterility 2-like protein [arabidopsis
 thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
 35 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|x99923|/ncgi
 http://www.ncgr.org/cgi-bin/ff?x99923
 (1710 letters)

 40 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

 Searching.....done

 45 Score E
 Sequences producing significant alignments: (bits) Value

 emb|AF149917|AF149917 *Simmondsia chinensis* acyl CoA reductase mR... 158 e-144
 emb|X99922|BNMS2PROT *B.napus* mRNA for male sterility protein 2. 137 2e-74
 50 emb|A45743|A45743 Sequence 22 from Patent WO9520668. 137 2e-74
 emb|AW615992|AW615992 EST325442 tomato flower buds 0-3 mm, Corne... 277 2e-73
 emb|AI730540|AI730540 BNLGHi7015 Six-day Cotton fiber *Gossypium* ... 153 4e-59
 emb|AW738637|AW738637 EST340064 tomato flower buds, anthesis, Co... 158 3e-51
 emb|AW931162|AW931162 EST357005 tomato fruit mature green, TAMU ... 201 1e-50
 55 emb|AW616784|AW616784 EST323195 *L. hirsutum* trichome, Cornell Un... 200 3e-50
 emb|AW308800|AW308800 sf72b03.y1 Gm-c1013 Glycine max cDNA clone... 141 7e-50
 emb|AW278653|AW278653 sf63e03.y1 Gm-c1013 Glycine max cDNA clone... 110 1e-46
 emb|AI727421|AI727421 BNLGHi7945 Six-day Cotton fiber *Gossypium* ... 106 3e-46
 emb|AI901240|AI901240 sc22e07.y1 Gm-c1013 Glycine max cDNA clone... 166 3e-40
 60 emb|AW306151|AW306151 se46e08.y1 Gm-c1017 Glycine max cDNA clone... 145 2e-39
 emb|AW688482|AW688482 NF008B06ST1F1000 Developing stem *Medicago* ... 127 6e-38

	emb AW648210 AW648210 EST326664 tomato germinating seedlings, TA...	107	1e-37
	emb AW279265 AW279265 sf68h11.y1 Gm-c1013 Glycine max cDNA clone...	123	3e-37
	emb AW671408 AW671408 LG1_343_A01.b1_A002 Light Grown 1 (LG1) So...	156	4e-37
	emb AW306626 AW306626 se53c07.y1 Gm-c1017 Glycine max cDNA clone...	145	5e-37
5	emb AW624291 AW624291 EST322152 tomato flower buds 3-8 mm, Corne...	121	1e-32
	emb AW688474 AW688474 NF008A09ST1F1000 Developing stem Medicago ...	106	5e-31
	emb AW781535 AW781535 sl81d04.y1 Gm-c1037 Glycine max cDNA clone...	109	7e-30
	emb AW622996 AW622996 EST320941 tomato flower buds 3-8 mm, Corne...	128	1e-28
	emb AI055562 AI055562 coau0004F11 Cotton Boll Abscission Zone cD...	98	1e-27
10	emb AW287082 AW287082 LG1_265_C07.b2_A002 Light Grown 1 (LG1) So...	119	7e-26
	emb AW691252 AW691252 NF042F05ST1F1000 Developing stem Medicago ...	100	3e-25
	emb AW649410 AW649410 EST327864 tomato germinating seedlings, TA...	115	1e-24
	emb AW705269 AW705269 sk59a03.y1 Gm-c1019 Glycine max cDNA clone...	70	3e-18
	emb AW217786 AW217786 EST296500 tomato flower buds 8 mm to pre-a...	92	6e-18
15	emb AW217788 AW217788 EST296502 tomato flower buds 8 mm to pre-a...	91	8e-18
	emb AW217787 AW217787 EST296501 tomato flower buds 8 mm to pre-a...	91	3e-17
	emb AW928598 AW928598 EST337386 tomato flower buds 8 mm to pre-a...	86	1e-16
	emb Z11889 MITTARRNG T.aestivum mitochondrion rm26 gene for rRN...	88	2e-16
	emb AW565061 AW565061 LG1_320_C11.b1_A002 Light Grown 1 (LG1) So...	78	2e-13
20	emb AW980920 AW980920 EST392073 GVN Medicago truncatula cDNA clo...	50	3e-13
	emb AV428628 AV428628 AV428628 Lotus japonicus young plants (two...	71	2e-11
	emb AV419850 AV419850 AV419850 Lotus japonicus young plants (two...	68	2e-10
	emb AF076792 AF076792 Irvingia gabonensis clone BM35, genomic su...	51	2e-08
	emb AW056631 AW056631 ST53H08 Pine TriplEx shoot tip library Pin...	36	7e-05
25	emb AW289724 AW289724 NXNV005H02F Nsf Xylem Normal wood Vertical...	48	2e-04
	gb BE057395 BE057395 sn02f06.y1 Gm-c1015 Glycine max cDNA clone ...	44	2e-04
	emb AZ050471 AZ050471 GSSTc11316 Trypanosoma cruzi random genomi...	48	2e-04
	emb AW758790 AW758790 NXNV_089_G03_F Nsf Xylem Normal wood Verti...	47	5e-04
	emb AA952454 AA952454 TENS1392 T. cruzi epimastigote normalized ...	46	0.001
30	emb AQ361876 AQ361876 mgxb0005G07r CUGI Rice Blast BAC Library P...	42	0.015
	emb AI069380 AI069380 mgae0006dC11f Magnaporthe grisea Appressor...	42	0.015
	emb AW649203 AW649203 EST327657 tomato germinating seedlings, TA...	41	0.021
	emb Y13967 PCLYS2 Penicillium chrysogenum lys2 gene.	41	0.021
	emb AW929360 AW929360 EST338148 tomato flower buds 8 mm to pre-a...	40	0.074
35	emb AW564691 AW564691 LG1_300_C05.b1_A002 Light Grown 1 (LG1) So...	37	0.50
	emb AF114171 AF114171 Sorghum bicolor BAC clone 25.M18, complete...	37	0.50
	gb BE033566 BE033566 MF03E04 MF Mesembryanthemum crystallinum cD...	36	0.69
	emb AI488290 AI488290 EST246612 tomato ovary, TAMU Lycopersicon ...	36	0.94
	emb AW932683 AW932683 EST358526 tomato fruit mature green, TAMU ...	36	0.94
40	emb AW932440 AW932440 EST358283 tomato fruit mature green, TAMU ...	36	0.94
	emb AQ874417 AQ874417 V108D3 mTn-3xHA/lacZ Insertion Library, st...	35	1.3
	emb AF156928 AF156928 Candida albicans folylpolyglutamate synthe...	28	1.4
	emb AW720470 AW720470 LjNEST192r Lotus japonicus nodule library...	35	1.8
	emb AW397976 AW397976 sg70f10.y1 Gm-c1007 Glycine max cDNA clone...	35	1.8
45	emb AV409049 AV409049 AV409049 Lotus japonicus young plants (two...	35	1.8
	emb AL353821 NC68B2 Neurospora crassa DNA linkage group V Cosmid...	35	2.4
	emb AW775233 AW775233 EST331955 GVN Medicago truncatula cDNA clo...	35	2.4
	emb AW694088 AW694088 NF072C08ST1F1065 Developing stem Medicago ...	35	2.4
	emb AW693849 AW693849 NF069G11ST1F1087 Developing stem Medicago ...	35	2.4
50	emb AW694067 AW694067 NF072D11ST1F1093 Developing stem Medicago ...	35	2.4
	emb AW773778 AW773778 EST332764 KV3 Medicago truncatula cDNA clo...	35	2.4
	emb AW774799 AW774799 EST333950 KV3 Medicago truncatula cDNA clo...	35	2.4
	emb AW774591 AW774591 EST333742 KV3 Medicago truncatula cDNA clo...	35	2.4
	emb AW689574 AW689574 NF021H08ST1F1000 Developing stem Medicago ...	35	2.4
55	emb AW694736 AW694736 NF079D09ST1F1077 Developing stem Medicago ...	35	2.4
	emb AI075585 AI075585 TENU3007 T. cruzi epimastigote normalized ...	35	2.4
	emb AW691920 AW691920 NF050F11ST1F1000 Developing stem Medicago ...	35	2.4
	emb AW690529 AW690529 NF035F03ST1F1000 Developing stem Medicago ...	35	2.4
	emb AA660549 AA660549 00435 MtRHE Medicago truncatula cDNA 5' si...	35	2.4
60	emb AQ841091 AQ841091 T132045b Medicago truncatula BAC library M...	35	2.4
	emb AW695358 AW695358 NF093H05ST1F1047 Developing stem Medicago ...	35	2.4

emb|AW299108|AW299108 EST305782 KV2 Medicago truncatula cDNA clo... 35 2.4
 gb|U46545|HAU46545 Helianthus annuus 17.7 kDa heat-shock protein... 34 3.4
 emb|AW309167|AW309167 sg05b03.y1 Gm-c1019 Glycine max cDNA clone... 34 3.4
 emb|AW234839|AW234839 sf19g08.y1 Gm-c1028 Glycine max cDNA clone... 34 3.4
 5 emb|AI960722|AI960722 sc89e06.y1 Gm-c1019 Glycine max cDNA clone... 34 3.4
 emb|AF233374|AF233374 Volvox carteri argininosuccinate lyase (VA... 34 4.6
 emb|AW925731|AW925731 HVSMEg0005F22 Hordeum vulgare pre-anthesis... 34 4.6
 gb|BE053807|BE053807 GA_Ea0014K20f Gossypium arboreum 7-10 dpa ... 34 4.6
 emb|AI213767|AI213767 z5b08a1.r1 Aspergillus nidulans 24hr asexu... 34 4.6
 10 gb|U58133|CAU58133 Candida albicans alpha-aminoadipate reductase... 26 6.1
 emb|AW686938|AW686938 NF004C01RT1F1004 Developing root Medicago ... 33 6.3
 emb|Z46881|SC3299 S.cerevisiae chromosome IX cosmid 3299. 33 6.3
 emb|AV391768|AV391768 AV391768 Chlamydomonas reinhardtii C9 Chla... 33 6.3
 emb|AW933793|AW933793 EST359636 tomato fruit mature green, TAMU ... 33 6.3
 15 emb|AW618444|AW618444 EST320430 L. pennellii trichome, Cornell U... 33 6.3
 gb|BE053260|BE053260 GA_Ea0035A01f Gossypium arboreum 7-10 dpa ... 33 6.3
 emb|AF082993|AF082993 Cryptosporidium parvum type I fatty acid s... 33 6.3
 emb|AZ220106|AZ220106 Sheared DNA-63H10.TR Sheared DNA Trypanoso... 33 6.3
 emb|AF072272|AF072272 Lactuca sativa resistance protein candidat... 33 6.3
 20 emb|AB012945|AB012945 Aspergillus oryzae gene for amyRp, complet... 33 8.7
 emb|AF180560|AF180560 Emericella nidulans sgdA gene, partial seq... 33 8.7
 dbj|D29761|YSACSH Candida maltosa gene for chitin synthase 2, p... 33 8.7
 emb|AJ273086|AJ273086 AJ273086 Metarhizium anisopliae ARSEF 2575... 33 8.7
 dbj|E12507|E12507 Promoter region of the agdA gene. 33 8.7
 25 dbj|D50617|YSCCHRVIN Saccharomyces cerevisiae chromosome VI comp... 33 8.7

Query= AL031804.245_at 19182_at /id_source genbank /description
 emb|caa21214.1| (al031804) putative protein [arabidopsis thaliana]
 30 /blast_score 0 /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031804| /ncgi
 http://www.ncgr.org/cgi-bin/ff?al031804
 (1467 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

emb|AI894665|AI894665 EST264108 tomato callus, TAMU Lycopersicon... 341 6e-93
 45 emb|AW032812|AW032812 EST276371 tomato callus, TAMU Lycopersicon... 325 5e-88
 emb|AW035000|AW035000 EST279229 tomato callus, TAMU Lycopersicon... 297 2e-79
 emb|AI896184|AI896184 EST265627 tomato callus, TAMU Lycopersicon... 282 5e-75
 emb|AI896887|AI896887 EST266330 tomato callus, TAMU Lycopersicon... 178 1e-72
 emb|AW030421|AW030421 EST273676 tomato callus, TAMU Lycopersicon... 254 1e-66
 50 gb|BE059595|BE059595 sn34c09.y1 Gm-c1016 Glycine max cDNA clone ... 177 2e-43
 emb|AW234683|AW234683 sf18a11.y1 Gm-c1028 Glycine max cDNA clone... 166 4e-40
 emb|AW687734|AW687734 NF012H03RT1F1031 Developing root Medicago ... 105 7e-39
 emb|AI728318|AI728318 BNLGHi10452 Six-day Cotton fiber Gossypium... 154 2e-36
 emb|AT000486|AT000486 AT000486 Brassica rapa guard cell Brassica... 92 1e-32
 55 emb|AI487311|AI487311 EST245633 tomato ovary, TAMU Lycopersicon ... 79 2e-30
 emb|AW220379|AW220379 EST302862 tomato root during/after fruit s... 133 2e-30
 emb|AI166722|AI166722 xylem.est.526 Poplar xylem Lambda ZAPII li... 103 3e-29
 emb|AW830251|AW830251 sm33a02.y1 Gm-c1028 Glycine max cDNA clone... 128 8e-29
 emb|AW777089|AW777089 M110842e GVSN Medicago truncatula cDNA clo... 126 5e-28
 60 emb|AT000492|AT000492 AT000492 Brassica rapa guard cell Brassica... 92 6e-28
 emb|AI895477|AI895477 EST264920 tomato callus, TAMU Lycopersicon... 125 1e-27

- emb|AV409317|AV409317 AV409317 Lotus japonicus young plants (two... 123 4e-27
emb|AI487156|AI487156 EST245478 tomato ovary, TAMU Lycopersicon ... 80 1e-25
emb|AV427085|AV427085 AV427085 Lotus japonicus young plants (two... 111 1e-23
emb|AT000641|AT000641 AT000641 Brassica rapa guard cell Brassica... 110 3e-23
5 emb|AW685452|AW685452 NF029F12NR1F1000 Nodulated root Medicago t... 104 2e-21
emb|AW719903|AW719903 LjNEST11g5r Lotus japonicus nodule library... 77 2e-21
emb|AI966612|AI966612 sc53d04.y1 Gm-c1015 Glycine max cDNA clone... 86 3e-19
emb|AW647985|AW647985 EST326439 tomato germinating seedlings, TA... 95 9e-19
emb|AI966597|AI966597 sc52h04.y1 Gm-c1015 Glycine max cDNA clone... 82 5e-18
10 emb|AW278350|AW278350 sf43a03.y1 Gm-c1009 Glycine max cDNA clone... 90 3e-17
emb|AW687571|AW687571 NF011A10RT1F1072 Developing root Medicago ... 90 3e-17
emb|AT000935|AT000935 AT000935 Brassica rapa guard cell Brassica... 89 1e-16
emb|AW684018|AW684018 NF011C08NR1F1000 Nodulated root Medicago t... 68 6e-16
gb|BE059565|BE059565 sn33g08.y1 Gm-c1016 Glycine max cDNA clone ... 78 3e-15
15 emb|AW934333|AW934333 EST360176 tomato fruit mature green, TAMU ... 84 4e-15
emb|AI781643|AI781643 EST262522 tomato susceptible, Cornell Lyco... 84 4e-15
emb|AW699630|AW699630 gb29d11.y1 Moss EST library PPN Physcomitr... 83 7e-15
emb|AW686556|AW686556 NF039E01NR1F1000 Nodulated root Medicago t... 81 2e-14
emb|AI736754|AI736754 sb33a10.y1 Gm-c1012 Glycine max cDNA clone... 68 6e-14
20 emb|AW687218|AW687218 NF007C06RT1F1049 Developing root Medicago ... 78 2e-13
emb|AI496521|AI496521 sb08h01.y1 Gm-c1004 Glycine max cDNA clone... 76 8e-13
emb|AQ448299|AQ448299 mgxb0020C15f CUGI Rice Blast BAC Library P... 75 1e-12
emb|AI731601|AI731601 BNLGHi10195 Six-day Cotton fiber Gossypium... 70 5e-11
emb|AW719552|AW719552 LjNEST6b3r Lotus japonicus nodule library,... 64 4e-10
25 emb|AI485751|AI485751 EST244072 tomato ovary, TAMU Lycopersicon ... 64 2e-09
emb|AL113765|CNS01B4D Botrytis cinerea strain T4 cDNA library un... 62 8e-09
emb|AW671559|AW671559 LG1_348_E04.b1_A002 Light Grown 1 (LG1) So... 62 1e-08
emb|AI484941|AI484941 EST243204 tomato ovary, TAMU Lycopersicon ... 60 5e-08
emb|AI486383|AI486383 EST244704 tomato ovary, TAMU Lycopersicon ... 58 2e-07
30 emb|AW564851|AW564851 LG1_310_D10.b1_A002 Light Grown 1 (LG1) So... 54 2e-06
emb|AW703782|AW703782 sk12e01.y1 Gm-c1023 Glycine max cDNA clone... 54 3e-06
emb|AW672524|AW672524 LG1_360_D10.b1_A002 Light Grown 1 (LG1) So... 49 8e-05
emb|AW348926|AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3... 47 3e-04
emb|AI960597|AI960597 sc86f09.y1 Gm-c1018 Glycine max cDNA clone... 41 0.024
35 emb|AW985394|AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti... 39 0.12
emb|X14399|TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su... 37 0.42
gb|M27164|TRBPOLI Trypanosoma brucei RNA polymerase I largest su... 37 0.42
emb|AW401287|AW401287 LamdiGest487est L.digitata gametophyte Lam... 36 0.58
emb|AJ276509|TAE276509 Triticum aestivum grp1 gene for glycine-r... 36 0.79
40 emb|AL133468|LMFL3238 Leishmania major Friedlin chromosome 19 co... 35 1.1
emb|AL353820|NC13E11 Neurospora crassa DNA linkage group V Cosmi... 35 2.1
emb|AQ947099|AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso... 35 2.1
emb|AI328270|AI328270 a2b05ne.r1 Neurospora crassa evening cDNA ... 35 2.1
emb|AW931221|AW931221 EST357064 tomato fruit mature green, TAMU ... 34 2.8
45 emb|X69461|HPURA3 H.polymorpha URA3 gene. 34 2.8
emb|AL355932|NCB5022 Neurospora crassa DNA linkage group II BAC ... 34 3.9
emb|AW461229|AW461229 NXNV052C08F Nsf Xylem Normal wood Vertical... 33 5.3
emb|AW283985|AW283985 LG1_264_D01.g1_A002 Light Grown 1 (LG1) So... 33 5.3
emb|AF104916|AF104916 Candida albicans protein mannosyltransfera... 33 5.3
50 emb|AF164200|AF164200 Trypanosoma brucei putative DNA replicatio... 33 5.3
emb|Z36169|SCYBR300C S.cerevisiae chromosome II reading frame OR... 33 5.3
emb|AQ655061|AQ655061 Sheared DNA-27K12.TF Sheared DNA Trypanoso... 33 5.3
emb|AF107804|AF107804 Pleospora herbarum DNA-dependent RNA polym... 33 5.3
emb|AC007865|AC007865 Trypanosoma brucei chromosome II clone RPC... 33 7.3
55 gb|U13054|LEU13054 Lycopersicon esculentum endo-1,4-beta-glucana... 33 7.3
emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 33 7.3
emb|AQ647629|AQ647629 RPCI93-EcoRI-6K22.TJ RPCI93-EcoRI Trypanos... 33 7.3
emb|AQ660459|AQ660459 Sheared DNA-24L7.TF Sheared DNA Trypanosom... 33 7.3
emb|AI727817|AI727817 BNLGHi9181 Six-day Cotton fiber Gossypium ... 33 7.3
60 emb|AI755342|AI755342 EtESTea36d07.y1 Eimeria S5-2 Sporozoite st... 33 7.3
emb|AC005506|AC005506 Plasmodium falciparum chromosome 12 clone ... 33 7.3

emb|AZ217295|AZ217295 Sheared DNA-112B7.TF Sheared DNA Trypanoso... 33 7.3
 emb|AW287840|AW287840 N100683e rootphos(-) Medicago truncatula c... 33 7.3

5 Query= AC003027.39_at 19229_at /id_source genbank /description
 gb|aad10694.1| (ac003027) lcl|prt_seq no definition line found
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&cuid=gb|ac003027|/ncgi
 10 http://www.ncgr.org/cgi-bin/ff?ac003027
 (1743 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

15 Searching.....done

		Score	E	
	Sequences producing significant alignments:			(bits) Value
20	emb AW218224 AW218224 EST303405 tomato radicle, 5 d post-imbibit...	270	4e-81	
	emb AW775278 AW775278 EST334343 DSIL Medicago truncatula cDNA cl...	276	6e-80	
	emb AW443927 AW443927 EST308857 tomato mixed elicitor, BTI Lycop...	225	3e-78	
	emb AW560040 AW560040 EST315088 DSIR Medicago truncatula cDNA cl...	276	1e-77	
25	emb AW560039 AW560039 EST315087 DSIR Medicago truncatula cDNA cl...	276	3e-73	
	gb BE033452 BE033452 ME02B10 ME Mesembryanthemum crystallinum cD...	264	2e-72	
	emb AI487716 AI487716 EST246038 tomato ovary, TAMU Lycopersicon ...	271	1e-71	
	emb AI486962 AI486962 EST245284 tomato ovary, TAMU Lycopersicon ...	269	4e-71	
	emb AW441974 AW441974 EST311370 tomato fruit red ripe, TAMU Lyco...	242	8e-71	
30	emb AW099977 AW099977 sd19c07.y2 Gm-c1012 Glycine max cDNA clone...	253	7e-69	
	emb AW733661 AW733661 sk83d11.y1 Gm-c1016 Glycine max cDNA clone...	223	4e-65	
	emb AW164658 AW164658 se75h05.y1 Gm-c1023 Glycine max cDNA clone...	162	1e-64	
	emb AW689466 AW689466 NF019F01ST1F1000 Developing stem Medicago ...	159	1e-62	
	emb AI441647 AI441647 sa65a03.y1 Gm-c1004 Glycine max cDNA clone...	212	9e-58	
35	emb AI729737 AI729737 BNLGHi14077 Six-day Cotton fiber Gossypium...	128	7e-55	
	emb AI771313 AI771313 EST252329 tomato ovary, TAMU Lycopersicon ...	137	3e-46	
	emb AW033056 AW033056 EST276615 tomato callus, TAMU Lycopersicon...	177	3e-43	
	emb AW623019 AW623019 EST320964 tomato flower buds 3-8 mm, Corne...	76	2e-41	
	emb AI728350 AI728350 BNLGHi10536 Six-day Cotton fiber Gossypium...	76	5e-40	
40	emb AW922217 AW922217 DG1_17_D01.b1_A002 Dark Grown 1 (DG1) Sorg...	162	6e-39	
	emb AI731527 AI731527 BNLGHi9654 Six-day Cotton fiber Gossypium ...	158	1e-37	
	gb BE056576 BE056576 894010C07.y1 C. reinhardtii CC-1690, normal...	129	9e-36	
	emb AI165184 AI165184 A077p80u Hybrid aspen plasmid library Popu...	142	1e-32	
	emb Z98600 SPAC20G4 S.pombe chromosome I cosmid c20G4.	133	6e-30	
45	emb AW056437 AW056437 ST51H06 Pine TriplEx shoot tip library Pin...	68	4e-27	
	gb BE020433 BE020433 sm40f12.y1 Gm-c1028 Glycine max cDNA clone ...	65	1e-26	
	gb BE053819 BE053819 GA_Ea0035C17f Gossypium arboreum 7-10 dpa ...	74	9e-26	
	emb AW726831 AW726831 GA_Ea0022N20 Gossypium arboreum 7-10 dpa ...	74	9e-26	
	dbj D50617 YSCCHRVIN Saccharomyces cerevisiae chromosome VI comp...	113	5e-24	
50	dbj D44595 YSCF6781C Saccharomyces cerevisiae chromosome VI phag...	113	5e-24	
	emb AA520817 AA520817 TgESTzz64d12.r1 TgME49 invivo Bradyzoite c...	80	1e-23	
	emb AW683126 AW683126 NF007H02LF1F1026 Developing leaf Medicago ...	66	2e-21	
	emb AW564299 AW564299 LG1_289_C04.b1_A002 Light Grown 1 (LG1) So...	47	4e-21	
	emb AW745946 AW745946 WS1_38_H09.b1_A002 Water-stressed 1 (WS1) ...	57	9e-21	
55	emb AW651005 AW651005 EST329459 tomato germinating seedlings, TA...	99	1e-19	
	emb AW760155 AW760155 sl58g05.y1 Gm-c1027 Glycine max cDNA clone...	94	7e-19	
	emb AW677014 AW677014 DG1_3_C03.b1_A002 Dark Grown 1 (DG1) Sorgh...	92	1e-17	
	emb AA556650 AA556650 505 Loblolly pine C Pinus taeda cDNA clone...	68	2e-16	
	emb AW681004 AW681004 WS1_9_D01.b1_A002 Water-stressed 1 (WS1) S...	73	3e-15	
60	emb AW686988 AW686988 NF004G03RT1F1023 Developing root Medicago ...	69	4e-15	
	emb AW650999 AW650999 EST329453 tomato germinating seedlings, TA...	83	6e-15	

- emb|AJ055048|AJ055048 coau0002O07 Cotton Boll Abscission Zone cD... 75 6e-13
emb|AW200862|AW200862 se94e02.y1 Gm-c1027 Glycine max cDNA clone... 53 1e-10
emb|AW693163|AW693163 NF062G06ST1F1000 Developing stem Medicago ... 56 4e-10
emb|AL111305|CNS01981 Botrytis cinerea strain T4 cDNA library un... 60 2e-09
5 emb|AW284408|AW284408 LG1_289_C04.g1_A002 Light Grown 1 (LG1) So... 47 2e-07
emb|AQ659916|AQ659916 Sheared DNA-16N2.TR Sheared DNA Trypanosom... 45 2e-07
emb|X79680|CAORF C.arietinum mRNA for open reading frame. 54 1e-06
gb|U19971|SCU19971 Saccharomyces cerevisiae ATP binding cassette... 54 4e-06
dbj|D44599|YSCF4233G Saccharomyces cerevisiae chromosome VI phag... 54 4e-06
10 emb|AW266043|AW266043 L30-2716T3 Ice plant Lambda Uni-Zap XR exp... 51 4e-05
emb|AA962925|AA962925 L30-456T3 Ice plant Lambda Uni-Zap XR expr... 42 5e-05
emb|AW982522|AW982522 HVSMEg0003H22f Hordeum vulgare pre-anthesi... 50 7e-05
emb|AQ953753|AQ953753 Sheared DNA-52P9.TF Sheared DNA Trypanosom... 49 1e-04
emb|AI776285|AI776285 EST257385 tomato resistant, Cornell Lycope... 48 2e-04
15 emb|AQ649643|AQ649643 Sheared DNA-16E5.TR Sheared DNA Trypanosom... 33 4e-04
emb|Z74816|SCYOL074C S.cerevisiae chromosome XV reading frame OR... 47 5e-04
emb|AL122011|SPCC825 S.pombe chromosome III cosmid c825. 47 5e-04
gb|T38919|T38919 EST104485 S. cerevisiae strain X2180-1A Sacchar... 46 9e-04
emb|Z99168|SPAC8C9 S.pombe chromosome I cosmid c8C9. 46 9e-04
20 emb|Z97208|SPAC15A10 S.pombe chromosome I cosmid c15A10. 46 9e-04
emb|AW746912|AW746912 WS1_56_G02.b1_A002 Water-stressed 1 (WS1) ... 46 0.001
emb|AC005893|AC005893 Leishmania major chromosome 3 clone L822 s... 46 0.001
emb|AC005767|AC005767 Leishmania major chromosome 3 clone L7535 ... 46 0.001
emb|AC005766|AC005766 Leishmania major chromosome 3 clone L4625 ... 46 0.001
25 emb|AQ640246|AQ640246 927P1-18B11.TP 927P1 Trypanosoma brucei ge... 45 0.002
emb|AQ642395|AQ642395 RPCI93-DpnII-29C18.TJ RPCI93-DpnII Trypano... 45 0.002
emb|AW043038|AW043038 ST28E05 Pine TriplEx shoot tip library Pin... 45 0.002
emb|AW226288|AW226288 ST80F04 Pine TriplEx shoot tip library Pin... 45 0.002
emb|AW870068|AW870068 NXNV_123_G02_F Nsf Xylem Normal wood Verti... 45 0.002
30 gb|U52079|STU52079 Solanum tuberosum P-glycoprotein (pmdr1) mRNA... 44 0.003
emb|AI780527|AI780527 EST261406 tomato susceptible, Cornell Lyco... 44 0.004
emb|AW934240|AW934240 EST360083 tomato fruit mature green, TAMU ... 44 0.004
emb|AV423490|AV423490 AV423490 Lotus japonicus young plants (two... 44 0.004
emb|AI328856|AI328856 a7c03ne.fl Neurospora crassa evening cDNA ... 44 0.004
35 emb|AI485412|AI485412 EST243733 tomato ovary, TAMU Lycopersicon ... 44 0.004
emb|AW625153|AW625153 EST319060 tomato radicle, 5 d post-imbibit... 44 0.004
gb|BE122564|BE122564 Ljirnp29-339-fl1 Ljirnp Lambda HybriZap ... 44 0.004
emb|AV419032|AV419032 AV419032 Lotus japonicus young plants (two... 44 0.004
emb|AW010587|AW010587 ST08E04 Pine TriplEx shoot tip library Pin... 44 0.004
40 emb|AW308969|AW308969 sf92d12.y1 Gm-c1019 Glycine max cDNA clone... 43 0.006
gb|BE021188|BE021188 sm47h12.y1 Gm-c1028 Glycine max cDNA clone ... 43 0.006
emb|AQ659914|AQ659914 Sheared DNA-16N2.TF Sheared DNA Trypanosom... 43 0.006
emb|AQ841079|AQ841079 T132031b Medicago truncatula BAC library M... 43 0.008
emb|AF137379|AF137379 Nephroselmis olivacea chloroplast DNA, com... 42 0.011
45 emb|AQ254520|AQ254520 CpG0676A CpIOWAgDNA1 Cryptosporidium parvu... 42 0.011
emb|AW761021|AW761021 sl70a03.y1 Gm-c1027 Glycine max cDNA clone... 42 0.011
gb|BE022040|BE022040 sm65g07.y1 Gm-c1028 Glycine max cDNA clone ... 42 0.011
emb|AW621316|AW621316 EST312114 tomato root during/after fruit s... 42 0.011
emb|Z14055|SPHMT1M S.pombe mRNA for HMT1. 42 0.016
50 emb|AB041505|AB041505 Populus nigra PnATH mRNA for ABC transport... 42 0.016
emb|AL109988|SPAC323 S.pombe chromosome I cosmid c323. 42 0.016
emb|Z98951|SPCC10D6 S.pombe chromosome I cosmid c10D6. 42 0.016
emb|AL031546|SPCC737 S.pombe chromosome III cosmid c737. 42 0.016
emb|Y10099|HVPGLYH H.vulgare mRNA for novel P-glycoprotein homol... 41 0.021
55 emb|AQ852914|AQ852914 LMAJFV1_lm93e10.y1 Leishmania major FV1 ra... 41 0.021
emb|AV410111|AV410111 AV410111 Lotus japonicus young plants (two... 41 0.029
emb|Z49212|SC9952X S.cerevisiae chromosome XIII cosmid 9952. 41 0.029
emb|X81715|SCMDYGENE S.cerevisiae partial MDY gene. 41 0.029
emb|AF166114|AF166114 Mesostigma viride chloroplast DNA, complet... 41 0.029
60

Query= AL080253.32_at 19415_at /id_source genbank /description
 emb|cab45805.1| (al080253) putative protein [arabidopsis thaliana]
 /blast_score 7.00e-83 /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 5 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al080253| /ncgi
 http://www.ncgr.org/cgi-bin/ff?al080253
 (594 letters)

10 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	
15	Sequences producing significant alignments:	(bits)	Value
	emb Z99969 MAZ99969 Musa acuminata mRNA for putative beta-1,3-gl...	62	3e-09
	emb AW725476 AW725476 GA__Ea0018C14 Gossypium arboreum 7-10 dpa ...	37	2e-08
	gb BE033791 BE033791 MF06E10 MF Mesembryanthemum crystallinum cD...	58	5e-08
20	gb BE034803 BE034803 ML04E10 ML Mesembryanthemum crystallinum cD...	58	5e-08
	emb AI728744 AI728744 BNLGHi11492 Six-day Cotton fiber Gossypium...	35	2e-07
	emb AW394608 AW394608 sh33e11.y1 Gm-c1017 Glycine max cDNA clone...	41	1e-06
	emb AW687017 AW687017 NF005A10RT1F1072 Developing root Medicago ...	40	2e-06
	emb AW685774 AW685774 NF035A03NR1F1000 Nodulated root Medicago t...	40	2e-06
25	emb AW220014 AW220014 EST302497 tomato root during/after fruit s...	45	2e-06
	emb AW277478 AW277478 sf82e11.y1 Gm-c1019 Glycine max cDNA clone...	37	8e-06
	emb AW728453 AW728453 GA__Ea0016L16 Gossypium arboreum 7-10 dpa ...	34	1e-05
	emb AW625648 AW625648 EST319555 tomato radicle, 5 d post-imbibit...	45	1e-05
	emb AW775954 AW775954 EST335019 DSIL Medicago truncatula cDNA cl...	39	2e-05
30	emb AW299135 AW299135 EST305809 KV2 Medicago truncatula cDNA clo...	47	1e-04
	gb BE033951 BE033951 MG02E05 MG Mesembryanthemum crystallinum cD...	46	2e-04
	emb AW697566 AW697566 ST64E03 Pine Triplex shoot tip library Pin...	34	8e-04
	emb AI812453 AI812453 11C3 Pine Lambda Zap Xylem library Pinus t...	44	0.001
	emb AW687794 AW687794 NF013E08RT1F1066 Developing root Medicago ...	32	0.003
35	emb AW423428 AW423428 sh66f08.y1 Gm-c1015 Glycine max cDNA clone...	38	0.003
	emb AW310121 AW310121 sf31d07.x1 Gm-c1028 Glycine max cDNA clone...	36	0.004
	emb AW704218 AW704218 sk17c12.y1 Gm-c1028 Glycine max cDNA clone...	38	0.004
	emb AW704640 AW704640 sk54f05.y1 Gm-c1019 Glycine max cDNA clone...	36	0.004
	emb AW395252 AW395252 sh45g06.y1 Gm-c1017 Glycine max cDNA clone...	36	0.004
40	emb AW704612 AW704612 sk54c11.y1 Gm-c1019 Glycine max cDNA clone...	36	0.004
	emb AW284126 AW284126 LG1_262_A05.g1_A002 Light Grown 1 (LG1) So...	41	0.008
	emb AW923658 AW923658 DG1_57_B06.g1_A002 Dark Grown 1 (DG1) Sorg...	39	0.040
	emb AW423359 AW423359 sh06g04.y1 Gm-c1016 Glycine max cDNA clone...	38	0.076
	emb AW649685 AW649685 EST328139 tomato germinating seedlings, TA...	28	0.35
45	emb AA520781 AA520781 TgESTzz64a03.r1 TgME49 invivo Bradyzoite c...	35	0.37
	emb AW620830 AW620830 sj47b03.y1 Gm-c1033 Glycine max cDNA clone...	30	0.48
	emb X65608 SCPDC2G S.cerevisiae PDC2 gene.	35	0.51
	emb Z74377 SCYDR081C S.cerevisiae chromosome IV reading frame OR...	35	0.51
	emb Z46796 SC8554 S.cerevisiae chromosome IV cosmid 8554.	35	0.51
50	emb X82086 SCCHROIV S.cerevisiae DNA for right arm of chromosome...	35	0.51
	gb L19880 YSCPDC2A Saccharomyces cerevisiae pdc2 gene, complete ...	35	0.51
	emb AW299176 AW299176 EST305986 KV2 Medicago truncatula cDNA clo...	35	0.70
	emb AW310120 AW310120 sf31d06.x1 Gm-c1028 Glycine max cDNA clone...	35	0.70
	emb AW309936 AW309936 sf26g12.x1 Gm-c1028 Glycine max cDNA clone...	35	0.70
55	emb AW278505 AW278505 sf45c08.y1 Gm-c1009 Glycine max cDNA clone...	35	0.70
	emb AW310598 AW310598 sg21h03.x1 Gm-c1024 Glycine max cDNA clone...	34	0.96
	emb AW233878 AW233878 sf31d07.y1 Gm-c1028 Glycine max cDNA clone...	34	0.96
	gb BE125775 BE125775 DG1_57_B06.b1_A002 Dark Grown 1 (DG1) Sorgh...	34	0.96
	gb M13237 BLYGLUCB Barley beta glucanase mRNA.	34	0.96
60	gb M62740 BLYGLB2 Hordeum vulgare 1,3-1,4-beta-D glucan 4-glucan...	34	0.96
	emb AW747074 AW747074 WS1_65_A07.g1_A002 Water-stressed 1 (WS1) ...	34	1.3

- emb|AJ228137|NTJ228137 *Nicotiana tomentosiformis* DNA for Tnt1 re... 34 1.3
 emb|AJ228118|NTJ228118 *Nicotiana tomentosiformis* DNA for Tnt1 re... 34 1.3
 emb|AE001365|AE001365 *Plasmodium falciparum* chromosome 2, sectio... 33 1.8
 emb|AW233798|AW233798 sf26g12.y1 Gm-cl028 Glycine max cDNA clone... 33 2.5
 5 emb|AV393790|AV393790 AV393790 *Chlamydomonas reinhardtii* C9 Chla... 33 2.5
 emb|AI920265|AI920265 1795 Pine Lambda Zap Xylem library Pinus t... 32 3.4
 emb|AL157415|LMFL8325 *Leishmania major* Friedlin chromosome 5 cos... 32 3.4
 emb|AQ935443|AQ935443 CpG2473A CpIOWAgDNA1 *Cryptosporidium parvu...* 32 3.4
 emb|AW686346|AW686346 NF040F08NR1F1000 Nodulated root *Medicago t...* 32 3.4
 10 emb|AW687188|AW687188 NF006H09RT1F1079 Developing root *Medicago ...* 32 3.4
 emb|AW684973|AW684973 NF023G04NR1F1000 Nodulated root *Medicago t...* 32 3.4
 emb|AQ851040|AQ851040 LMAJFV1_lm43g10.x1 *Leishmania major* FV1 ra... 32 3.4
 emb|AW687098|AW687098 NF006A02RT1F1007 Developing root *Medicago ...* 32 3.4
 emb|AQ855101|AQ855101 CpG1965B CpIOWAgDNA1 *Cryptosporidium parvu...* 32 3.4
 15 emb|Y08937|CRNII *Chlamydomonas reinhardtii* mRNA for nitrite red... 32 3.4
 gb|C96140|C96140 C96140 *Marchantia polymorpha* immature sex organ... 32 4.7
 emb|AI162427|AI162427 A017P38U Hybrid aspen plasmid library Popu... 31 6.5
 emb|Z98549|PFSC03014 *Plasmodium falciparum* DNA *** SEQUENCING IN... 31 6.5
 emb|AC013353|AC013353 *Trypanosoma brucei* chromosome VI clone RPC... 31 6.5
 20 emb|AC013484|AC013484 *Trypanosoma brucei* chromosome IX clone RPC... 31 6.5
 emb|AC009463|AC009463 *Trypanosoma brucei* chromosome II clone RPC... 31 6.5
 emb|AW696295|AW696295 NF105E11ST1F1086 Developing stem *Medicago ...* 31 6.5
 emb|AI213146|AI213146 y8b01a1.rl *Aspergillus nidulans* 24hr asexu... 31 6.5
 emb|AC009259|AC009259 *Trypanosoma brucei* chromosome VI clone RPC... 31 6.5
 25 emb|AC007863|AC007863 *Trypanosoma brucei* chromosome VI clone RPC... 31 6.5
 emb|AV418253|AV418253 AV418253 *Lotus japonicus* young plants (two... 31 6.5
 emb|A85864|A85864 Sequence 523 from Patent EP0866129. 31 6.5
 emb|Z98547|PFMAL3P3 *Plasmodium falciparum* MAL3P3, complete seque... 31 6.5
 gb|BE056773|BE056773 894011F02.y1 *C. reinhardtii* CC-1690, normal... 31 6.5
 30 emb|AQ945249|AQ945249 Sheared DNA-54D15.TR Sheared DNA *Trypanoso...* 31 6.5
 emb|AC008368|AC008368 *Trypanosoma brucei* chromosome II clone RPC... 31 6.5
 emb|AF226997|AF226997 *Cladosporium fulvum* methionine synthase ge... 31 8.9
 emb|AW687565|AW687565 NF011A04RT1F1024 Developing root *Medicago ...* 31 8.9
 emb|AF186185|AF186185 Glycine max retrovirus-like element Calyps... 31 8.9
 35 emb|AW569976|AW569976 si85a11.y1 Gm-cl031 Glycine max cDNA clone... 31 8.9
 emb|AI441553|AI441553 sa67c12.y1 Gm-cl004 Glycine max cDNA clone... 31 8.9
 emb|AI759235|AI759235 EtESTea26d12.y1 *Eimeria* S5-2 Sporozoite st... 27 9.6

Query= X98321.2_i_at 19594_i_at /id_source genbank /description
 40 emb|caa66965.1| (x98321) peroxidase [*arabidopsis thaliana*]
 /blast_score 1.00e-174 /ec_number /family peroxidase /chip nova
 /gb_link [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x98321|/ncgi)
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|x98321|/ncgi
 http://www.ncgr.org/cgi-bin/ff?x98321
 45 (1212 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

50 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

- 55 gb|U51191|GMU51191 Glycine max peroxidase precursor (sEPa1) mRNA... 388 e-129
 gb|U51192|GMU51192 Glycine max peroxidase precursor (sEPa2) mRNA... 385 e-128
 gb|L13653|TOMTPX2A *Lycopersicon esculentum* peroxidase (TPX2) mRN... 326 e-122
 gb|L13654|TOMTPX1A *Lycopersicon esculentum* peroxidase (TPX1) mRN... 204 e-118
 emb|Y16776|SOY16776 *Spinacia oleracea* mRNA for peroxidase, prx10... 210 e-113
 60 emb|Z22920|SPPEROXDS *S. polyrrhiza* mRNA for peroxidase. 183 5e-90
 emb|AI495190|AI495190 sa89c07.y1 Gm-cl004 Glycine max cDNA clone... 325 6e-88

- emb|AW219258|AW219258 EST301740 tomato root during/after fruit s... 212 5e-85
emb|AW621449|AW621449 EST312247 tomato root during/after fruit s... 212 7e-85
emb|AW625780|AW625780 EST319687 tomato radicle, 5 d post-imbibit... 211 1e-84
emb|AW622057|AW622057 EST312855 tomato root during/after fruit s... 182 2e-83
5 emb|AW329363|AW329363 N200592e rootphos(-) Medicago truncatula c... 307 1e-82
emb|AW647641|AW647641 EST307119 tomato germinating seedlings, TA... 190 9e-82
emb|AW625441|AW625441 EST319348 tomato radicle, 5 d post-imbibit... 187 7e-80
emb|AW621198|AW621198 EST311996 tomato root during/after fruit s... 206 9e-80
emb|AW704698|AW704698 sk39d06.y1 Gm-cl028 Glycine max cDNA clone... 297 1e-79
10 emb|AW219160|AW219160 EST301642 tomato root during/after fruit s... 190 2e-79
emb|AW622012|AW622012 EST312810 tomato root during/after fruit s... 205 2e-79
emb|AW622593|AW622593 EST313393 tomato root during/after fruit s... 188 1e-77
emb|AW626302|AW626302 EST320209 tomato radicle, 5 d post-imbibit... 205 1e-77
emb|AW621202|AW621202 EST312000 tomato root during/after fruit s... 187 3e-77
15 emb|AW220017|AW220017 EST302500 tomato root during/after fruit s... 197 7e-77
emb|AB024437|AB024437 Scutellaria baicalensis mRNA for peroxidase... 212 6e-76
emb|AW622066|AW622066 EST312864 tomato root during/after fruit s... 211 6e-76
emb|AF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 196 6e-76
emb|AW625860|AW625860 EST319767 tomato radicle, 5 d post-imbibit... 181 2e-75
20 emb|AI771103|AI771103 EST252203 tomato ovary, TAMU Lycopersicon ... 190 8e-75
emb|AW218917|AW218917 EST301399 tomato root during/after fruit s... 180 2e-74
emb|AW831524|AW831524 sm27c05.y1 Gm-cl028 Glycine max cDNA clone... 279 3e-74
emb|AW220442|AW220442 EST302925 tomato root during/after fruit s... 192 9e-73
gb|BE020787|BE020787 sm52h01.y1 Gm-cl028 Glycine max cDNA clone ... 274 1e-72
25 emb|AW649146|AW649146 EST327600 tomato germinating seedlings, TA... 178 3e-71
emb|AW219955|AW219955 EST302438 tomato root during/after fruit s... 178 3e-71
gb|BE020269|BE020269 sm42f09.y1 Gm-cl028 Glycine max cDNA clone ... 165 3e-71
emb|AW219743|AW219743 EST302225 tomato root during/after fruit s... 173 9e-70
emb|AW218390|AW218390 EST303573 tomato radicle, 5 d post-imbibit... 191 8e-69
30 gb|BE020135|BE020135 sm41f03.y1 Gm-cl028 Glycine max cDNA clone ... 184 1e-68
emb|AI895098|AI895098 EST264541 tomato callus, TAMU Lycopersicon... 169 2e-68
emb|AW219511|AW219511 EST301909 tomato root during/after fruit s... 193 6e-68
emb|AW154826|AW154826 EST290219 tomato root deficiency, Cornell ... 154 1e-67
gb|L36112|SSNPEROXIC Stylosanthes humilis peroxidase mRNA. 105 8e-67
35 emb|AW625509|AW625509 EST319416 tomato radicle, 5 d post-imbibit... 167 2e-65
dbj|D42065|TOBCPI40KB Tobacco mRNA for cationic peroxidase isozy... 122 3e-65
gb|U51193|GMU51193 Glycine max peroxidase (sEPb1) mRNA, partial ... 95 5e-65
dbj|D42064|TOBCPI38KA Tobacco mRNA for cationic peroxidase isozy... 119 6e-65
gb|U51194|GMU51194 Glycine max peroxidase (sEPb2) mRNA, partial ... 100 6e-65
40 emb|AW621545|AW621545 EST312343 tomato root during/after fruit s... 166 8e-65
emb|AW704193|AW704193 sk17a09.y1 Gm-cl028 Glycine max cDNA clone... 244 8e-64
gb|M37637|ARCPNC2 A.hypogaea cationic peroxidase mRNA, complete ... 100 2e-63
emb|X90694|MSRNAPE1C M.sativa mRNA for peroxidase 1C. 164 3e-63
emb|AW621842|AW621842 EST312640 tomato root during/after fruit s... 151 4e-63
45 emb|X94943|LECEVI16G L.esculentum mRNA for peroxidase. 104 4e-63
emb|AI487546|AI487546 EST245868 tomato ovary, TAMU Lycopersicon ... 150 5e-63
emb|AW625242|AW625242 EST319245 tomato radicle, 5 d post-imbibit... 149 9e-63
emb|AF149279|AF149279 Phaseolus vulgaris peroxidase 4 precursor ... 100 2e-62
emb|AW621971|AW621971 EST312769 tomato root during/after fruit s... 147 6e-62
50 emb|AW218589|AW218589 EST303772 tomato radicle, 5 d post-imbibit... 147 6e-62
emb|AW621728|AW621728 EST312526 tomato root during/after fruit s... 136 8e-62
gb|L36157|ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple... 151 2e-61
emb|AW569722|AW569722 si79f03.y1 Gm-cl031 Glycine max cDNA clone... 160 2e-61
emb|AW649624|AW649624 EST328078 tomato germinating seedlings, TA... 145 2e-61
55 emb|AW621885|AW621885 EST312683 tomato root during/after fruit s... 145 2e-61
gb|J02979|TOBPXDLF Nicotiana tabacum lignin-forming peroxidase m... 235 6e-61
emb|AW625097|AW625097 EST313914 tomato radicle, 5 d post-imbibit... 143 8e-61
emb|AB027753|AB027753 Nicotiana tabacum mRNA for peroxidase, com... 105 1e-60
emb|Y16778|SPY16778 Spinacia oleracea mRNA for peroxidase, prx11... 109 3e-60
60 emb|X71593|LECEVI1A L.esculentum CEVI-1 mRNA. 174 4e-60
emb|X90693|MSRNAPE1B M.sativa mRNA for peroxidase 1B. 153 6e-60

- gb|BE057477|BE057477 sm58f06.y1 Gm-cl028 Glycine max cDNA clone ... 231 6e-60
 emb|X90692|MSRNAPE1A M.sativa mRNA for peroxidase 1A. 149 9e-60
 emb|AW666051|AW666051 sk31e03.y1 Gm-cl028 Glycine max cDNA clone... 154 3e-59
 emb|AW219008|AW219008 EST301490 tomato root during/after fruit s... 149 2e-58
 5 gb|L36111|SSNPEROXIB Stylosanthes humilis peroxidase mRNA. 161 2e-58
 emb|AW351229|AW351229 GM210011A10H11R Gm-r1021 Glycine max cDNA ... 149 2e-58
 emb|AF149277|AF149277 Phaseolus vulgaris peroxidase 1 precursor ... 151 3e-58
 emb|AW666205|AW666205 sk33f10.y1 Gm-cl028 Glycine max cDNA clone... 199 3e-58
 10 emb|X56011|TAPERO Wheat mRNA for peroxidase. 146 6e-58
 emb|AW132575|AW132575 se05h10.y1 Gm-cl013 Glycine max cDNA clone... 102 7e-58
 emb|AJ242742|IBA242742 Ipomoea batatas mRNA for peroxidase (pod ... 154 1e-57
 emb|AW218512|AW218512 EST303695 tomato radicle, 5 d post-imbibit... 124 4e-57
 emb|AF007211|AF007211 Glycine max peroxidase precursor (GMIPER1)... 157 6e-57
 15 emb|AB024438|AB024438 Scutellaria baicalensis mRNA for peroxidase... 141 6e-57
 emb|AJ250121|PAB250121 Picea abies mRNA for SPI2 protein (spi2 g... 109 8e-57
 emb|AW559660|AW559660 EST314772 DSIR Medicago truncatula cDNA cl... 154 1e-56
 emb|AW774581|AW774581 EST333732 KV3 Medicago truncatula cDNA clo... 154 1e-56
 emb|AW775762|AW775762 EST334827 DSIL Medicago truncatula cDNA cl... 154 1e-56
 20 emb|AW981426|AW981426 EST392579 DSIL Medicago truncatula cDNA cl... 154 1e-56
 emb|AF244924|AF244924 Spinacia oleracea peroxidase prx15 precurs... 171 2e-56
 emb|Y10467|SOPRXXR6 S.oleracea mRNA for peroxidase, clone PC23. 151 4e-56
 emb|AW035958|AW035958 EST282817 tomato callus, TAMU Lycopersicon... 106 3e-55
 emb|X91232|MARNAPRX M.annua mRNA for peroxidase. 163 4e-55
 25 emb|AW625144|AW625144 EST319051 tomato radicle, 5 d post-imbibit... 123 8e-55
 emb|AF049881|AF049881 Linum usitatissimum peroxidase FLXPER4 (PE... 146 1e-54
 gb|L36158|ALFPXDD Medicago sativa peroxidase (pxdD) mRNA, 3' end. 136 1e-54
 emb|AW441632|AW441632 EST311028 tomato fruit red ripe, TAMU Lyco... 165 2e-54
 emb|Y10468|SOPRXXR7 S.oleracea mRNA for peroxidase, clone PC36. 96 2e-54
 30 emb|AB042103|AB042103 Asparagus officinalis AspPOX1 mRNA for per... 158 2e-54
 emb|AW218519|AW218519 EST303702 tomato radicle, 5 d post-imbibit... 122 2e-54
 emb|AW622418|AW622418 EST313205 tomato root during/after fruit s... 122 2e-54
 emb|AF149280|AF149280 Phaseolus vulgaris peroxidase 5 precursor ... 141 3e-54
 35
 Query= AC004561.78_at 19640_at /id_source genbank /description
 gb|aac95192.1| (ac004561) putative glutathione s-transferase
 [arabidopsis thaliana] /blast_score 1.00e-118 /ec_number /family
 transferase /chip nova /gb_link
 40 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004561|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004561|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004561|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac004561>
 (675 letters)
 45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
 Searching.....done
 50 Score E
 Sequences producing significant alignments: (bits) Value
 emb|AW624985|AW624985 EST313814 tomato radicle, 5 d post-imbibit... 73 1e-42
 emb|AW041029|AW041029 EST283893 tomato mixed elicitor, BTI Lycop... 110 7e-41
 55 emb|AW728749|AW728749 GA_Ea0028D12 Gossypium arboreum 7-10 dpa ... 112 5e-40
 emb|AW622625|AW622625 EST313425 tomato root during/after fruit s... 73 6e-40
 emb|AW267974|AW267974 EST306196 DSIR Medicago truncatula cDNA cl... 115 1e-39
 emb|AW224728|AW224728 EST303171 tomato root, plants pre-anthesis... 88 1e-37
 emb|AW597347|AW597347 si91f07.y1 Gm-cl031 Glycine max cDNA clone... 92 2e-36
 60 emb|AW186185|AW186185 se64f07.y1 Gm-cl019 Glycine max cDNA clone... 112 3e-36
 emb|AW760657|AW760657 sl53c04.y1 Gm-cl027 Glycine max cDNA clone... 89 2e-35

	gb BE021138 BE021138 sm55h05.yl Gm-cl028 Glycine max cDNA clone ...	89 2e-35
	gb BE021010 BE021010 sm54f05.yl Gm-cl028 Glycine max cDNA clone ...	89 2e-35
	emb AW569900 AW569900 si83a10.yl Gm-cl031 Glycine max cDNA clone...	89 2e-35
	emb AW423852 AW423852 sh52g05.yl Gm-cl017 Glycine max cDNA clone...	86 4e-35
5	gb U20809 VRU20809 Vigna radiata clone MII-4 auxin-induced prote...	75 4e-35
	emb AW234458 AW234458 sf25d08.yl Gm-cl028 Glycine max cDNA clone...	89 5e-35
	emb AV422068 AV422068 AV422068 Lotus japonicus young plants (two...	93 1e-34
	emb AV422051 AV422051 AV422051 Lotus japonicus young plants (two...	93 1e-34
	emb AW234826 AW234826 sf19f07.yl Gm-cl028 Glycine max cDNA clone...	89 2e-34
10	gb BE057428 BE057428 sm58a10.yl Gm-cl028 Glycine max cDNA clone ...	89 2e-34
	emb X56264 NTAUX110 N.tabacum auxin-induced mRNA (pCNT110).	82 7e-34
	emb AW761562 AW761562 sl69c11.yl Gm-cl027 Glycine max cDNA clone...	89 7e-34
	emb AW704357 AW704357 sk18c09.yl Gm-cl028 Glycine max cDNA clone...	82 7e-34
	gb BE020410 BE020410 sm43h07.yl Gm-cl028 Glycine max cDNA clone ...	85 9e-34
15	emb AW234420 AW234420 sf25a01.yl Gm-cl028 Glycine max cDNA clone...	89 9e-34
	emb X56265 NTAUX111 N.tabacum auxin-induced mRNA (pCNT111).	83 2e-33
	emb X56263 NTAUX103 N.tabacum auxin-induced mRNA (pCNT103).	79 2e-33
	emb AV417399 AV417399 AV417399 Lotus japonicus young plants (two...	89 2e-33
	emb AW569893 AW569893 si82h12.yl Gm-cl031 Glycine max cDNA clone...	93 3e-33
20	emb AW981250 AW981250 EST392403 DSIL Medicago truncatula cDNA cl...	84 4e-33
	gb BE057291 BE057291 sn01b03.yl Gm-cl015 Glycine max cDNA clone ...	89 1e-32
	emb AW560886 AW560886 EST315934 DSIR Medicago truncatula cDNA cl...	84 4e-32
	emb AV427433 AV427433 AV427433 Lotus japonicus young plants (two...	84 4e-32
	emb AW626046 AW626046 EST319953 tomato radicle, 5 d post-imbibit...	88 7e-32
25	emb AW776845 AW776845 EST335910 DSIL Medicago truncatula cDNA cl...	84 2e-31
	emb AW776620 AW776620 EST335685 DSIL Medicago truncatula cDNA cl...	79 2e-31
	emb AV422089 AV422089 AV422089 Lotus japonicus young plants (two...	115 3e-31
	emb AW234602 AW234602 sf17b10.yl Gm-cl028 Glycine max cDNA clone...	85 4e-31
	emb AW278309 AW278309 sf42d10.yl Gm-cl009 Glycine max cDNA clone...	85 5e-31
30	emb AW684397 AW684397 NF016E02NR1F1000 Nodulated root Medicago t...	84 6e-31
	emb AW234437 AW234437 sf25b07.yl Gm-cl028 Glycine max cDNA clone...	82 8e-31
	emb AW307015 AW307015 sf51g02.yl Gm-cl009 Glycine max cDNA clone...	82 2e-30
	emb AW306150 AW306150 se46e07.yl Gm-cl017 Glycine max cDNA clone...	85 7e-30
	emb AW397802 AW397802 sg68e08.yl Gm-cl007 Glycine max cDNA clone...	81 1e-29
35	emb AW234580 AW234580 sf15h12.yl Gm-cl028 Glycine max cDNA clone...	81 2e-29
	emb AW690032 AW690032 NF027E09ST1F1000 Developing stem Medicago ...	79 2e-29
	emb AW569497 AW569497 si87h06.yl Gm-cl031 Glycine max cDNA clone...	83 3e-29
	gb M20363 SOYHSP Soybean heat-shock protein (Gmhsp26-A) gene, co...	90 3e-29
	emb AW350224 AW350224 GM210007B10H2R Gm-r1021 Glycine max cDNA 3...	107 3e-29
40	emb AF239928 AF239928 Euphorbia esula glutathione S-transferase ...	84 4e-29
	emb AW907271 AW907271 EST343394 potato stolon, Cornell Universit...	81 5e-29
	emb AW980323 AW980323 EST391476 GVN Medicago truncatula cDNA clo...	84 6e-29
	emb AW569022 AW569022 si74e07.yl Gm-cl031 Glycine max cDNA clone...	85 7e-29
45	emb AW218869 AW218869 EST301351 tomato root during/after fruit s...	62 8e-29
	emb AW224727 AW224727 EST303170 tomato root, plants pre-anthesis...	77 1e-28
	emb AW394813 AW394813 sh35f08.yl Gm-cl017 Glycine max cDNA clone...	81 1e-28
	emb AW233937 AW233937 sf32c05.yl Gm-cl028 Glycine max cDNA clone...	92 2e-28
	emb AJ441991 AJ441991 sa82g05.yl Gm-cl004 Glycine max cDNA clone...	99 2e-28
50	emb AJ010448 AMY010448 Alopecurus myosuroides mRNA for glutathio...	63 2e-28
	emb AJ010449 AMY010449 Alopecurus myosuroides mRNA for glutathio...	64 2e-28
	emb AW687500 AW687500 NF010C06RT1F1049 Developing root Medicago ...	84 3e-28
	emb AB027501 AB027501 Daucus carota Dcarg-1 mRNA, complete cds.	62 4e-28
	emb AW684848 AW684848 NF022C03NR1F1000 Nodulated root Medicago t...	84 4e-28
55	emb AW684915 AW684915 NF023A04NR1F1000 Nodulated root Medicago t...	75 4e-28
	emb AW830445 AW830445 sm27a05.yl Gm-cl028 Glycine max cDNA clone...	89 5e-28
	gb BE020437 BE020437 sm40g05.yl Gm-cl028 Glycine max cDNA clone ...	89 5e-28
	emb AW677374 AW677374 DG1_6_A02.b1_A002 Dark Grown 1 (DG1) Sorgh...	66 8e-28
	emb AW040981 AW040981 EST283845 tomato mixed elicitor, BTI Lycop...	88 9e-28
60	emb AW759593 AW759593 sl45c12.yl Gm-cl027 Glycine max cDNA clone...	87 2e-27
	gb BE124079 BE124079 EST394204 DSIL Medicago truncatula cDNA clo...	75 3e-27

emb|X56268|NTAUX1 N.tabacum gene for an auxin-induced protein (p... 79 4e-27
 emb|AW687359|AW687359 NF008G06RT1F1051 Developing root Medicago ... 84 4e-27
 emb|AW625637|AW625637 EST319544 tomato radicle, 5 d post-imbibit... 60 7e-27
 emb|AW685686|AW685686 NF033F09NR1F1000 Nodulated root Medicago t... 72 8e-27
 5 emb|AI778504|AI778504 EST259383 tomato susceptible, Cornell Lyco... 72 1e-26
 emb|AW508224|AW508224 si51d09.y1 Gm-r1030 Glycine max cDNA clone... 86 1e-26
 emb|AI776426|AI776426 EST257526 tomato resistant, Cornell Lycop... 77 2e-26
 emb|X56269|NTAUX35 N.tabacum gene for an auxin-induced protein (... 82 3e-26
 gb|BE124113|BE124113 EST394238 DSIL Medicago truncatula cDNA clo... 75 3e-26
 10 emb|AW774063|AW774063 EST333293 KV3 Medicago truncatula cDNA clo... 79 4e-26
 emb|AW775514|AW775514 EST334579 DSIL Medicago truncatula cDNA cl... 72 6e-26
 emb|AW685579|AW685579 NF029C01NR1F1000 Nodulated root Medicago t... 72 6e-26
 emb|AW693566|AW693566 NF067F08ST1F1074 Developing stem Medicago ... 72 6e-26
 emb|AW776395|AW776395 EST335460 DSIL Medicago truncatula cDNA cl... 72 6e-26
 15 emb|AW775759|AW775759 EST334824 DSIL Medicago truncatula cDNA cl... 72 6e-26
 emb|AW775247|AW775247 EST331969 GVN Medicago truncatula cDNA clo... 72 6e-26
 emb|AW684399|AW684399 NF016E04NR1F1000 Nodulated root Medicago t... 72 6e-26
 emb|AW559724|AW559724 EST314716 DSIR Medicago truncatula cDNA cl... 72 6e-26
 emb|AW776111|AW776111 EST335176 DSIL Medicago truncatula cDNA cl... 72 6e-26
 20 emb|AW775816|AW775816 EST334881 DSIL Medicago truncatula cDNA cl... 72 6e-26
 emb|AW684443|AW684443 NF017A06NR1F1000 Nodulated root Medicago t... 72 6e-26
 emb|AW573792|AW573792 EST316383 GVN Medicago truncatula cDNA clo... 72 6e-26
 emb|AI778968|AI778968 EST259847 tomato susceptible, Cornell Lyco... 78 1e-25
 emb|AW031747|AW031747 EST275201 tomato callus, TAMU Lycopersicon... 78 1e-25
 25 emb|AW127655|AW127655 M110397 DSLC Medicago truncatula cDNA clon... 84 1e-25
 emb|AW559360|AW559360 EST314408 DSIR Medicago truncatula cDNA cl... 72 2e-25
 emb|AJ010450|AMY010450 Alopeurus myosuroides mRNA for glutathio... 61 3e-25
 emb|AI777263|AI777263 EST258228 tomato resistant, Cornell Lycop... 75 5e-25
 emb|AW685702|AW685702 NF033B01NR1F1000 Nodulated root Medicago t... 77 5e-25
 30 emb|AW443955|AW443955 EST308885 tomato mixed elicitor, BTI Lycop... 75 5e-25
 emb|AW040833|AW040833 EST283697 tomato mixed elicitor, BTI Lycop... 75 5e-25

35 Query= AL050351.172_at 19664_at /id_source genbank /description
 "emb|cab43638.1| (al050351) nad(p)h oxidoreductase, isoflavone
 reductase-like protein [arabidopsis thaliana]" /blast_score 1.00e-177
 /ec_number /family reductase /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al050351|/ncgi
 40 http://www.ncgr.org/cgi-bin/ff?al050351
 (927 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

45 Searching.....done

	Score	E	(bits)	Value
Sequences producing significant alignments:				
50 emb AF071477 AF071477 Pyrus communis isoflavone reductase relate...	583	e-166		
emb AF202184 AF202184 Glycine max isoflavone reductase homolog 2...	581	e-165		
emb X92075 STISORED H S.tuberosum mRNA for isoflavone reductase h...	542	e-153		
emb AF135127 AF135127 Betula pendula isoflavone reductase homolo...	534	e-151		
55 emb AF242491 AF242491 Forsythia x intermedia clone 1 phenylcouma...	527	e-149		
emb AF242492 AF242492 Forsythia x intermedia clone 2 phenylcouma...	512	e-144		
emb AJ005806 PTR5806 Populus trichocarpa mRNA for phenylcoumaran...	497	e-140		
emb AJ005805 PTR5805 Populus trichocarpa mRNA for phenylcoumaran...	497	e-140		
emb AJ005804 PTR5804 Populus trichocarpa mRNA for phenylcoumaran...	497	e-140		
60 emb AJ005803 PTR5803 Populus trichocarpa mRNA for phenylcoumaran...	495	e-139		
emb AF201458 AF201458 Medicago sativa isoflavone reductase-like ...	294	e-136		

	dbj D28505 TOBA622A Tobacco mRNA for A622, complete cds.	462 e-129
	emb AF242498 AF242498 Tsuga heterophylla clone 6 phenylcoumaran ...	417 e-124
	emb AF202183 AF202183 Glycine max isoflavone reductase homolog 1...	403 e-124
	emb AF242497 AF242497 Tsuga heterophylla clone 5 phenylcoumaran ...	416 e-123
5	emb AW164323 AW164323 se71a03.y1 Gm-c1023 Glycine max cDNA clone...	426 e-118
	emb AF242494 AF242494 Tsuga heterophylla clone 2 phenylcoumaran ...	363 e-117
	emb AF242495 AF242495 Tsuga heterophylla clone 3 phenylcoumaran ...	363 e-117
	emb AI960922 AI960922 sc92f06.y1 Gm-c1019 Glycine max cDNA clone...	420 e-117
	emb AW560052 AW560052 EST315100 DSIR Medicago truncatula cDNA cl...	369 e-114
10	emb AW560051 AW560051 EST315099 DSIR Medicago truncatula cDNA cl...	410 e-113
	emb AI960719 AI960719 sc89e03.y1 Gm-c1019 Glycine max cDNA clone...	396 e-109
	emb AF242490 AF242490 Pinus taeda phenylcoumaran benzylic ether ...	358 e-106
	emb AF081678 AF081678 Pinus taeda phenylcoumaran benzylic ether ...	358 e-106
	emb AF242496 AF242496 Tsuga heterophylla clone 4 phenylcoumaran ...	356 e-105
15	emb AF242493 AF242493 Tsuga heterophylla clone 1 phenylcoumaran ...	356 e-105
	emb AF242499 AF242499 Tsuga heterophylla clone 7 phenylcoumaran ...	345 e-102
	emb X58078 MSISREDMR M.sativa mRNA for isoflavone reductase.	308 e-100
	emb AJ003245 GMAJ3245 Glycine max mRNA for putative NADPH:isofla...	311 2e-99
	emb AW306732 AW306732 sf47f07.y1 Gm-c1009 Glycine max cDNA clone...	222 2e-99
20	gb S72472 S72472 isoflavone reductase [Pisum sativum=peas, seedl...	300 2e-98
	emb AW277911 AW277911 sf89a12.y1 Gm-c1019 Glycine max cDNA clone...	357 7e-98
	emb AW423683 AW423683 sh50d08.y1 Gm-c1017 Glycine max cDNA clone...	258 2e-96
	emb AW560880 AW560880 EST315928 DSIR Medicago truncatula cDNA cl...	335 3e-91
	emb X60755 CANADPHIO C.arietinum mRNA for NADPH:isoflavone oxido...	302 2e-90
25	emb AW308968 AW308968 sf92d11.y1 Gm-c1019 Glycine max cDNA clone...	331 5e-90
	gb BE020712 BE020712 sm52a04.y1 Gm-c1028 Glycine max cDNA clone ...	191 2e-88
	emb AW508698 AW508698 si35d01.y1 Gm-r1030 Glycine max cDNA clone...	321 4e-87
	emb AI897693 AI897693 EST267136 tomato ovary, TAMU Lycopersicon ...	320 8e-87
	gb BE022340 BE022340 sm73f05.y1 Gm-c1028 Glycine max cDNA clone ...	289 3e-86
30	emb AI167005 AI167005 xylem.est.781 Poplar xylem Lambda ZAPII li...	317 7e-86
	emb AW980520 AW980520 EST391673 GVN Medicago truncatula cDNA clo...	316 2e-85
	emb AW568970 AW568970 si73g05.y1 Gm-c1031 Glycine max cDNA clone...	264 5e-85
	emb AW100852 AW100852 sd62c02.y1 Gm-c1008 Glycine max cDNA clone...	310 8e-84
	emb AW736641 AW736641 EST333133 KV3 Medicago truncatula cDNA clo...	308 3e-83
35	emb AW980642 AW980642 EST391795 GVN Medicago truncatula cDNA clo...	308 6e-83
	emb AW234069 AW234069 sf33h03.y1 Gm-c1028 Glycine max cDNA clone...	291 7e-78
	emb AI812729 AI812729 18D5 Pine Lambda Zap Xylem library Pinus t...	291 7e-78
	emb AW687040 AW687040 NF005C11RT1F1085 Developing root Medicago ...	259 2e-77
	emb AI901007 AI901007 sc18c12.y1 Gm-c1013 Glycine max cDNA clone...	288 3e-77
40	emb AW706449 AW706449 sj58e10.y1 Gm-c1033 Glycine max cDNA clone...	280 4e-77
	emb AF242506 AF242506 Thuja plicata clone 4 pinoresinol-laricire...	166 4e-77
	emb AI899794 AI899794 sb92g12.y1 Gm-c1017 Glycine max cDNA clone...	286 1e-76
	emb AW278000 AW278000 sf89e04.y1 Gm-c1019 Glycine max cDNA clone...	286 2e-76
	emb AW348609 AW348609 GM210002B22F12R Gm-r1021 Glycine max cDNA ...	263 5e-76
45	emb AF242504 AF242504 Thuja plicata clone 2 pinoresinol-laricire...	160 7e-76
	emb AF242503 AF242503 Thuja plicata clone 1 pinoresinol-laricire...	120 7e-76
	emb AW623613 AW623613 EST321558 tomato flower buds 3-8 mm, Corne...	199 3e-75
	emb AW164589 AW164589 se73h03.y1 Gm-c1023 Glycine max cDNA clone...	281 6e-75
	emb AW719567 AW719567 LjNEST6f2r Lotus japonicus nodule library,...	281 8e-75
50	emb AI726822 AI726822 BNLGHi6647 Six-day Cotton fiber Gossypium ...	279 2e-74
	emb AW695822 AW695822 NF099E10ST1F1082 Developing stem Medicago ...	203 3e-74
	emb AI812838 AI812838 19H8 Pine Lambda Zap Xylem library Pinus t...	243 9e-73
	emb AI730069 AI730069 BNLGHi6078 Six-day Cotton fiber Gossypium ...	273 1e-72
	emb AW277687 AW277687 sf85c09.y1 Gm-c1019 Glycine max cDNA clone...	270 2e-72
55	emb AF242505 AF242505 Thuja plicata clone 3 pinoresinol-laricire...	112 2e-72
	emb AF242500 AF242500 Thuja plicata phenylcoumaran benzylic ethe...	112 2e-72
	emb AW559440 AW559440 EST314488 DSIR Medicago truncatula cDNA cl...	269 3e-72
	emb AF242501 AF242501 Tsuga heterophylla clone 1 pinoresinol-lar...	171 6e-72
	emb AW278307 AW278307 sf42d08.y1 Gm-c1009 Glycine max cDNA clone...	271 6e-72
60	emb AF242502 AF242502 Tsuga heterophylla clone 2 pinoresinol-lar...	171 8e-72
	emb AW687008 AW687008 NF004H12RT1F1103 Developing root Medicago ...	255 1e-71

emb|AW310288|AW310288 sf33h03.x1 Gm-c1028 Glycine max cDNA clone... 263 2e-71
 gb|U81158|FXU81158 Forsythia x intermedia (+)-pinoresinol/(+)-la... 166 1e-70
 emb|AI488036|AI488036 EST246358 tomato ovary, TAMU Lycopersicon ... 265 4e-70
 emb|AW685137|AW685137 NF025H12NR1F1000 Nodulated root Medicago t... 262 2e-69
 5 emb|Y12689|CPRLP C.paradisi mRNA isoflavone reductase-like prot... 123 1e-68
 emb|AI485705|AI485705 EST244026 tomato ovary, TAMU Lycopersicon ... 253 4e-68
 emb|AW348311|AW348311 GM210001B23E3R Gm-r1021 Glycine max cDNA 3... 257 8e-68
 gb|BE020979|BE020979 sm54c03.y1 Gm-c1028 Glycine max cDNA clone ... 257 8e-68
 emb|AI162702|AI162702 A022P17U Hybrid aspen plasmid library Popu... 231 3e-66
 10 emb|AW774032|AW774032 EST333018 KV3 Medicago truncatula cDNA clo... 226 3e-66
 emb|AW775908|AW775908 EST334973 DSIL Medicago truncatula cDNA cl... 226 2e-65
 emb|AW684683|AW684683 NF019G01NR1F1000 Nodulated root Medicago t... 249 2e-65
 gb|U48590|LAU48590 Lupinus albus isoflavone reductase-like prote... 151 2e-65
 emb|AW038676|AW038676 EST280537 tomato mixed elicitor, BTI Lycop... 197 2e-65
 15 emb|AI443821|AI443821 sa30d07.y1 Gm-c1004 Glycine max cDNA clone... 248 3e-65
 emb|AW773814|AW773814 EST332800 KV3 Medicago truncatula cDNA clo... 223 4e-65
 emb|AI162699|AI162699 A022P13U Hybrid aspen plasmid library Popu... 243 4e-65
 emb|AI437725|AI437725 sa38g09.y1 Gm-c1004 Glycine max cDNA clone... 221 8e-65
 emb|AW985148|AW985148 NXNV_133_E11_F Nsf Xylem Normal wood Verti... 227 3e-64
 20 emb|AW696352|AW696352 NF107B01ST1F1011 Developing stem Medicago ... 216 7e-64
 emb|AJ132262|PBA132262 Populus balsamifera subsp. trichocarpa pc... 141 7e-64
 emb|AW736640|AW736640 EST333132 KV3 Medicago truncatula cDNA clo... 243 1e-63
 emb|AW278044|AW278044 sf89h09.y1 Gm-c1019 Glycine max cDNA clone... 242 3e-63
 emb|AW928288|AW928288 G200003e KV0 Medicago truncatula cDNA clon... 206 2e-62
 25 emb|AW776834|AW776834 EST335899 DSIL Medicago truncatula cDNA cl... 214 2e-62
 emb|AW775218|AW775218 EST331940 GVN Medicago truncatula cDNA clo... 214 2e-62
 emb|AW289885|AW289885 NXNV007E10F Nsf Xylem Normal wood Vertical... 238 4e-62
 emb|AI496272|AI496272 sb01f07.y1 Gm-c1004 Glycine max cDNA clone... 236 2e-61

30

Query= AC005687.19_at 19672_at /id_source genbank /description
 gb|aac36019.1| (ac005687) rap2.6 [arabidopsis thaliana] /blast_score
 1.00e-105 /ec_number /family /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005687|/ncgi)
 35 [post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005687|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005687|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac005687>
 (734 letters)

Database: plantfungal
 40 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 45 Sequences producing significant alignments: (bits) Value

emb|AI488999|AI488999 EST247338 tomato ovary, TAMU Lycopersicon ... 123 2e-27
 emb|AI483510|AI483510 EST249359 tomato ovary, TAMU Lycopersicon ... 122 2e-27
 emb|AI489709|AI489709 EST248048 tomato ovary, TAMU Lycopersicon ... 122 3e-27
 50 emb|AI771834|AI771834 EST252934 tomato ovary, TAMU Lycopersicon ... 122 4e-27
 emb|AI771755|AI771755 EST252855 tomato ovary, TAMU Lycopersicon ... 122 4e-27
 emb|AI490296|AI490296 EST248622 tomato ovary, TAMU Lycopersicon ... 122 4e-27
 emb|AI486929|AI486929 EST245251 tomato ovary, TAMU Lycopersicon ... 122 4e-27
 emb|AI899397|AI899397 EST268840 tomato ovary, TAMU Lycopersicon ... 122 4e-27
 55 emb|AI897787|AI897787 EST267230 tomato ovary, TAMU Lycopersicon ... 122 4e-27
 emb|AI483636|AI483636 EST249507 tomato ovary, TAMU Lycopersicon ... 122 4e-27
 emb|AI485460|AI485460 EST243781 tomato ovary, TAMU Lycopersicon ... 122 4e-27
 emb|AI771795|AI771795 EST252895 tomato ovary, TAMU Lycopersicon ... 122 4e-27
 emb|AI489199|AI489199 EST247538 tomato ovary, TAMU Lycopersicon ... 122 4e-27
 60 emb|AI483501|AI483501 EST249322 tomato ovary, TAMU Lycopersicon ... 122 4e-27
 emb|AI483741|AI483741 EST249612 tomato ovary, TAMU Lycopersicon ... 122 4e-27

	emb AI489919 AI489919 EST248258 tomato ovary, TAMU Lycopersicon ...	121	8e-27
	emb AW033743 AW033743 EST277314 tomato callus, TAMU Lycopersicon...	120	1e-26
	emb AI485175 AI485175 EST243479 tomato ovary, TAMU Lycopersicon ...	120	1e-26
	emb AW685799 AW685799 NF030D09NR1F1000 Nodulated root Medicago t...	119	2e-26
5	emb AW032669 AW032669 EST276228 tomato callus, TAMU Lycopersicon...	117	1e-25
	emb AI484721 AI484721 EST242982 tomato ovary, TAMU Lycopersicon ...	117	1e-25
	emb AI484063 AI484063 EST249934 tomato ovary, TAMU Lycopersicon ...	116	3e-25
	emb AV428124 AV428124 AV428124 Lotus japonicus young plants (two...	115	4e-25
	emb AI490297 AI490297 EST248623 tomato ovary, TAMU Lycopersicon ...	114	9e-25
10	emb AW782252 AW782252 sm03d11.y1 Gm-c1027 Glycine max cDNA clone...	113	1e-24
	emb AW203601 AW203601 sF36b02.y1 Gm-c1028 Glycine max cDNA clone...	111	4e-24
	emb AI898190 AI898190 EST267633 tomato ovary, TAMU Lycopersicon ...	111	8e-24
	emb AI483545 AI483545 EST249394 tomato ovary, TAMU Lycopersicon ...	109	2e-23
	emb AI485260 AI485260 EST243564 tomato ovary, TAMU Lycopersicon ...	108	6e-23
15	emb AF071893 AF071893 Prunus armeniaca AP2 domain containing pro...	108	6e-23
	emb AI897176 AI897176 EST266715 tomato ovary, TAMU Lycopersicon ...	107	8e-23
	emb AW560196 AW560196 EST315244 DSIR Medicago truncatula cDNA cl...	107	8e-23
	emb AW560968 AW560968 EST316016 DSIR Medicago truncatula cDNA cl...	107	8e-23
	emb AW559374 AW559374 EST314422 DSIR Medicago truncatula cDNA cl...	105	3e-22
20	emb AW267756 AW267756 EST305884 DSIR Medicago truncatula cDNA cl...	105	5e-22
	emb AW560135 AW560135 EST315183 DSIR Medicago truncatula cDNA cl...	105	5e-22
	emb AW560134 AW560134 EST315182 DSIR Medicago truncatula cDNA cl...	105	5e-22
	emb AW256448 AW256448 EST304585 KV2 Medicago truncatula cDNA clo...	105	5e-22
	emb AW094484 AW094484 EST287664 tomato mixed elicitor, BTI Lycop...	105	5e-22
25	gb BE022152 BE022152 sm68b06.y1 Gm-c1028 Glycine max cDNA clone ...	104	1e-21
	emb AW831226 AW831226 sm12d11.y1 Gm-c1027 Glycine max cDNA clone...	104	1e-21
	emb AW760676 AW760676 sl53e01.y1 Gm-c1027 Glycine max cDNA clone...	104	1e-21
	gb BE024062 BE024062 sm96c01.y1 Gm-c1015 Glycine max cDNA clone ...	104	1e-21
	emb AW568625 AW568625 si60b05.y1 Gm-r1030 Glycine max cDNA clone...	104	1e-21
30	emb AW458893 AW458893 sh16c04.y1 Gm-c1016 Glycine max cDNA clone...	104	1e-21
	emb AW156366 AW156366 se25b08.y1 Gm-c1015 Glycine max cDNA clone...	103	1e-21
	emb AW185126 AW185126 se87b08.y1 Gm-c1023 Glycine max cDNA clone...	103	2e-21
	emb AW328989 AW328989 N200181e rootphos(-) Medicago truncatula c...	103	2e-21
	emb AW152963 AW152963 se33c03.y1 Gm-c1015 Glycine max cDNA clone...	98	2e-21
35	emb AW441775 AW441775 EST311171 tomato fruit red ripe, TAMU Lyco...	102	3e-21
	emb AW221854 AW221854 EST298665 tomato fruit red ripe, TAMU Lyco...	102	3e-21
	emb AW441715 AW441715 EST311111 tomato fruit red ripe, TAMU Lyco...	102	3e-21
	emb AW219198 AW219198 EST301680 tomato root during/after fruit s...	102	3e-21
	emb AV417624 AV417624 AV417624 Lotus japonicus young plants (two...	102	3e-21
40	emb AV407462 AV407462 AV407462 Lotus japonicus young plants (two...	102	3e-21
	emb AI895742 AI895742 EST265185 tomato callus, TAMU Lycopersicon...	102	3e-21
	emb AW931667 AW931667 EST357510 tomato fruit mature green, TAMU ...	101	4e-21
	emb AW931028 AW931028 EST356871 tomato fruit mature green, TAMU ...	101	4e-21
	emb AW040033 AW040033 EST282524 tomato mixed elicitor, BTI Lycop...	101	5e-21
45	emb AW040028 AW040028 EST282519 tomato mixed elicitor, BTI Lycop...	101	5e-21
	emb AI487067 AI487067 EST245389 tomato ovary, TAMU Lycopersicon ...	101	5e-21
	emb AW442735 AW442735 EST307665 tomato mixed elicitor, BTI Lycop...	101	5e-21
	emb AW218830 AW218830 EST301310 tomato root during/after fruit s...	101	5e-21
	emb AI483782 AI483782 EST249653 tomato ovary, TAMU Lycopersicon ...	101	5e-21
50	emb AW218836 AW218836 EST301316 tomato root during/after fruit s...	101	5e-21
	emb AI483900 AI483900 EST249771 tomato ovary, TAMU Lycopersicon ...	101	5e-21
	emb AI482665 AI482665 EST241988 tomato shoot, Cornell Lycopersic...	101	5e-21
	emb AW760204 AW760204 sl59d04.y1 Gm-c1027 Glycine max cDNA clone...	101	5e-21
	emb AI496139 AI496139 sa95h06.y1 Gm-c1004 Glycine max cDNA clone...	101	5e-21
55	emb AW308962 AW308962 sF92d05.y1 Gm-c1019 Glycine max cDNA clone...	101	7e-21
	emb AW926284 AW926284 HVSMEg0006M23 Hordeum vulgare pre-anthesis...	101	7e-21
	emb AI966369 AI966369 sc37h09.y1 Gm-c1014 Glycine max cDNA clone...	101	7e-21
	emb AI855585 AI855585 sc28b12.y1 Gm-c1014 Glycine max cDNA clone...	101	7e-21
	emb AW038227 AW038227 EST279884 tomato mixed elicitor, BTI Lycop...	101	7e-21
60	emb AI855661 AI855661 sc32e04.y1 Gm-c1014 Glycine max cDNA clone...	101	7e-21
	emb AW234175 AW234175 sF22b03.y1 Gm-c1028 Glycine max cDNA clone...	101	7e-21

emb|AW598575|AW598575 sj93c10.y1 Gm-cl023 Glycine max cDNA clone... 101 7e-21
 emb|AW615838|AW615838 EST325336 tomato flower buds 0-3 mm, Corne... 100 9e-21
 gb|T14923|T14923 crs406 lambdaZAPST Ricinus communis cDNA clone ... 100 9e-21
 emb|AW093577|AW093577 EST286757 tomato mixed elicitor, BTI Lycop... 100 9e-21
 5 emb|AW621852|AW621852 EST312650 tomato root during/after fruit s... 100 9e-21
 emb|AI781904|AI781904 EST262783 tomato susceptible, Cornell Lyco... 100 9e-21
 emb|AW738052|AW738052 EST339479 tomato flower buds, anthesis, Co... 100 1e-20
 emb|AW726761|AW726761 GA__Ea0022K12 Gossypium arboreum 7-10 dpa ... 100 1e-20
 emb|AV422603|AV422603 AV422603 Lotus japonicus young plants (two... 100 1e-20
 10 emb|AW574073|AW574073 EST316664 GVN Medicago truncatula cDNA clo... 100 1e-20
 gb|BE057468|BE057468 sm58e08.y1 Gm-cl028 Glycine max cDNA clone ... 100 2e-20
 emb|AW755737|AW755737 sl08e02.y1 Gm-cl036 Glycine max cDNA clone... 100 2e-20
 emb|AW747259|AW747259 WS1_67_A03.b1_A002 Water-stressed 1 (WS1) ... 100 2e-20
 emb|AI489450|AI489450 EST247789 tomato ovary, TAMU Lycopersicon ... 100 2e-20
 15 emb|AW037553|AW037553 EST278880 tomato mixed elicitor, BTI Lycop... 100 2e-20
 emb|AW745488|AW745488 WS1_35_E09.b1_A002 Water-stressed 1 (WS1) ... 100 2e-20
 emb|AI900301|AI900301 sc03g01.y1 Gm-cl012 Glycine max cDNA clone... 99 4e-20
 emb|AI771801|AI771801 EST252901 tomato ovary, TAMU Lycopersicon ... 99 4e-20
 emb|AW329209|AW329209 N200421e rootphos(-) Medicago truncatula c... 98 6e-20
 20 emb|AI974084|AI974084 sd16c06.y1 Gm-cl020 Glycine max cDNA clone... 98 6e-20
 emb|AW267914|AW267914 EST306256 DSIR Medicago truncatula cDNA cl... 98 6e-20
 emb|AI772393|AI772393 EST253493 tomato resistant, Cornell Lycope... 98 8e-20
 emb|AW397723|AW397723 sg83e11.y1 Gm-cl026 Glycine max cDNA clone... 97 1e-19
 emb|AW034241|AW034241 EST277812 tomato callus, TAMU Lycopersicon... 97 2e-19
 25

Query= AC005770.30_at 19892_at /id_source genbank /description
 gb|aac79626.1| (ac005770) putative protease inhibitor [arabidopsis
 thaliana] /blast_score 2.00e-36 /ec_number /family protease /chip
 30 nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005770|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005770|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005770|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac005770>
 (378 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

	Score	E	
			(bits) Value
Sequences producing significant alignments:			
45	gb BE057244 BE057244 sm99e04.y1 Gm-cl015 Glycine max cDNA clone ...	87	7e-17
	gb BE057597 BE057597 sn04d12.y1 Gm-cl015 Glycine max cDNA clone ...	87	7e-17
	gb BE022905 BE022905 sm89a05.y1 Gm-cl015 Glycine max cDNA clone ...	87	7e-17
	gb BE022697 BE022697 sm87c09.y1 Gm-cl015 Glycine max cDNA clone ...	87	7e-17
	emb AW156430 AW156430 se26b01.y1 Gm-cl015 Glycine max cDNA clone...	87	7e-17
	emb AI938252 AI938252 sc41h01.y1 Gm-cl014 Glycine max cDNA clone...	87	7e-17
50	emb Z46949 SNPR6JT11 S.nigra mRNA for pathogenesis-related prote...	86	9e-17
	gb BE024084 BE024084 sm96e02.y1 Gm-cl015 Glycine max cDNA clone ...	85	2e-16
	emb AI938085 AI938085 sc41h07.x1 Gm-cl014 Glycine max cDNA clone...	84	3e-16
	emb AI930853 AI930853 sb43c07.y1 Gm-cl015 Glycine max cDNA clone...	84	6e-16
	emb AW156600 AW156600 se27e01.y1 Gm-cl015 Glycine max cDNA clone...	83	1e-15
55	emb AI966712 AI966712 sc55h06.y1 Gm-cl015 Glycine max cDNA clone...	80	6e-15
	gb BE023986 BE023986 sm95a07.y1 Gm-cl015 Glycine max cDNA clone ...	78	2e-14
	emb AW433320 AW433320 sh55e08.y1 Gm-cl015 Glycine max cDNA clone...	78	2e-14
	gb BE057243 BE057243 sm99e03.y1 Gm-cl015 Glycine max cDNA clone ...	78	2e-14
	emb AI522988 AI522988 sb07e02.y1 Gm-cl004 Glycine max cDNA clone...	78	2e-14
60	emb AI937952 AI937952 sc06b01.y1 Gm-cl012 Glycine max cDNA clone...	78	2e-14
	emb AI966518 AI966518 sc51b12.y1 Gm-cl015 Glycine max cDNA clone...	78	3e-14

	emb AI938255 AI938255 sc41h04.y1 Gm-cl014 Glycine max cDNA clone...	78 3e-14
	emb AI966697 AI966697 sc55e03.y1 Gm-cl015 Glycine max cDNA clone...	78 3e-14
	emb AW433162 AW433162 sh53b01.y1 Gm-cl015 Glycine max cDNA clone...	77 5e-14
	emb AW432522 AW432522 sh75d04.y1 Gm-cl015 Glycine max cDNA clone...	76 1e-13
5	emb AW432580 AW432580 sh76c09.y1 Gm-cl015 Glycine max cDNA clone...	75 3e-13
	emb AJ132473 AHY132473 Amaranthus hypochondriacus mRNA for tryps...	75 3e-13
	emb AW309047 AW309047 sf94c03.y1 Gm-cl019 Glycine max cDNA clone...	74 4e-13
	emb AW432514 AW432514 sh75c07.y1 Gm-cl015 Glycine max cDNA clone...	72 2e-12
	emb AI966650 AI966650 sc54d10.y1 Gm-cl015 Glycine max cDNA clone...	71 3e-12
10	emb AW460209 AW460209 sh56d11.y1 Gm-cl015 Glycine max cDNA clone...	70 6e-12
	emb AI966675 AI966675 sc54h10.y1 Gm-cl015 Glycine max cDNA clone...	68 2e-11
	emb AI488671 AI488671 EST247010 tomato ovary, TAMU Lycopersicon ...	68 3e-11
	emb AW033471 AW033471 EST277042 tomato callus, TAMU Lycopersicon...	52 4e-11
	emb AW041367 AW041367 EST284231 tomato mixed elicitor, BTI Lycop...	52 4e-11
15	gb J04099 TOMERIP II Tomato fruit-ripening protein (ethylene resp...	52 4e-11
	emb AI930895 AI930895 sb44a05.y1 Gm-cl015 Glycine max cDNA clone...	68 4e-11
	emb AW041591 AW041591 EST284455 tomato mixed elicitor, BTI Lycop...	67 8e-11
	emb AW929951 AW929951 EST354221 tomato flower buds 8 mm to pre-a...	50 9e-11
	emb AI483878 AI483878 EST249749 tomato ovary, TAMU Lycopersicon ...	50 9e-11
20	emb AW944751 AW944751 EST336801 tomato flower buds 3-8 mm, Corne...	50 1e-10
	gb M59427 TOMTRYINH I L.peruvianum proteinase inhibitor I gene, c...	50 2e-10
	gb J05094 TOMP II L.peruvianum proteinase inhibitor I mRNA, compl...	50 2e-10
	emb AW010812 AW010812 ST14C10 Pine TriplEx shoot tip library Pin...	64 4e-10
	emb AI485251 AI485251 EST243555 tomato ovary, TAMU Lycopersicon ...	47 4e-10
25	dbj D26455 TOBTID44 Nicotiana glauca X Nicotiana langsdorffii mR...	51 5e-10
	emb Z12623 NTPII3PI N.tabacum pre-pro-PI-Ib gene encoding pre-pr...	50 8e-10
	emb Z12619 NTPII4PI N.tabacum PI-Ia gene encoding pre-pro-protei...	50 8e-10
	emb X67075 NTTIMPB N.tabacum TIMPB mRNA for inhibitor of microbi...	50 8e-10
	emb X67076 NTTIMPA N.tabacum TIMPa mRNA for inhibitor of microbi...	50 9e-10
30	emb AW929928 AW929928 EST354198 tomato flower buds 8 mm to pre-a...	46 2e-09
	emb AW616209 AW616209 EST307248 L. hirsutum trichome, Cornell Un...	48 3e-09
	emb AW432477 AW432477 sh74f01.y1 Gm-cl015 Glycine max cDNA clone...	61 4e-09
	emb AW092750 AW092750 EST285930 tomato mixed elicitor, BTI Lycop...	45 4e-09
	gb M74102 TOBCPII Nicotiana sylvestris serine proteinase inhibit...	52 6e-09
35	emb AW622766 AW622766 EST306752 tomato flower buds 3-8 mm, Corne...	46 1e-08
	emb AI563053 AI563053 EST00177 watermelon lambda zap library Cit...	58 3e-08
	emb AI563140 AI563140 EST00264 watermelon lambda zap library Cit...	58 3e-08
	emb AI723907 AI723907 RHIZ1_32_B07.y1_A001 Rhizome1 Sorghum hale...	57 5e-08
	emb AI724626 AI724626 RHIZ1_11_A01.y1_A001 Rhizome1 Sorghum hale...	57 5e-08
40	emb AJ250663 HVU250663 Hordeum vulgare partial mRNA for putative...	57 5e-08
	emb AI724485 AI724485 RHIZ1_10_F03.y1_A001 Rhizome1 Sorghum hale...	57 5e-08
	dbj D13662 TOBGTI Nicotiana glauca X Nicotiana langsdorffii mRNA...	51 7e-08
	gb L06137 POTINH I X Solanum tuberosum proteinase inhibitor I (pin...	44 1e-07
	gb L06985 POTPIN I A Solanum tuberosum proteinase inhibitor I mRNA...	43 1e-07
45	gb M13938 TOMWPIG Tomato (L.esculentum) wound-inducible protein...	42 2e-07
	emb AI771798 AI771798 EST252898 tomato ovary, TAMU Lycopersicon ...	42 2e-07
	emb AI490242 AI490242 EST248568 tomato ovary, TAMU Lycopersicon ...	42 2e-07
	emb AI486930 AI486930 EST245252 tomato ovary, TAMU Lycopersicon ...	42 2e-07
	gb BE049671 BE049671 NXNV_140_C03_F Nsf Xylem Normal wood Vertic...	55 2e-07
50	gb K03290 TOMWPII Tomato leaf wound-induced proteinase inhibitor...	42 2e-07
	emb X67950 STPIN1MR S.tuberosum pin1 mRNA for proteinase inhibit...	41 5e-07
	emb X67675 STPIN1 S.tuberosum mRNA for proteinase inhibitor I.	41 5e-07
	emb AW443358 AW443358 EST308288 tomato mixed elicitor, BTI Lycop...	42 5e-07
	emb X57035 HVICA2 H.vulgare chymotrypsin inhibitor-2 gene.	53 8e-07
55	emb AI899242 AI899242 EST268685 tomato ovary, TAMU Lycopersicon ...	41 9e-07
	emb AI487831 AI487831 EST246153 tomato ovary, TAMU Lycopersicon ...	41 9e-07
	emb Z12611 STPROINI S.tuberosum proteinase inhibitor I.	44 9e-07
	emb AW944847 AW944847 EST336897 tomato flower buds 3-8 mm, Corne...	41 1e-06
	emb AW443908 AW443908 EST308838 tomato mixed elicitor, BTI Lycop...	41 1e-06
60	emb AW040832 AW040832 EST283696 tomato mixed elicitor, BTI Lycop...	41 1e-06
	emb AI485812 AI485812 EST244133 tomato ovary, TAMU Lycopersicon ...	41 1e-06

emb|AW442733|AW442733 EST307663 tomato mixed elicitor, BTI Lycop... 41 1e-06
emb|X05404|HVC12A Barley mRNA or chymotrypsin inhibitor-2 (CI-2A). 53 1e-06
gb|C95416|C95416 C95416 Citrus unshiu Miyagawa-wase maturation s... 52 2e-06
emb|AW746262|AW746262 WS1_40_H09.b1_A002 Water-stressed 1 (WS1) ... 52 2e-06
5 emb|AW746284|AW746284 WS1_40_H09.g1_A002 Water-stressed 1 (WS1) ... 52 2e-06
emb|AW437904|AW437904 ST78A12 Pine TriplEx shoot tip library Pin... 52 2e-06
emb|AW093975|AW093975 EST287155 tomato mixed elicitor, BTI Lycop... 35 4e-06
emb|AI781668|AI781668 EST262547 tomato susceptible, Cornell Lyco... 35 4e-06
emb|AW092485|AW092485 EST285665 tomato mixed elicitor, BTI Lycop... 35 4e-06
10 emb|AI772725|AI772725 EST253825 tomato resistant, Cornell Lycop... 35 5e-06
emb|AI778944|AI778944 EST259823 tomato susceptible, Cornell Lyco... 35 5e-06
emb|AI774403|AI774403 EST255503 tomato resistant, Cornell Lycop... 35 5e-06
emb|AI772154|AI772154 EST253254 tomato resistant, Cornell Lycop... 35 5e-06
emb|AW094311|AW094311 EST287491 tomato mixed elicitor, BTI Lycop... 35 5e-06
15 emb|AW092125|AW092125 EST285221 tomato mixed elicitor, BTI Lycop... 35 5e-06
emb|AW039975|AW039975 EST282466 tomato mixed elicitor, BTI Lycop... 35 5e-06
emb|AW039971|AW039971 EST282462 tomato mixed elicitor, BTI Lycop... 35 5e-06
emb|AW040872|AW040872 EST283736 tomato mixed elicitor, BTI Lycop... 35 5e-06
emb|AW093509|AW093509 EST286689 tomato mixed elicitor, BTI Lycop... 35 5e-06
20 emb|AI938012|AI938012 sc40a06.x1 Gm-cl014 Glycine max cDNA clone... 51 5e-06
emb|AW039063|AW039063 EST281036 tomato mixed elicitor, BTI Lycop... 38 8e-06

Query= AJ001809.1_at 19894_at /id_source genbank /description
25 emb|caa05025.1| (aj001809) succinate dehydrogenase flavoprotein alpha
subunit [arabidopsis thaliana] /blast_score 0 /ec_number /family
dehydrogenase /chip nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|aj001809| /ncgi
30 http://www.ncgr.org/cgi-bin/ff?aj001809
(2247 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters
35 Searching.....done

Score E
Sequences producing significant alignments: (bits) Value

40 emb|AL132984|SPAC1556 S.pombe chromosome I cosmid c1556. 637 0.0
emb|Z26877|SCDCHR11 S.cerevisiae (S288C) 36.2kb DNA fragment fro... 408 0.0
emb|Z49320|SCYJL045W S.cerevisiae chromosome X reading frame ORF... 403 0.0
gb|M86909|YSCSDH1A Saccharomyces cerevisiae succinate dehydrogen... 408 0.0
45 gb|M94874|YSCSDH1B Saccharomyces cerevisiae succinate dehydrogen... 408 0.0
emb|Z28148|SCYKL148C S.cerevisiae chromosome XI reading frame OR... 408 0.0
gb|M86746|YSCSDHA Saccharomyces cerevisiae succinate dehydrogena... 408 0.0
dbj|D86573|D86573 Plasmodium falciparum DNA for flavoprotein sub... 676 0.0
emb|AB031741|AB031741 Trypanosoma cruzi mRNA for succinate dehyd... 456 0.0
50 dbj|D89263|D89263 Schizosaccharomyces pombe mRNA, partial cds, c... 637 0.0
emb|Y10377|CATOP2 C.albicans TOP2 gene. 635 0.0
emb|AI771965|AI771965 EST253065 tomato resistant, Cornell Lycop... 495 e-139
emb|AW720194|AW720194 LjNEST16f8r Lotus japonicus nodule library... 440 e-122
emb|AI898950|AI898950 EST268393 tomato ovary, TAMU Lycopersicon ... 434 e-121
55 emb|AI727777|AI727777 BNLGHi9047 Six-day Cotton fiber Gossypium ... 391 e-114
emb|AW775119|AW775119 EST334270 KV3 Medicago truncatula cDNA clo... 407 e-112
emb|AL110721|CNS018RU Botrytis cinerea strain T4 cDNA library un... 323 e-110
emb|AW729362|AW729362 GA_Ea0024M24 Gossypium arboreum 7-10 dpa ... 314 4e-94
emb|AW687411|AW687411 NF009C11RT1F1085 Developing root Medicago ... 208 2e-85
60 emb|AW180257|AW180257 MgA0347fMgA Library Mycosphaerella gramin... 309 4e-83
emb|AA660851|AA660851 00746 MtrHE Medicago truncatula cDNA 5' si... 163 3e-82

- emb|AW760184|AW760184 sl59b01.y1 Gm-cl027 Glycine max cDNA clone... 304 1e-81
 emb|AI676411|AI676411 etmEST0165 EtH1 Eimeria tenella cDNA clone... 261 7e-81
 emb|AW278355|AW278355 sf43a10.y1 Gm-cl009 Glycine max cDNA clone... 301 1e-80
 emb|AW703689|AW703689 sk23b10.y1 Gm-cl028 Glycine max cDNA clone... 298 1e-79
 5 emb|AW350842|AW350842 GM210009B10E8R Gm-r1021 Glycine max cDNA 3... 293 3e-78
 emb|AW350838|AW350838 GM210009B10E7R Gm-r1021 Glycine max cDNA 3... 276 4e-73
 emb|AW563308|AW563308 LG1_228_B12.g1_A002 Light Grown 1 (LG1) So... 274 2e-72
 emb|AW398787|AW398787 EST309287 L. pennellii trichome, Cornell U... 246 4e-67
 emb|AW688181|AW688181 NF004D03ST1F1000 Developing stem Medicago ... 204 5e-67
 10 emb|AW667947|AW667947 GA_Ea0012A06 Gossypium arboreum 7-10 dpa ... 250 4e-65
 emb|AW685660|AW685660 NF033C09NR1F1000 Nodulated root Medicago t... 235 4e-65
 emb|AQ873013|AQ873013 V57F7 mTn-3xHA/lacZ Insertion Library, str... 170 2e-63
 emb|X54702|LPPLB08M L.polyphyllus pPLB08 mRNA. 159 5e-63
 emb|AW180015|AW180015 MgA0071f MgA Library Mycosphaerella gramin... 233 4e-60
 15 emb|AI495497|AI495497 sa98g08.y1 Gm-cl004 Glycine max cDNA clone... 219 8e-56
 emb|AQ659505|AQ659505 Sheared DNA-5G1.TR Sheared DNA Trypanosoma... 212 1e-53
 emb|AI391973|AI391973 NCC1F7T3 Conidial Neurospora crassa cDNA c... 162 4e-50
 emb|AW774144|AW774144 EST333227 KV3 Medicago truncatula cDNA clo... 184 2e-48
 emb|AI055409|AI055409 coau0003O20 Cotton Boll Abcission Zone cD... 177 1e-47
 20 emb|AQ659508|AQ659508 Sheared DNA-5G3.TF Sheared DNA Trypanosoma... 140 2e-46
 emb|AW730892|AW730892 GA_Ea0029E17 Gossypium arboreum 7-10 dpa ... 157 1e-45
 emb|AW922507|AW922507 DGI_20_E07.g1_A002 Dark Grown 1 (DG1) Sorg... 184 3e-45
 emb|AW218470|AW218470 EST303653 tomato radicle, 5 d post-imbibit... 168 2e-40
 emb|AW180288|AW180288 MgA0381f MgA Library Mycosphaerella gramin... 167 2e-40
 25 emb|AW334279|AW334279 S32G2 AGS-1 Pneumocystis carinii f. sp. ca... 158 5e-39
 gb|T15234|T15234 crs828 lambdaZAPST Ricinus communis cDNA clone ... 161 2e-38
 emb|AQ873266|AQ873266 V62G2 mTn-3xHA/lacZ Insertion Library, str... 129 5e-37
 emb|AW736632|AW736632 EST333124 KV3 Medicago truncatula cDNA clo... 136 4e-34
 emb|AW287458|AW287458 LG1_228_B12.b1_A002 Light Grown 1 (LG1) So... 145 1e-33
 30 emb|AV409739|AV409739 AV409739 Lotus japonicus young plants (two... 138 6e-33
 emb|AW255532|AW255532 ML565 peppermint glandular trichome Mentha... 87 9e-33
 emb|AQ646390|AQ646390 RPCI93-DpnII-29L18.TJ RPCI93-DpnII Trypano... 120 2e-32
 emb|AW350507|AW350507 GM210008B20H12R Gm-r1021 Glycine max cDNA ... 140 4e-32
 35 emb|AW736633|AW736633 EST333125 KV3 Medicago truncatula cDNA clo... 128 6e-32
 emb|AA051852|AA051852 Cn0030-5 Cryptococcus neoformans, Stratage... 117 3e-31
 emb|AW759819|AW759819 sl54d12.y1 Gm-cl027 Glycine max cDNA clone... 131 2e-29
 gb|BE020875|BE020875 sm53d08.y1 Gm-cl028 Glycine max cDNA clone ... 127 2e-28
 emb|AW703733|AW703733 sk23g01.y1 Gm-cl028 Glycine max cDNA clone... 127 2e-28
 40 emb|AW991033|AW991033 SsS0224 Suaeda salsa ZAP cDNA library Suae... 95 9e-28
 gb|BE057332|BE057332 sn01g03.y1 Gm-cl015 Glycine max cDNA clone ... 117 3e-25
 emb|AW180944|AW180944 MgA0071r MgA Library Mycosphaerella gramin... 108 1e-22
 emb|AI496172|AI496172 sa96c04.y1 Gm-cl004 Glycine max cDNA clone... 98 3e-19
 gb|BE024378|BE024378 894002F01.y1 C. reinhardtii CC-1690, normal... 96 8e-19
 45 emb|AW830714|AW830714 sm35c05.y1 Gm-cl028 Glycine max cDNA clone... 81 3e-18
 emb|AW568440|AW568440 si70g12.y1 Gm-cl031 Glycine max cDNA clone... 88 2e-16
 emb|AQ873304|AQ873304 V63D7 mTn-3xHA/lacZ Insertion Library, str... 57 3e-16
 gb|BE125576|BE125576 DG1_28_E07.b1_A002 Dark Grown 1 (DG1) Sorgh... 76 1e-12
 gb|BE034538|BE034538 MK01A06 MK Mesembryanthemum crystallinum cD... 74 3e-12
 50 emb|AW773033|AW773033 925002H09.y1 C. reinhardtii CC-2290, norma... 52 4e-12
 gb|BE122635|BE122635 Ljirnp30-425-h1 Ljirnp Lambda HybriZap t... 53 5e-12
 emb|AQ872933|AQ872933 V55G2 mTn-3xHA/lacZ Insertion Library, str... 49 2e-10
 emb|AU006770|AU006770 AU006770 Schizosaccharomyces pombe late lo... 65 2e-09
 gb|L46545|L46545 BNAF1848 Mustard flower buds Brassica rapa cDNA... 61 4e-08
 55 gb|L36344|YSCGTGMS Saccharomyces cerevisiae tRNA-Met, tRNA-Ser, ... 47 1e-06
 gb|L26347|YSCSEQA Saccharomyces cerevisiae COR gene cluster, iso... 47 1e-06
 emb|Z49551|SCYJR051W S.cerevisiae chromosome X reading frame ORF... 47 1e-06
 emb|AQ502406|AQ502406 V17H2 mTn-3xHA/lacZ Insertion Library Sacc... 55 3e-06
 gb|U18779|SCE8199 Saccharomyces cerevisiae chromosome V cosmid 8... 46 1e-05
 60 emb|AC011017|AC011017 Leishmania major chromosome 35 clone L3184... 45 1e-05
 emb|AL356456|LMFLUNK01 Leishmania major Friedlin cosmid clones L... 45 2e-05

emb|AL110853|CNS018VI Botrytis cinerea strain T4 cDNA library un... 38 1e-04
 emb|AC022284|AC022284 Leishmania major chromosome 35 clone L3377... 43 2e-04
 emb|AQ912027|AQ912027 LMAJFV1_ln10g05.y1 Leishmania major FV1 ra... 37 2e-04
 emb|Z99292|SPAC17A2 S.pombe chromosome I cosmid c17A2. 44 7e-04
 5 emb|AI897849|AI897849 EST267292 tomato ovary, TAMU Lycopersicon ... 46 0.002
 emb|AZ218322|AZ218322 Sheared DNA-81H6.TF Sheared DNA Trypanosom... 46 0.002
 emb|AQ652406|AQ652406 Sheared DNA-22G19.TR Sheared DNA Trypanoso... 40 0.003
 emb|AW401245|AW401245 LamdiGest417est L.digitata gametophyte Lam... 38 0.009
 emb|AQ948036|AQ948036 Sheared DNA-45P20.TF Sheared DNA Trypanoso... 42 0.020
 10 emb|AA785876|AA785876 h8g02a1.rl Aspergillus nidulans 24hr asexu... 40 0.053
 gb|BE036039|BE036039 MO18H07 MO Mesembryanthemum crystallinum cD... 40 0.099
 emb|AQ850793|AQ850793 LMAJFV1_lm31g07.x1 Leishmania major FV1 ra... 39 0.14
 emb|AF163958|AF163958 Saccharomyces cerevisiae isolate wt-13 tel... 29 0.19
 emb|AW649153|AW649153 EST327607 tomato germinating seedlings, TA... 34 0.46
 15 emb|AW618015|AW618015 EST313981 L. pennellii trichome, Cornell U... 37 0.49
 emb|AW398425|AW398425 EST298272 L. pennellii trichome, Cornell U... 37 0.49
 emb|AW678775|AW678775 WS1_1_B06.b2_A002 Water-stressed 1 (WS1) S... 37 0.67
 emb|AW678627|AW678627 WS1_1_B06.b1_A002 Water-stressed 1 (WS1) S... 37 0.67
 emb|AF136006|AF136006 Triticum aestivum eukaryotic initiation fa... 37 0.67
 20

Query= AC005727.175_at 19914_at /id_source genbank /description
 gb|aac79593.1| (ac005727) unknown protein [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link
 25 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005727|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005727|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005727|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac005727>
 (2008 letters)

30 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

35 Score E
 Sequences producing significant alignments: (bits) Value

emb|AW234376|AW234376 sf24e02.y1 Gm-c1028 Glycine max cDNA clone... 315 7e-85
 emb|AW234848|AW234848 sf19h05.y1 Gm-c1028 Glycine max cDNA clone... 240 2e-62
 40 emb|AI782064|AI782064 EST262943 tomato susceptible, Cornell Lyco... 220 4e-56
 emb|AW290802|AW290802 NXNV047A02F Nsf Xylem Normal wood Vertical... 204 2e-51
 emb|AA856223|AA856223 L30-246T3 Ice plant Lambda Uni-Zap XR expr... 182 1e-45
 gb|BE058219|BE058219 sn13b08.y1 Gm-c1016 Glycine max cDNA clone ... 184 2e-45
 emb|AW458125|AW458125 sh78e12.y1 Gm-c1016 Glycine max cDNA clone... 183 5e-45
 45 emb|AW030539|AW030539 EST273794 tomato callus, TAMU Lycopersicon... 163 2e-43
 emb|AW565896|AW565896 LG1_353_C06.g1_A002 Light Grown 1 (LG1) So... 156 5e-37
 emb|AW569925|AW569925 si83d03.y1 Gm-c1031 Glycine max cDNA clone... 153 4e-36
 emb|AT000567|AT000567 AT000567 Brassica rapa guard cell Brassica... 106 4e-33
 emb|AW648540|AW648540 EST326994 tomato germinating seedlings, TA... 69 2e-24
 50 emb|AW033885|AW033885 EST277456 tomato callus, TAMU Lycopersicon... 108 1e-22
 emb|AW284143|AW284143 LG1_262_C03.g1_A002 Light Grown 1 (LG1) So... 101 1e-20
 emb|AW676943|AW676943 DG1_2_E04.b1_A002 Dark Grown 1 (DG1) Sorgh... 101 2e-20
 emb|AW277624|AW277624 sf84e05.y1 Gm-c1019 Glycine max cDNA clone... 95 2e-18
 emb|AV428005|AV428005 AV428005 Lotus japonicus young plants (two... 91 2e-17
 55 emb|AW399438|AW399438 EST309938 L. pennellii trichome, Cornell U... 64 2e-16
 emb|AF097667|AF097667 Mesembryanthemum crystallinum protein phos... 52 4e-15
 emb|AW617510|AW617510 EST323921 L. hirsutum trichome, Cornell Un... 64 6e-15
 emb|AW698259|AW698259 NXNV_070_G08_F Nsf Xylem Normal wood Verti... 83 6e-15
 emb|AW560259|AW560259 EST315307 DSIR Medicago truncatula cDNA cl... 53 2e-14
 60 emb|AW698260|AW698260 NXNV_070_G09_F Nsf Xylem Normal wood Verti... 81 3e-14
 emb|AW560258|AW560258 EST315306 DSIR Medicago truncatula cDNA cl... 51 6e-14

- emb|AW626583|AW626583 NXNV067A10 Nsf Xylem Normal wood Vertical ... 70 6e-14
emb|AW163982|AW163982 Ljirnp18-406-a10 Ljirnp Lambda HybriZap... 73 6e-14
emb|AW698258|AW698258 NXNV_070_G07_F Nsf Xylem Normal wood Verti... 79 1e-13
5 gb|BE058708|BE058708 sn19g01.y1 Gm-c1016 Glycine max cDNA clone ... 51 5e-13
emb|AI167089|AI167089 xylem.est.857 Poplar xylem Lambda ZAPII li... 49 7e-13
emb|AF079355|AF079355 Mesembryanthemum crystallinum protein phos... 51 2e-12
emb|X94335|SC130KBXV S.cerevisiae 130kb DNA fragment from chromo... 50 2e-12
emb|Z74998|SCYOR090C S.cerevisiae chromosome XV reading frame OR... 50 2e-12
emb|AJ277744|FSY277744 Fagus sylvatica mRNA for ABA and calcium ... 56 2e-12
10 emb|AI485178|AI485178 EST243482 tomato ovary, TAMU Lycopersicon ... 51 3e-12
emb|AW932792|AW932792 EST358635 tomato fruit mature green, TAMU ... 51 8e-12
emb|AW676913|AW676913 DG1_2_G04.b1_A002 Dark Grown 1 (DG1) Sorgh... 72 2e-11
emb|AW164418|AW164418 se72c06.y1 Gm-c1023 Glycine max cDNA clone... 47 3e-11
emb|AI726381|AI726381 BNLGHi5700 Six-day Cotton fiber Gossypium ... 44 7e-11
15 emb|AW348221|AW348221 GM210001B12B8R Gm-r1021 Glycine max cDNA 3... 48 5e-10
emb|AW650300|AW650300 EST328754 tomato germinating seedlings, TA... 46 6e-10
gb|BE053500|BE053500 GA_Ea0001P09f Gossypium arboreum 7-10 dpa ... 53 1e-09
gb|C23895|C23895 C23895 Miyagawa-wase satsuma mandarin orange (M... 65 2e-09
emb|AI896264|AI896264 EST265707 tomato callus, TAMU Lycopersicon... 53 2e-09
20 emb|AW687126|AW687126 NF006C06RT1F1049 Developing root Medicago ... 53 7e-09
emb|AI897957|AI897957 EST267400 tomato ovary, TAMU Lycopersicon ... 48 1e-08
emb|AW030242|AW030242 EST273497 tomato callus, TAMU Lycopersicon... 38 2e-08
emb|AV420315|AV420315 AV420315 Lotus japonicus young plants (two... 52 3e-08
emb|AW729643|AW729643 GA_Ea0025K03 Gossypium arboreum 7-10 dpa ... 59 8e-08
25 emb|AI897759|AI897759 EST267202 tomato ovary, TAMU Lycopersicon ... 54 6e-07
emb|AI897074|AI897074 EST266517 tomato ovary, TAMU Lycopersicon ... 56 1e-06
emb|AI899132|AI899132 EST268575 tomato ovary, TAMU Lycopersicon ... 56 1e-06
emb|AW256742|AW256742 EST304879 KV2 Medicago truncatula cDNA clo... 55 2e-06
emb|AI489557|AI489557 EST247896 tomato ovary, TAMU Lycopersicon ... 54 3e-06
30 emb|AI898184|AI898184 EST267627 tomato ovary, TAMU Lycopersicon ... 54 3e-06
emb|AI895459|AI895459 EST264902 tomato callus, TAMU Lycopersicon... 54 4e-06
emb|AW398099|AW398099 EST297982 L. pennellii trichome, Cornell U... 54 5e-06
emb|AW207933|AW207933 M111162e DSIR Medicago truncatula cDNA clo... 54 5e-06
emb|AV427908|AV427908 AV427908 Lotus japonicus young plants (two... 54 5e-06
35 emb|AL355926|NCB17C10 Neurospora crassa DNA linkage group II BAC... 42 7e-06
emb|AI486082|AI486082 EST244403 tomato ovary, TAMU Lycopersicon ... 53 7e-06
emb|AW093348|AW093348 EST286528 tomato mixed elicitor, BTI Lycop... 53 1e-05
emb|AW746773|AW746773 WS1_55_B12.b1_A002 Water-stressed 1 (WS1) ... 53 1e-05
emb|AW666538|AW666538 GA_Ea0005H20 Gossypium arboreum 7-10 dpa ... 53 1e-05
40 emb|AW309762|AW309762 sf24e02.x1 Gm-c1028 Glycine max cDNA clone... 52 1e-05
emb|AW624350|AW624350 EST322295 tomato flower buds 3-8 mm, Corne... 51 3e-05
emb|AV417021|AV417021 AV417021 Lotus japonicus young plants (two... 51 3e-05
emb|AW290215|AW290215 NXNV015C12F Nsf Xylem Normal wood Vertical... 51 4e-05
emb|AI484987|AI484987 EST243250 tomato ovary, TAMU Lycopersicon ... 51 4e-05
45 emb|AI728047|AI728047 BNLGHi9685 Six-day Cotton fiber Gossypium ... 51 4e-05
emb|AI771145|AI771145 EST252341 tomato ovary, TAMU Lycopersicon ... 51 4e-05
emb|AI939275|AI939275 sc69f06.y1 Gm-c1016 Glycine max cDNA clone... 50 5e-05
emb|AI052977|AI052977 Mpc4 Ice plant seedlings, RT-PCR, pCRII M... 50 5e-05
emb|AW349802|AW349802 GM210006A20E6R Gm-r1021 Glycine max cDNA 3... 49 9e-05
50 emb|AW349791|AW349791 GM210006A20E12R Gm-r1021 Glycine max cDNA ... 49 9e-05
emb|AW933759|AW933759 EST359602 tomato fruit mature green, TAMU ... 49 9e-05
emb|AI731667|AI731667 BNLGHi10427 Six-day Cotton fiber Gossypium... 43 1e-04
emb|AW598662|AW598662 sj94c01.y1 Gm-c1023 Glycine max cDNA clone... 49 2e-04
emb|AW037487|AW037487 EST275994 tomato mixed elicitor, BTI Lycop... 49 2e-04
55 emb|AW328948|AW328948 N200140e rootphos(-) Medicago truncatula c... 48 2e-04
emb|AI442775|AI442775 sa26c12.x1 Gm-c1004 Glycine max cDNA clone... 48 2e-04
emb|AW399213|AW399213 EST309713 L. pennellii trichome, Cornell U... 48 3e-04
emb|AI779659|AI779659 EST260538 tomato susceptible, Cornell Lyco... 48 3e-04
emb|AI486266|AI486266 EST244587 tomato ovary, TAMU Lycopersicon ... 41 4e-04
60 emb|AW677101|AW677101 DG1_4_D08.b1_A002 Dark Grown 1 (DG1) Sorgh... 47 5e-04
emb|AB029099|AB029099 AB029099 Cucumis sativus library (Chono M)... 47 5e-04

emb|AI897604|AI897604 EST267047 tomato ovary, TAMU Lycopersicon ... 47 6e-04
 emb|AI898276|AI898276 EST267719 tomato ovary, TAMU Lycopersicon ... 47 6e-04
 emb|AW101984|AW101984 sd81e10.y1 Gm-c1009 Glycine max cDNA clone... 46 9e-04
 emb|AW696975|AW696975 NF111A04ST1F1024 Developing stem Medicago ... 46 0.001
 5 emb|AL035475|PFMAL4P2 Plasmodium falciparum MAL4P2, complete seq... 46 0.001
 emb|AW396281|AW396281 sh26f02.y1 Gm-c1016 Glycine max cDNA clone... 38 0.002
 emb|AW926387|AW926387 HVSMEg0007B08 Hordeum vulgare pre-anthesis... 38 0.002
 emb|AF075581|AF075581 Mesembryanthemum crystallinum clone Mpc6 p... 42 0.002
 emb|AI900423|AI900423 sc05e10.y1 Gm-c1012 Glycine max cDNA clone... 45 0.002
 10 emb|AI060327|AI060327 Mpc6 Ice plant seedlings, RT-PCR, pCRII M... 42 0.002
 emb|AI897958|AI897958 EST267401 tomato ovary, TAMU Lycopersicon ... 40 0.003
 emb|AW982223|AW982223 HVSMEg0002G04f Hordeum vulgare pre-anthesi... 44 0.003
 gb|BE124122|BE124122 EST394247 DSIL Medicago truncatula cDNA clo... 35 0.004
 emb|AW126333|AW126333 N100440e rootphos(-) Medicago truncatula c... 44 0.004
 15 emb|AI461042|AI461042 sa73c01.y1 Gm-c1004 Glycine max cDNA clone... 44 0.006

Query= AC005395.47_at 19951_at /id_source genbank /description
 gb|aac42241.1| (ac005395) unknown protein [arabidopsis thaliana]
 20 /blast_score 1.00e-157 /ec_number /family /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005395|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005395|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005395|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac005395>
 (938 letters)

25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

30 Score E
 Sequences producing significant alignments: (bits) Value

gb|BE036593|BE036593 MP01G10 MP Mesembryanthemum crystallinum cD... 387 e-119
 35 gb|BE054676|BE054676 GA_Ea0032C08f Gossypium arboreum 7-10 dpa ... 405 e-113
 emb|AW728038|AW728038 GA_Ea0029I18 Gossypium arboreum 7-10 dpa ... 395 e-109
 emb|AW329378|AW329378 N200608e rootphos(-) Medicago truncatula c... 386 e-107
 emb|AW725467|AW725467 GA_Ea0018B18 Gossypium arboreum 7-10 dpa ... 275 e-105
 emb|AI966343|AI966343 sc37e08.y1 Gm-c1014 Glycine max cDNA clone... 260 6e-97
 40 emb|AW442228|AW442228 EST311624 tomato fruit red ripe, TAMU Lyco... 308 5e-95
 emb|AW255529|AW255529 ML562 peppermint glandular trichome Mentha... 319 3e-93
 emb|AW221896|AW221896 EST298707 tomato fruit red ripe, TAMU Lyco... 215 2e-78
 emb|AW678275|AW678275 WS1_14_A02.b1_A002 Water-stressed 1 (WS1) ... 157 1e-77
 emb|AW668498|AW668498 GA_Ea0014E02 Gossypium arboreum 7-10 dpa ... 259 3e-75
 45 emb|AI730573|AI730573 BNLGHi7295 Six-day Cotton fiber Gossypium ... 272 3e-72
 emb|AW219191|AW219191 EST301673 tomato root during/after fruit s... 211 5e-54
 emb|AV409540|AV409540 AV409540 Lotus japonicus young plants (two... 211 7e-54
 emb|AV423705|AV423705 AV423705 Lotus japonicus young plants (two... 207 1e-52
 emb|AA231842|AA231842 CDO920.R cDNA from oat Avena sativa cDNA c... 175 9e-46
 50 emb|AW695662|AW695662 NF097C11ST1F1085 Developing stem Medicago ... 166 4e-45
 emb|AI960056|AI960056 sc37e08.x1 Gm-c1014 Glycine max cDNA clone... 98 2e-44
 emb|AI759880|AI759880 sb65e12.y1 Gm-c1017 Glycine max cDNA clone... 152 3e-41
 emb|AW677045|AW677045 DG1_4_G06.b1_A002 Dark Grown 1 (DG1) Sorgh... 135 4e-31
 emb|AW598595|AW598595 sj93f10.y1 Gm-c1023 Glycine max cDNA clone... 118 5e-26
 55 emb|AW684174|AW684174 NF013F01NR1F1000 Nodulated root Medicago t... 112 3e-24
 emb|AW677664|AW677664 WS1_10_G12.b1_A002 Water-stressed 1 (WS1) ... 100 1e-20
 emb|AW677709|AW677709 WS1_10_G12.g1_A002 Water-stressed 1 (WS1) ... 100 1e-20
 emb|AW757178|AW757178 sl30b05.y1 Gm-c1027 Glycine max cDNA clone... 95 4e-20
 emb|AA231890|AA231890 CDO920.F cDNA from oat Avena sativa cDNA c... 82 8e-15
 60 emb|AE001381|AE001381 Plasmodium falciparum chromosome 2, sectio... 57 2e-07
 emb|AW734973|AW734973 sk92g05.y1 Gm-c1035 Glycine max cDNA clone... 56 4e-07

emb|AI612519|AI612519 TENGO335 T. Cruzi epimastigote normalised ... 47 2e-04
 emb|AA926384|AA926384 TENS1006 T. cruzi epimastigote normalized ... 38 0.13
 emb|AA555388|AA555388 CpEST.617 uniZAPCp|OWAsporoLib3 Cryptospor... 37 0.25
 emb|AW666632|AW666632 GA_Ea0005D10 Gossypium arboreum 7-10 dpa ... 37 0.25
 5 emb|AW695873|AW695873 NF100C01ST1F1004 Developing stem Medicago ... 36 0.48
 emb|AW685637|AW685637 NF032F04NR1F1000 Nodulated root Medicago t... 35 0.66
 emb|AW930970|AW930970 EST356813 tomato fruit mature green, TAMU ... 35 0.91
 emb|AW930458|AW930458 EST340831 tomato fruit mature green, TAMU ... 35 0.91
 emb|AW035833|AW035833 EST281987 tomato callus, TAMU Lycopersicon... 35 0.91
 10 emb|AI211536|AI211536 p0h06a1.r1 Aspergillus nidulans 24hr asexu... 35 0.91
 emb|AQ640157|AQ640157 927P1-18A7.TP 927P1 Trypanosoma brucei gen... 35 1.2
 emb|AW349276|AW349276 GM210004B21H2R Gm-r1021 Glycine max cDNA 3... 34 2.4
 emb|AQ324698|AQ324698 mgxb0019F05r CUGI Rice Blast BAC Library P... 34 2.4
 emb|AA550044|AA550044 1130m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 34 2.4
 15 gb|U19028|YSCL8300 Saccharomyces cerevisiae chromosome XII cosmi... 34 2.4
 emb|X06689|PCLIGH8 Phanerochaete chrysosporium gene for ligninas... 29 2.5
 gb|M27401|PHALIGH8 Phanerochaete chrysosporium ligninase isozyme... 29 2.5
 emb|X51590|PCGLG3 P. chrysosporium GLG3 (LIP) gene for lignin pe... 29 2.5
 gb|M27884|PHALPIA P.chrysosporium lignin peroxidase isozyme H8 ge... 29 2.5
 20 emb|AW693181|AW693181 NF061C03ST1F1000 Developing stem Medicago ... 33 3.2
 emb|AW761196|AW761196 sl64d11.y1 Gm-c1027 Glycine max cDNA clone... 33 4.4
 emb|AQ502162|AQ502162 V8A9 mTn-3xHA/lacZ Insertion Library Sacch... 33 4.4
 gb|M37701|PHALPO P.chrysosporium lignin peroxidase genes, comple... 28 5.7
 emb|Z75009|SCYOR101W S.cerevisiae chromosome XV reading frame OR... 32 6.1
 25 gb|U32307|SCU32307 Saccharomyces cerevisiae oligosaccharyltransf... 32 6.1
 emb|AW201959|AW201959 sf09d01.y1 Gm-c1027 Glycine max cDNA clone... 32 6.1
 emb|Z70690|SPAC1F3 S.pombe chromosome I cosmid c1F3. 32 6.1
 emb|X94335|SC130KBXV S.cerevisiae 130kb DNA fragment from chromo... 32 6.1
 emb|AL022070|SPBC3B9 S.pombe chromosome II cosmid c3B9. 32 6.1
 30 emb|AI416552|AI416552 sa10f05.y1 Gm-c1003 Glycine max cDNA clone... 32 6.1
 gb|M33139|YSPRPA3 S.pombe ribosomal protein A3 (rpa2+) gene, com... 32 6.1
 gb|BE056330|BE056330 00241 leafy spurge Lambda HybriZAP 2.1 two-... 32 8.4
 emb|AF136004|AF136004 Triticum aestivum eukaryotic initiation fa... 32 8.4
 emb|AW395197|AW395197 sh45b04.y1 Gm-c1017 Glycine max cDNA clone... 32 8.4
 35 emb|AW671822|AW671822 LG1_351_G04.g1_A002 Light Grown 1 (LG1) So... 32 8.4
 emb|AQ648854|AQ648854 Sheared DNA-18A21.TR Sheared DNA Trypanoso... 32 8.4
 gb|BE059776|BE059776 sn37a01.y1 Gm-c1016 Glycine max cDNA clone ... 32 8.4
 emb|X12698|PCLIGNINA P. chrysosporium mRNA for ligninase (rLDM(T... 29 8.5

40

Query= AC002986.28_at 19982_at /id_source genbank /description
 "gb|aac17040.1| (ac002986) similarity to a. thaliana gene product
 f21m12.20, gb|ac000132. est gb|z25651 comes from this gene.
 [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova
 45 /gb_link [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002986|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002986|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002986|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac002986>
 (1593 letters)

50

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

55

Score E
 Sequences producing significant alignments: (bits) Value

gb|BE053277|BE053277 GA_Ea0035A14f Gossypium arboreum 7-10 dpa ... 205 1e-78
 emb|AW831229|AW831229 sm12g02.y1 Gm-c1027 Glycine max cDNA clone... 207 3e-78
 60 emb|AW678776|AW678776 WS1_1_A04.b2_A002 Water-stressed 1 (WS1) S... 224 1e-77
 emb|AW678614|AW678614 WS1_1_A04.b1_A002 Water-stressed 1 (WS1) S... 224 1e-77

	emb AW688577 AW688577 NF009B11ST1F1000 Developing stem Medicago ...	214	5e-75
	emb AW757260 AW757260 sl32a03.y1 Gm-c1027 Glycine max cDNA clone...	194	1e-74
	emb AW684123 AW684123 NF012F07NR1F1000 Nodulated root Medicago t...	179	7e-70
	emb AW933688 AW933688 EST359531 tomato fruit mature green, TAMU ...	261	1e-68
5	emb AW035607 AW035607 EST281345 tomato callus, TAMU Lycopersicon...	255	8e-67
	emb AW508601 AW508601 si34b06.y1 Gm-r1030 Glycine max cDNA clone...	166	8e-66
	emb AW680760 AW680760 WS1_7_B05.b1_A002 Water-stressed 1 (WS1) S...	168	1e-65
	emb AW564408 AW564408 LG1_292_D08.b1_A002 Light Grown 1 (LG1) So...	251	1e-65
	emb AV411756 AV411756 AV411756 Lotus japonicus young plants (two...	186	3e-65
10	emb AW926737 AW926737 HVSMEg0008A08 Hordeum vulgare pre-anthesis...	210	6e-64
	emb AW443003 AW443003 EST307933 tomato mixed elicitor, BTI Lycop...	160	8e-64
	emb AW928933 AW928933 EST337817 tomato flower buds 8 mm to pre-a...	244	1e-63
	emb AW684792 AW684792 NF021B07NR1F1000 Nodulated root Medicago t...	221	1e-63
	emb AW508690 AW508690 si35c03.y1 Gm-r1030 Glycine max cDNA clone...	159	3e-62
15	emb AI731330 AI731330 BNLGHi9231 Six-day Cotton fiber Gossypium ...	236	4e-61
	emb AW759875 AW759875 sl55c03.y1 Gm-c1027 Glycine max cDNA clone...	216	3e-60
	emb AW508088 AW508088 si50f10.y1 Gm-r1030 Glycine max cDNA clone...	156	4e-60
	emb AW737936 AW737936 EST339363 tomato flower buds, anthesis, Co...	230	2e-59
	emb AW983534 AW983534 HVSMEg0010P13f Hordeum vulgare pre-anthesi...	144	3e-58
20	emb AW208258 AW208258 M110914e GVSNN Medicago truncatula cDNA clo...	201	2e-57
	emb AI899909 AI899909 sb96a05.y1 Gm-c1012 Glycine max cDNA clone...	216	3e-55
	emb AW746930 AW746930 WS1_56_B01.b1_A002 Water-stressed 1 (WS1) ...	132	7e-55
	emb AW127622 AW127622 M110358 DSLC Medicago truncatula cDNA clon...	208	1e-52
	emb AW094255 AW094255 EST287435 tomato mixed elicitor, BTI Lycop...	195	1e-48
25	emb AV424875 AV424875 AV424875 Lotus japonicus young plants (two...	159	3e-48
	emb AW216607 AW216607 EST295321 tomato callus, TAMU Lycopersicon...	191	2e-47
	emb AW622247 AW622247 EST313045 tomato root during/after fruit s...	190	2e-47
	emb AW761408 AW761408 sl67b04.y1 Gm-c1027 Glycine max cDNA clone...	185	7e-46
	emb AW441544 AW441544 EST310940 tomato fruit red ripe, TAMU Lyco...	184	1e-45
30	emb AW203607 AW203607 sf36b08.y1 Gm-c1028 Glycine max cDNA clone...	174	2e-42
	emb AW746061 AW746061 WS1_39_D07.b1_A002 Water-stressed 1 (WS1) ...	168	1e-40
	emb AI794979 AI794979 sb74e06.y1 Gm-c1010 Glycine max cDNA clone...	108	1e-40
	emb AW755419 AW755419 sl03g08.y1 Gm-c1036 Glycine max cDNA clone...	104	3e-40
	emb AW329571 AW329571 N200823e rootphos(-) Medicago truncatula c...	97	1e-37
35	emb AW774738 AW774738 EST333889 KV3 Medicago truncatula cDNA clo...	157	1e-37
	emb AW201668 AW201668 sf05h05.y1 Gm-c1027 Glycine max cDNA clone...	155	7e-37
	emb AW781444 AW781444 sl78f03.y1 Gm-c1037 Glycine max cDNA clone...	154	2e-36
	emb AW037635 AW037635 EST279093 tomato mixed elicitor, BTI Lycop...	148	1e-34
	emb AI823132 AI823132 L30-1015T3 Ice plant Lambda Uni-Zap XR exp...	142	6e-33
40	emb AW595996 AW595996 si96e10.y1 Gm-c1032 Glycine max cDNA clone...	138	1e-31
	emb AI896179 AI896179 EST265622 tomato callus, TAMU Lycopersicon...	135	1e-30
	emb AW756882 AW756882 sk82d02.y1 Gm-c1016 Glycine max cDNA clone...	131	2e-29
	emb AW756279 AW756279 sl18d04.y1 Gm-c1036 Glycine max cDNA clone...	130	2e-29
	emb AW621046 AW621046 sj95c02.y1 Gm-c1023 Glycine max cDNA clone...	123	3e-27
45	gb U28373 YSCD9481 Saccharomyces cerevisiae chromosome IV cosmid...	64	2e-25
	emb AW924277 AW924277 WS1_52_D12.b1_A002 Water-stressed 1 (WS1) ...	109	7e-23
	emb AI960559 AI960559 sc86a02.y1 Gm-c1018 Glycine max cDNA clone...	109	7e-23
	gb BE060234 BE060234 HVSMEg0011K15f Hordeum vulgare pre-anthesis...	107	3e-22
	emb AW736643 AW736643 EST333135 KV3 Medicago truncatula cDNA clo...	104	2e-21
50	emb AA231652 AA231652 BCD98.F cDNA from barley Hordeum vulgare c...	99	1e-19
	emb AW736642 AW736642 EST333134 KV3 Medicago truncatula cDNA clo...	92	8e-18
	emb AW568172 AW568172 si57d03.y1 Gm-r1030 Glycine max cDNA clone...	84	2e-15
	emb AW256616 AW256616 EST304753 KV2 Medicago truncatula cDNA clo...	84	3e-15
	emb AI960723 AI960723 sc89e07.y1 Gm-c1019 Glycine max cDNA clone...	78	2e-13
55	emb AI728294 AI728294 BNLGHi10384 Six-day Cotton fiber Gossypium...	76	6e-13
	emb AI822771 AI822771 L30-604T3 Ice plant Lambda Uni-Zap XR expr...	76	9e-13
	emb AW564841 AW564841 LG1_310_B02.b1_A002 Light Grown 1 (LG1) So...	74	3e-12
	emb AW278636 AW278636 sf63b11.y1 Gm-c1013 Glycine max cDNA clone...	70	5e-11
	emb AW350463 AW350463 GM210008A20F3R Gm-r1021 Glycine max cDNA 3...	64	4e-09
60	emb AW563245 AW563245 LG1_204_C07.g1_A002 Light Grown 1 (LG1) So...	61	2e-08
	emb AW760716 AW760716 sl36b09.y1 Gm-c1027 Glycine max cDNA clone...	45	2e-07

emb|AW318040|AW318040 sg60d08.y1 Gm-c1007 Glycine max cDNA clone... 56 6e-07
 emb|AW706467|AW706467 sj58g06.y1 Gm-c1033 Glycine max cDNA clone... 54 4e-06
 emb|AW704696|AW704696 sk39d04.y1 Gm-c1028 Glycine max cDNA clone... 45 1e-05
 emb|AW350967|AW350967 GM210010B10H7R Gm-r1021 Glycine max cDNA 3... 51 2e-05
 5 emb|Z98547|PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque... 38 2e-04
 emb|AW981040|AW981040 EST392193 GVN Medicago truncatula cDNA clo... 45 0.002
 gb|L44100|BLYFQ Hordeum vulgare (clone CD98) STS mRNA, sequence ... 43 0.006
 emb|AW618476|AW618476 EST320462 L. pennellii trichome, Cornell U... 42 0.014
 emb|AW678071|AW678071 WS1_13_E01.b1_A002 Water-stressed 1 (WS1) ... 41 0.026
 10 emb|AB024989|AB024989 Cicer arietinum mRNA for chalcone reductas... 40 0.036
 emb|AW329724|AW329724 N200990e rootphos(-) Medicago truncatula c... 40 0.050
 emb|AW684697|AW684697 NF019H04NR1F1000 Nodulated root Medicago t... 40 0.050
 emb|AW256585|AW256585 EST304722 KV2 Medicago truncatula cDNA clo... 40 0.050
 emb|AW309364|AW309364 sf16d12.x1 Gm-c1028 Glycine max cDNA clone... 38 0.24
 15 emb|AW348632|AW348632 GM210002B22H5R Gm-r1021 Glycine max cDNA 3... 38 0.24
 emb|AW348958|AW348958 GM210004A12C5R Gm-r1021 Glycine max cDNA 3... 38 0.24
 emb|AW309230|AW309230 sf29a01.x1 Gm-c1028 Glycine max cDNA clone... 38 0.24
 emb|AW101404|AW101404 sd79e02.y1 Gm-c1009 Glycine max cDNA clone... 37 0.44
 emb|Z36281|TBI17RN T.brucei I17 mRNA for flagellar antigen. 36 0.45
 20 emb|X82366|MSCHR1A M.sativa mRNA for chalcone reductase (1202 bp). 36 0.61
 emb|AW757198|AW757198 sl30d08.y1 Gm-c1027 Glycine max cDNA clone... 36 0.61
 emb|AW650600|AW650600 EST329054 tomato germinating seedlings, TA... 36 0.61
 emb|AW649434|AW649434 EST327888 tomato germinating seedlings, TA... 36 0.61
 emb|AW329584|AW329584 N200836e rootphos(-) Medicago truncatula c... 36 0.83
 25 gb|BE059817|BE059817 sn37e05.y1 Gm-c1016 Glycine max cDNA clone ... 35 1.2
 emb|AW760667|AW760667 sl53d03.y1 Gm-c1027 Glycine max cDNA clone... 35 1.2
 emb|AW782226|AW782226 sm03b02.y1 Gm-c1027 Glycine max cDNA clone... 35 1.2
 emb|AW760912|AW760912 sl60e10.y1 Gm-c1027 Glycine max cDNA clone... 35 1.2
 gb|BE023356|BE023356 sm70h01.y1 Gm-c1028 Glycine max cDNA clone ... 35 1.2
 30 emb|AW200818|AW200818 se93h05.y1 Gm-c1027 Glycine max cDNA clone... 35 1.2
 emb|AI210832|AI210832 l0f05a1.fl Aspergillus nidulans 24hr asexu... 29 1.4
 dbj|D83718|GYCPKR Glycyrrhiza echinata mRNA for polyketide reduc... 35 1.6
 emb|AW472504|AW472504 si26b06.y1 Gm-r1030 Glycine max cDNA clone... 35 1.6
 emb|Z99173|NTCYSTPRO Nicotiana tabacum mRNA for cysteine protein... 35 1.6
 35 dbj|D86558|D86558 Glycyrrhiza glabra mRNA for polyketide reducta... 35 1.6

Query= AC007017.124_at 19991_at /id_source genbank /description
 gb|aad21459.1| (ac007017) similar to harpin-induced protein hin1 from
 40 tobacco [arabidopsis thaliana] /blast_score 1.00e-112 /ec_number
 /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac007017|/ncgi
 http://www.ncgr.org/cgi-bin/ff?ac007017
 45 (713 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

50 Searching.....done

	Score	E
Sequences producing significant alignments:	(bits)	Value
55 emb AF212183 AF212183 Nicotiana tabacum harpin inducing protein ...	221	3e-62
emb AW216692 AW216692 EST295406 tomato callus, TAMU Lycopersicon...	215	6e-61
emb Y07563 NTHIN1 N.tabacum mRNA for hin1 gene.	212	2e-59
emb AW621495 AW621495 EST312293 tomato root during/after fruit s...	215	2e-59
emb AW032166 AW032166 EST275620 tomato callus, TAMU Lycopersicon...	212	1e-58
60 emb AI484933 AI484933 EST243196 tomato ovary, TAMU Lycopersicon ...	214	8e-55
emb AI779911 AI779911 EST260790 tomato susceptible, Cornell Lyco...	209	2e-53

	emb AW216459 AW216459 EST295089 tomato callus, TAMU Lycopersicon...	189 3e-53
	emb AW596126 AW596126 si98d02.y1 Gm-cl032 Glycine max cDNA clone...	126 1e-49
	emb AW034324 AW034324 EST277895 tomato callus, TAMU Lycopersicon...	182 2e-49
	emb AI895898 AI895898 EST265341 tomato callus, TAMU Lycopersicon...	180 5e-49
5	emb AW096867 AW096867 EST20D16 potato shoot cDNA library Solanum...	193 9e-49
	emb AI896063 AI896063 EST265506 tomato callus, TAMU Lycopersicon...	179 1e-48
	emb AW030430 AW030430 EST273685 tomato callus, TAMU Lycopersicon...	171 6e-48
	emb AW033033 AW033033 EST276592 tomato callus, TAMU Lycopersicon...	170 1e-47
	emb AW030771 AW030771 EST274026 tomato callus, TAMU Lycopersicon...	170 1e-47
10	emb AW032046 AW032046 EST275500 tomato callus, TAMU Lycopersicon...	170 1e-47
	emb AW032073 AW032073 EST275527 tomato callus, TAMU Lycopersicon...	168 5e-47
	emb AW030260 AW030260 EST273515 tomato callus, TAMU Lycopersicon...	166 2e-46
	emb AI489927 AI489927 EST248266 tomato ovary, TAMU Lycopersicon ...	165 5e-46
	emb AI488082 AI488082 EST246404 tomato ovary, TAMU Lycopersicon ...	184 5e-46
15	emb AI486820 AI486820 EST245142 tomato ovary, TAMU Lycopersicon ...	184 7e-46
	emb AW034205 AW034205 EST277776 tomato callus, TAMU Lycopersicon...	163 1e-45
	emb AW030158 AW030158 EST273413 tomato callus, TAMU Lycopersicon...	163 2e-45
	emb AW034505 AW034505 EST278121 tomato callus, TAMU Lycopersicon...	180 6e-45
	emb AW036026 AW036026 EST276742 tomato callus, TAMU Lycopersicon...	166 8e-45
20	emb AW032069 AW032069 EST275523 tomato callus, TAMU Lycopersicon...	158 5e-44
	emb AW032994 AW032994 EST276553 tomato callus, TAMU Lycopersicon...	160 7e-43
	emb AW216803 AW216803 EST295517 tomato callus, TAMU Lycopersicon...	160 7e-43
	emb AW033731 AW033731 EST277302 tomato callus, TAMU Lycopersicon...	159 1e-42
	emb AW685851 AW685851 NF035H03NR1F1000 Nodulated root Medicago t...	112 2e-41
25	emb AI776989 AI776989 EST252081 tomato callus, TAMU Lycopersicon...	166 1e-40
	emb AW035944 AW035944 EST282803 tomato callus, TAMU Lycopersicon...	144 7e-40
	emb AW034103 AW034103 EST277598 tomato callus, TAMU Lycopersicon...	144 7e-40
	emb AW032974 AW032974 EST276533 tomato callus, TAMU Lycopersicon...	144 7e-40
	emb AI896142 AI896142 EST265585 tomato callus, TAMU Lycopersicon...	144 7e-40
30	gb BE022800 BE022800 sm88f04.y1 Gm-cl015 Glycine max cDNA clone ...	117 1e-38
	emb AI777033 AI777033 EST252000 tomato callus, TAMU Lycopersicon...	148 2e-38
	emb AW423417 AW423417 sh66e06.y1 Gm-cl015 Glycine max cDNA clone...	105 3e-37
	emb AW099273 AW099273 sd37e04.y1 Gm-cl016 Glycine max cDNA clone...	89 5e-37
	emb AW220190 AW220190 EST302673 tomato root during/after fruit s...	138 1e-36
35	emb AI896428 AI896428 EST265859 tomato callus, TAMU Lycopersicon...	132 2e-36
	emb AW033867 AW033867 EST277438 tomato callus, TAMU Lycopersicon...	127 1e-34
	emb AI896215 AI896215 EST265658 tomato callus, TAMU Lycopersicon...	126 1e-34
	emb AW423696 AW423696 sh50e10.y1 Gm-cl017 Glycine max cDNA clone...	117 4e-34
	emb AW706093 AW706093 sj51g03.y1 Gm-cl033 Glycine max cDNA clone...	144 1e-33
40	emb AI780237 AI780237 EST261116 tomato susceptible, Cornell Lyco...	139 2e-32
	emb AI352735 AI352735 MB56-1G PZ204.BNlib Brassica napus cDNA cl...	138 3e-32
	emb AW217026 AW217026 EST295740 tomato callus, TAMU Lycopersicon...	123 6e-32
	emb AW570043 AW570043 sj17a02.y1 Gm-cl032 Glycine max cDNA clone...	135 3e-31
	emb AW099281 AW099281 sd37f04.y1 Gm-cl016 Glycine max cDNA clone...	72 7e-31
45	emb AW573938 AW573938 EST316529 GVN Medicago truncatula cDNA clo...	77 7e-31
	emb AW032507 AW032507 EST276066 tomato callus, TAMU Lycopersicon...	113 9e-31
	emb AW032075 AW032075 EST275529 tomato callus, TAMU Lycopersicon...	112 2e-30
	emb AW033024 AW033024 EST276583 tomato callus, TAMU Lycopersicon...	111 3e-30
	emb AW216908 AW216908 EST295622 tomato callus, TAMU Lycopersicon...	108 4e-29
50	emb AW311014 AW311014 sg31e08.x1 Gm-cl024 Glycine max cDNA clone...	127 6e-29
	emb AV427017 AV427017 AV427017 Lotus japonicus young plants (two...	66 3e-28
	emb AI440724 AI440724 sa62g06.y1 Gm-cl004 Glycine max cDNA clone...	74 3e-28
	emb AV417820 AV417820 AV417820 Lotus japonicus young plants (two...	74 8e-28
	emb AW432916 AW432916 sh99g05.y1 Gm-cl016 Glycine max cDNA clone...	113 2e-27
55	emb AV415500 AV415500 AV415500 Lotus japonicus young plants (two...	74 2e-27
	emb AI896041 AI896041 EST265484 tomato callus, TAMU Lycopersicon...	102 2e-27
	emb AV426857 AV426857 AV426857 Lotus japonicus young plants (two...	74 5e-27
	emb AW596730 AW596730 sj16a08.y1 Gm-cl032 Glycine max cDNA clone...	120 1e-26
	emb AW776958 AW776958 EST336023 DSIL Medicago truncatula cDNA cl...	117 7e-26
60	emb AW573973 AW573973 EST316564 GVN Medicago truncatula cDNA clo...	67 3e-24
	emb AW216899 AW216899 EST295613 tomato callus, TAMU Lycopersicon...	86 3e-23

emb|AV414410|AV414410 AV414410 Lotus japonicus young plants (two... 62 2e-22
emb|AI776990|AI776990 EST252082 tomato callus, TAMU Lycopersicon... 105 4e-22
emb|AW032747|AW032747 EST276306 tomato callus, TAMU Lycopersicon... 82 3e-21
emb|AW349817|AW349817 GM210005B12D5R Gm-r1021 Glycine max cDNA 3... 100 9e-21
5
emb|AW216349|AW216349 EST295093 tomato callus, TAMU Lycopersicon... 100 2e-20
emb|AI960775|AI960775 sc90c07.y1 Gm-cl019 Glycine max cDNA clone... 63 3e-20
emb|AW686891|AW686891 NF003F09RT1F1000 Developing root Medicago ... 62 1e-19
emb|AI055043|AI055043 coau0002O01 Cotton Boll Abscission Zone cD... 68 8e-19
10
emb|AW687417|AW687417 NF009D05RT1F1045 Developing root Medicago ... 93 2e-18
emb|AV426494|AV426494 AV426494 Lotus japonicus young plants (two... 63 2e-18
emb|AW102192|AW102192 sd84e05.y1 Gm-cl009 Glycine max cDNA clone... 93 3e-18
emb|AV419918|AV419918 AV419918 Lotus japonicus young plants (two... 63 4e-18
emb|AV426405|AV426405 AV426405 Lotus japonicus young plants (two... 63 1e-17
15
emb|AT000898|AT000898 AT000898 Brassica rapa guard cell Brassica... 90 2e-17
emb|AW101413|AW101413 sd79f01.y1 Gm-cl009 Glycine max cDNA clone... 55 2e-17
emb|AW035459|AW035459 EST281197 tomato callus, TAMU Lycopersicon... 73 5e-17
emb|AW102127|AW102127 sd83e05.y1 Gm-cl009 Glycine max cDNA clone... 88 9e-17
emb|AV427127|AV427127 AV427127 Lotus japonicus young plants (two... 63 1e-16
20
emb|AW738963|AW738963 gb16h01.y1 Moss EST library PPN Physcomitr... 85 3e-16
emb|AV420136|AV420136 AV420136 Lotus japonicus young plants (two... 63 4e-16
emb|AV423861|AV423861 AV423861 Lotus japonicus young plants (two... 63 4e-16
emb|AI960004|AI960004 sc36e08.x1 Gm-cl014 Glycine max cDNA clone... 83 2e-15
emb|AW065130|AW065130 ST40A06 Pine TriplEx shoot tip library Pin... 72 2e-15
25
emb|AW207915|AW207915 M111138e DSIR Medicago truncatula cDNA clo... 65 1e-14
gb|C96147|C96147 C96147 Marchantia polymorpha immature sex organ... 46 3e-14
emb|AV426062|AV426062 AV426062 Lotus japonicus young plants (two... 62 4e-14
emb|AW133380|AW133380 se18b08.y1 Gm-cl015 Glycine max cDNA clone... 77 2e-13
emb|AV408625|AV408625 AV408625 Lotus japonicus young plants (two... 60 2e-13
30
emb|AI725475|AI725475 BNLGHi12255 Six-day Cotton fiber Gossypium... 54 4e-13
emb|AI487763|AI487763 EST246085 tomato ovary, TAMU Lycopersicon ... 73 3e-12
emb|AW573972|AW573972 EST316563 GVN Medicago truncatula cDNA clo... 54 6e-12
emb|AW625608|AW625608 EST319515 tomato radicle, 5 d post-imbibit... 54 7e-12
35
Query= AC005489.2_at 20189_at /id_source genbank /description
gb|aad32864.1|ac005489_2 (ac005489) fl4n23.2 [arabidopsis thaliana]
/blast_score 2.00e-57 /ec_number /family /chip nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-
40
post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005489|/ncgi
http://www.ncgr.org/cgi-bin/ff?ac005489
(504 letters)
Database: plantfungal
45
661,018 sequences; 426,114,510 total letters
Searching.....done
Score E
50
Sequences producing significant alignments: (bits) Value
emb|AW703956|AW703956 sk14d08.y1 Gm-cl023 Glycine max cDNA clone... 64 4e-18
emb|AW102211|AW102211 sd84g10.y1 Gm-cl009 Glycine max cDNA clone... 64 8e-18
emb|AW102144|AW102144 sd83g10.y1 Gm-cl009 Glycine max cDNA clone... 64 1e-16
55
emb|AW687497|AW687497 NF010C03RT1F1020 Developing root Medicago ... 53 6e-12
emb|AW255241|AW255241 ML241 peppermint glandular trichome Mentha... 50 1e-10
emb|AV425186|AV425186 AV425186 Lotus japonicus young plants (two... 55 1e-10
emb|AW597737|AW597737 sj97d03.y1 Gm-cl023 Glycine max cDNA clone... 39 1e-09
emb|AW472079|AW472079 si19f11.y1 Gm-cl029 Glycine max cDNA clone... 46 9e-09
60
emb|AI965429|AI965429 sc71f12.y1 Gm-cl016 Glycine max cDNA clone... 44 2e-08
emb|AV409094|AV409094 AV409094 Lotus japonicus young plants (two... 55 5e-07

	emb AW040753 AW040753 EST283617 tomato mixed elicitor, BTI Lycop...	37	6e-07
	emb AW040757 AW040757 EST283621 tomato mixed elicitor, BTI Lycop...	37	8e-07
	emb AV420178 AV420178 AV420178 Lotus japonicus young plants (two...	41	0.007
	emb AI812313 AI812313 10G1 Pine Lambda Zap Xylem library Pinus t...	33	0.026
5	emb AW985454 AW985454 NXNV_136_G09_F Nsf Xylem Normal wood Verti...	33	0.026
	emb AW985465 AW985465 NXNV_136_H10_F Nsf Xylem Normal wood Verti...	37	0.084
	emb AW216679 AW216679 EST295393 tomato callus, TAMU Lycopersicon...	37	0.084
	emb AW324783 AW324783 NXNV026E10F Nsf Xylem Normal wood Vertical...	28	0.71
	emb AW754722 AW754722 PC07A05 Pine TriplEx pollen cone library P...	26	1.5
10	emb AW094476 AW094476 EST287656 tomato mixed elicitor, BTI Lycop...	33	2.0
	gb U71016 DGU71016 Dactylis glomerata NADH dehydrogenase subunit...	32	2.8
	gb U71028 HBU71028 Hordeum brevisubulatum NADH dehydrogenase sub...	32	2.8
	emb AF056181 AF056181 Hordeum bogdanii NADH dehydrogenase subuni...	32	2.8
	gb U22260 NTU22260 Nicotiana tabacum UMP synthase (pyr5-6) mRNA,...	32	3.8
15	emb AF236867 AF236867 Poa secunda NADH dehydrogenase subunit F (...	31	5.2
	gb U21924 ORU21924 Oryzopsis racemosa NADH dehydrogenase F (ndhF...	31	5.2
	gb U71025 TAU71025 Triticum aestivum NADH dehydrogenase subunit ...	31	5.2
	gb U71047 ORU71047 Oryzopsis racemosa NADH dehydrogenase subunit...	31	5.2
	gb U71049 MCU71049 Melica ciliata NADH dehydrogenase subunit F (...	31	5.2
20	gb U71023 SMU71023 Secale montanum NADH dehydrogenase subunit F ...	31	5.2
	gb U71015 FRU71015 Festuca rubra NADH dehydrogenase subunit F (n...	31	5.2
	gb U71027 ERU71027 Elytrigia repens NADH dehydrogenase subunit F...	31	5.2
	gb U71033 BEU71033 Bromopsis erecta NADH dehydrogenase subunit F...	31	5.2
	emb AW287747 AW287747 LG1_271_H07.b1_A002 Light Grown 1 (LG1) So...	31	5.2
25	emb AF108029 AF108029 Elymus elymoides NADH dehydrogenase subuni...	31	5.2
	emb AF108028 AF108028 Elymus elymoides x Leymus salinus subsp. s...	31	5.2
	emb AF056180 AF056180 Pseudoroegneria spicata NADH dehydrogenase...	31	5.2
	emb AF056179 AF056179 Leymus cinereus NADH dehydrogenase subunit...	31	5.2
	emb AF056178 AF056178 Pascopyrum smithii cultivar Atkins142 NADH...	31	5.2
30	emb AF056177 AF056177 Pascopyrum smithii cultivar Walsh NADH deh...	31	5.2
	emb AF056176 AF056176 Pascopyrum smithii cultivar Epc-8 NADH deh...	31	5.2
	emb AF056175 AF056175 Pascopyrum smithii cultivar Rosanna NADH d...	31	5.2
	emb AF056174 AF056174 Pascopyrum smithii cultivar Barton NADH de...	31	5.2
	emb AF056173 AF056173 Pascopyrum smithii cultivar Atkins172 NADH...	31	5.2
35	emb AF056172 AF056172 Pascopyrum smithii cultivar Arriba NADH de...	31	5.2
	emb AF056171 AF056171 Pascopyrum smithii cultivar R-9-1-5 NADH ...	31	5.2
	emb AF056170 AF056170 Pascopyrum smithii cultivar Rodan NADH deh...	31	5.2
	emb AF056169 AF056169 Pascopyrum smithii cultivar Flintlock NADH...	31	5.2
	emb AF056168 AF056168 Elymus lanceolatus subsp. wawawaiensis NAD...	31	5.2
40	emb AF056167 AF056167 Psathyrostachys juncea NADH dehydrogenase ...	31	5.2
	emb AF056166 AF056166 Elymus lanceolatus subsp. lanceolatus NADH...	31	5.2
	emb AF056165 AF056165 Leymus triticoides NADH dehydrogenase subu...	31	5.2
	gb U22003 HVVU22003 Hordeum vulgare NADH dehydrogenase F (ndhF) g...	31	5.2
	gb U21999 DOU21999 Diarrhena obovata NADH dehydrogenase F (ndhF)...	31	5.2
45	gb U71011 SAU71011 Sesleria argentea NADH dehydrogenase subunit ...	31	7.1
	gb U22006 PGU22006 Phaenosperma globosa NADH dehydrogenase F (nd...	31	7.1
	gb U22000 ASU22000 Avena sativa NADH dehydrogenase F (ndhF) gene...	31	7.1
	emb AZ214488 AZ214488 Sheared DNA-78B7.TF Sheared DNA Trypanosom...	31	7.1
	emb AI736210 AI736210 sb24h08.y1 Gm-c1008 Glycine max cDNA clone...	31	7.1
50	gb U71048 GDU71048 Glyceria declinata NADH dehydrogenase subunit...	31	7.1
	gb U71018 AFU71018 Avena fatua NADH dehydrogenase subunit F (ndh...	31	7.1
	gb M31615 TRBESAGF T.brucei metacyclic expression site-associate...	31	7.1
	emb AQ944873 AQ944873 Sheared DNA-36B24.TF Sheared DNA Trypanoso...	31	7.1
	emb AF108030 AF108030 Leymus salinus subsp. salmonis NADH dehydr...	31	7.1
55	emb AI856529 AI856529 sb40e03.y1 Gm-c1014 Glycine max cDNA clone...	31	7.1
	gb U71041 BPU71041 Brachypodium pinnatum NADH dehydrogenase subu...	30	9.8
	gb U71042 BAU71042 Brachypodium arbuscula NADH dehydrogenase sub...	30	9.8
	emb AQ640138 AQ640138 927P1-18A6.TP 927P1 Trypanosoma brucei gen...	30	9.8
	emb AQ655335 AQ655335 Sheared DNA-25B9.TF Sheared DNA Trypanosom...	30	9.8
60	Query= AL022347.145_at 20223_at /id_source genbank /description		

emb|caal8469.1| (al022347) serine/threonine kinase-like protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family kinase /chip
 nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 5 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022347| /ncgi
 http://www.ncgr.org/cgi-bin/ff?al022347
 (2703 letters)

Database: plantfungal
 10 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	
15	Sequences producing significant alignments:	(bits)	Value
	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k...	318	e-148
	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2.	289	3e-96
	emb Y18260 BOY18260 Brassica oleracea mRNA for SRK15 protein, pa...	280	8e-93
20	emb AB024416 AB024416 Brassica oleracea SRK2-b mRNA, complete cds.	281	3e-92
	emb Y18259 BOY18259 Brassica oleracea mRNA for SRK5 protein, par...	280	1e-91
	emb Y14285 BOY14285 Brassica oleracea mRNA for SFR1 protein.	268	1e-91
	emb AB008191 AB008191 Brassica rapa mRNA for SRK29, complete cds.	278	3e-91
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	271	8e-90
25	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	272	2e-89
	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR...	221	5e-88
	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	277	9e-88
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	272	9e-88
	emb Y12530 BOARLKGEN B.oleraceae gene encoding serine/threonine ...	133	1e-85
30	dbj D30049 BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti...	277	2e-85
	emb AW620957 AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone...	252	5e-84
	gb BE034855 BE034855 ML05C11 ML Mesembryanthemum crystallinum cD...	272	5e-84
	gb U20948 ITU20948 Ipomoea trifida receptor protein kinase (IRK1...	224	6e-84
	emb Y14286 BOY14286 Brassica oleracea SFR3 gene, partial.	182	6e-84
35	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	275	2e-82
	emb AB000970 AB000970 Brassica campestris gene for receptor kina...	129	6e-82
	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti...	266	4e-81
	emb AF088885 AF088885 Nicotiana tabacum receptor-like kinase CHR...	258	1e-80
	emb AB032474 AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc...	265	2e-80
40	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	273	1e-79
	gb BE057261 BE057261 sm99f12.y1 Gm-c1015 Glycine max cDNA clone ...	297	3e-79
	emb AB000971 AB000971 Brassica campestris pseudogene for recepto...	115	3e-78
	dbj D38563 BOLRPKA Brassica campestris mRNA for receptor protein...	262	9e-77
	dbj D38564 BOLRPKB Brassica campestris mRNA for receptor protein...	264	2e-76
45	emb AW031255 AW031255 EST274630 tomato callus, TAMU Lycopersicon...	279	2e-76
	emb AJ245480 BNA245480 Brassica napus slg gene for S-locus glyco...	126	3e-76
	emb Y12531 BOBRLKGEN B.oleraceae gene encoding serine/threonine ...	128	2e-75
	emb AW760240 AW760240 sl59g07.y1 Gm-c1027 Glycine max cDNA clone...	280	3e-74
	emb X79432 BOSRK3 B.oleracea SRK3 gene.	117	4e-74
50	emb AI895838 AI895838 EST265281 tomato callus, TAMU Lycopersicon...	266	5e-70
	emb AW442344 AW442344 EST311740 tomato fruit red ripe, TAMU Lyco...	200	5e-68
	emb AJ245479 BNA245479 Brassica napus Sl13, slk, srk, CePP, Fmt,...	122	2e-67
	dbj D88193 D88193 Brassica rapa DNA for S-receptor kinase, compl...	122	1e-65
	emb Z18921 BOSRKL B.oleracea gene for S-receptor kinase-like pro...	113	6e-65
55	emb AB024422 AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ...	108	7e-65
	emb AW831390 AW831390 sm22a06.y1 Gm-c1028 Glycine max cDNA clone...	184	9e-65
	gb BE034949 BE034949 ML07F03 ML Mesembryanthemum crystallinum cD...	216	4e-64
	emb Z30211 BOSRK29G B.oleracea (alboglabra) srk29 gene.	120	2e-63
	emb AB024420 AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,...	108	1e-62
60	emb AB013718 AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,...	106	3e-62
	emb AW309544 AW309544 sf20h08.x1 Gm-c1028 Glycine max cDNA clone...	235	8e-62

	emb AW220676 AW220676 EST297145 tomato fruit mature green, TAMU ...	227	7e-61
	emb AI486193 AI486193 EST244514 tomato ovary, TAMU Lycopersicon ...	164	1e-60
	emb AW666141 AW666141 sk32f11.y1 Gm-cl028 Glycine max cDNA clone...	174	1e-58
	emb AW220677 AW220677 EST297146 tomato fruit mature green, TAMU ...	221	4e-58
5	emb AW220675 AW220675 EST297144 tomato fruit mature green, TAMU ...	225	1e-57
	emb AI897876 AI897876 EST267319 tomato ovary, TAMU Lycopersicon ...	158	1e-56
	emb AI486584 AI486584 EST244905 tomato ovary, TAMU Lycopersicon ...	158	2e-55
	emb Y16999 TCA16999 Theobroma cacao microsatellite DNA, clone mT...	133	3e-55
	emb AI901283 AI901283 sc31d08.y1 Gm-cl014 Glycine max cDNA clone...	179	1e-54
10	emb Z18884 BOSRKRPC B.oleracea encoding S-receptor kinase relate...	133	5e-54
	emb AW736407 AW736407 EST332421 KV3 Medicago truncatula cDNA clo...	192	1e-53
	emb AI967314 AI967314 Ljimpest00-017 Ljimp Lambda HybriZap two...	119	2e-53
	emb AW203661 AW203661 sf36g06.y1 Gm-cl028 Glycine max cDNA clone...	183	4e-53
	emb AW033458 AW033458 EST277029 tomato callus, TAMU Lycopersicon...	191	3e-50
15	emb AW039406 AW039406 EST281663 tomato mixed elicitor, BTI Lycop...	111	9e-50
	emb AI896953 AI896953 EST266396 tomato callus, TAMU Lycopersicon...	168	9e-50
	emb AI895623 AI895623 EST265066 tomato callus, TAMU Lycopersicon...	199	1e-49
	emb AW684339 AW684339 NF015G04NR1F1000 Nodulated root Medicago t...	111	2e-49
	emb AI896155 AI896155 EST265598 tomato callus, TAMU Lycopersicon...	181	6e-49
20	emb AW667985 AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ...	91	3e-48
	emb AI899009 AI899009 EST268452 tomato ovary, TAMU Lycopersicon ...	140	2e-47
	emb AF142596 AF142596 Nicotiana tabacum LRR receptor-like protei...	77	2e-46
	emb AB041503 AB041503 Populus nigra PnPK1 mRNA for protein kinas...	119	2e-46
	emb AI771857 AI771857 EST252957 tomato ovary, TAMU Lycopersicon ...	136	3e-46
25	emb AI488101 AI488101 EST246423 tomato ovary, TAMU Lycopersicon ...	136	3e-46
	emb AI729170 AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium...	128	3e-46
	emb AW034624 AW034624 EST278308 tomato callus, TAMU Lycopersicon...	170	4e-46
	emb AW031816 AW031816 EST275270 tomato callus, TAMU Lycopersicon...	126	6e-46
	emb AI898581 AI898581 EST268024 tomato ovary, TAMU Lycopersicon ...	140	8e-46
30	emb AI899156 AI899156 EST268599 tomato ovary, TAMU Lycopersicon ...	140	8e-46
	emb Z18883 BOSRKRPB B.oleracea encoding S-receptor kinase relate...	183	2e-45
	emb AI486331 AI486331 EST244652 tomato ovary, TAMU Lycopersicon ...	140	7e-45
	emb AA738545 AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg...	117	2e-44
	emb AI484701 AI484701 EST242962 tomato ovary, TAMU Lycopersicon ...	99	2e-44
35	emb Z18862 BOSRKRPD B.oleracea encoding S-receptor kinase protein...	93	4e-44
	emb Z18861 BOSRKRPA B.oleracea encoding S-receptor kinase relate...	113	1e-43
	emb AI772117 AI772117 EST253217 tomato resistant, Cornell Lycop...	142	3e-43
	emb AW668493 AW668493 GA_Ea0014C20 Gossypium arboreum 7-10 dpa ...	121	4e-43
	emb AB030083 AB030083 Populus nigra PnLPK mRNA for lectin-like p...	79	9e-43
40	emb AI822355 AI822355 L0-804T3 Ice plant Lambda Uni-Zap XR expre...	123	7e-42
	emb AI822907 AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr...	123	7e-42
	emb AW687233 AW687233 NF007D09RT1F1077 Developing root Medicago ...	84	8e-42
	emb Y14600 SBRLK1 Sorghum bicolor mRNA for protein serine/threon...	73	1e-41
	emb AB041504 AB041504 Populus nigra PnPK2 mRNA for protein kinas...	73	1e-41
45	emb AW706972 AW706972 sk20a03.y1 Gm-cl028 Glycine max cDNA clone...	148	2e-41
	emb AW279355 AW279355 sf65g10.y1 Gm-cl013 Glycine max cDNA clone...	103	6e-41
	emb AW776492 AW776492 EST335557 DSIL Medicago truncatula cDNA cl...	169	8e-41
	gb U51330 TAU51330 Triticum aestivum leaf rust resistance kinase...	83	8e-41
	emb AI896318 AI896318 EST265761 tomato callus, TAMU Lycopersicon...	85	1e-40
50	emb AI731504 AI731504 BNLGHi9991 Six-day Cotton fiber Gossypium ...	69	1e-40
	emb AF085164 AF085164 Hordeum vulgare receptor-like kinase LRK10...	83	2e-40
	gb BE058691 BE058691 sn19e05.y1 Gm-cl016 Glycine max cDNA clone ...	87	3e-40
	emb AW597214 AW597214 si71g06.y1 Gm-cl031 Glycine max cDNA clone...	91	1e-39
	emb AF220603 AF220603 Lycopersicon esculentum VFNT Cherry Pto lo...	68	1e-39
55	gb U59316 LEU59316 Lycopersicon esculentum serine/threonine prot...	68	1e-39

Query= AL022347.12_s_at 20232_s_at /id_source genbank /description
emb|caa18460.1| (al022347) protein kinase-like protein [arabidopsis
60 thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
/ncgi

(1953 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5

Searching.....done

		Score	E	
	Sequences producing significant alignments:	(bits)	Value	
10	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k...	330	e-134	
	gb U20948 ITU20948 Ipomoea trifida receptor protein kinase (IRK1...	224	e-107	
	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR...	215	e-105	
	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	297	e-104	
15	dbj D30049 BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti...	285	e-103	
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	287	e-103	
	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	304	e-102	
	emb AB032474 AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc...	289	e-102	
	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti...	292	e-102	
20	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	291	e-101	
	emb AB008191 AB008191 Brassica rapa mRNA for SRK29, complete cds.	303	e-101	
	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2.	299	e-101	
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	294	e-101	
	emb Y18260 BOY18260 Brassica oleracea mRNA for SRK15 protein, pa...	301	e-101	
25	emb AB024416 AB024416 Brassica oleracea SRK2-b mRNA, complete cds.	302	e-101	
	dbj D38564 BOLRPKB Brassica campestris mRNA for receptor protein...	287	e-100	
	emb Y14285 BOY14285 Brassica oleracea mRNA for SFR1 protein.	295	e-100	
	dbj D38563 BOLRPKA Brassica campestris mRNA for receptor protein...	288	e-100	
	emb Y18259 BOY18259 Brassica oleracea mRNA for SRK5 protein, par...	303	e-100	
30	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	290	2e-99	
	emb AW620957 AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone...	270	3e-93	
	emb AF088885 AF088885 Nicotiana tabacum receptor-like kinase CHR...	264	3e-93	
	gb BE034855 BE034855 ML05C11 ML Mesembryanthemum crystallinum cD...	286	2e-92	
	emb Y14286 BOY14286 Brassica oleracea SFR3 gene, partial.	199	6e-92	
35	gb BE057261 BE057261 sm99f12.y1 Gm-c1015 Glycine max cDNA clone ...	310	3e-83	
	emb AW031255 AW031255 EST274630 tomato callus, TAMU Lycopersicon...	277	1e-80	
	emb Y12531 BOBRLKGEN B.oleraceae gene encoding serine/threonine ...	127	7e-80	
	emb Y12530 BOARLKGEN B.oleraceae gene encoding serine/threonine ...	129	3e-76	
	emb AW760240 AW760240 sl59g07.y1 Gm-c1027 Glycine max cDNA clone...	284	2e-75	
40	emb AJ245480 BNA245480 Brassica napus slg gene for S-locus glyco...	126	3e-75	
	emb AJ245479 BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,...	126	4e-75	
	emb AB000970 AB000970 Brassica campestris gene for receptor kina...	126	2e-74	
	emb Z18921 BOSRKL B.oleracea gene for S-receptor kinase-like pro...	119	3e-74	
	emb X79432 BOSRK3 B.oleracea SRK3 gene.	118	8e-74	
45	emb AB024422 AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ...	117	1e-73	
	emb AB024420 AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,...	116	2e-73	
	emb Z30211 BOSRK29G B.oleracea (alboglabra) srk29 gene.	121	8e-73	
	emb AI895838 AI895838 EST265281 tomato callus, TAMU Lycopersicon...	275	8e-73	
	emb AB013718 AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,...	116	1e-72	
50	dbj D88193 D88193 Brassica rapa DNA for S-receptor kinase, compl...	124	1e-71	
	emb AW831390 AW831390 sm22a06.y1 Gm-c1028 Glycine max cDNA clone...	211	3e-71	
	emb AB000971 AB000971 Brassica campestris pseudogene for recepto...	109	3e-68	
	emb AW442344 AW442344 EST311740 tomato fruit red ripe, TAMU Lyco...	206	9e-67	
	emb AW309544 AW309544 sf20h08.x1 Gm-c1028 Glycine max cDNA clone...	254	1e-66	
55	emb AI486193 AI486193 EST244514 tomato ovary, TAMU Lycopersicon ...	179	3e-66	
	gb BE034949 BE034949 ML07F03 ML Mesembryanthemum crystallinum cD...	225	2e-65	
	emb AI896155 AI896155 EST265598 tomato callus, TAMU Lycopersicon...	186	4e-64	
	emb AI486584 AI486584 EST244905 tomato ovary, TAMU Lycopersicon ...	176	4e-63	
	emb AI897876 AI897876 EST267319 tomato ovary, TAMU Lycopersicon ...	176	1e-62	
60	emb AW203661 AW203661 sf36g06.y1 Gm-c1028 Glycine max cDNA clone...	202	4e-61	
	emb AW666141 AW666141 sk32f11.y1 Gm-c1028 Glycine max cDNA clone...	178	7e-61	

- emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 231 1e-59
 emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 231 2e-59
 emb|AW220677|AW220677 EST297146 tomato fruit mature green, TAMU ... 227 2e-58
 emb|AI901283|AI901283 sc31d08.y1 Gm-cl014 Glycine max cDNA clone... 180 3e-57
 5 emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 124 8e-57
 emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 194 2e-56
 emb|AW667985|AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ... 91 4e-56
 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 127 1e-54
 emb|Y16999|TCA16999 Theobroma cacao microsatellite DNA, clone mT... 125 1e-53
 10 emb|Z18884|BOSRKRPC B.oleracea encoding S-receptor kinase relate... 129 2e-53
 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 141 2e-53
 emb|AI896953|AI896953 EST266396 tomato callus, TAMU Lycopersicon... 184 3e-53
 emb|AI967314|AI967314 Ljimpest00-017 Ljimp Lambda HybriZap two... 143 6e-53
 emb|AW033458|AW033458 EST277029 tomato callus, TAMU Lycopersicon... 184 8e-53
 15 emb|AI899009|AI899009 EST268452 tomato ovary, TAMU Lycopersicon ... 161 4e-52
 emb|AI771857|AI771857 EST252957 tomato ovary, TAMU Lycopersicon ... 157 5e-51
 emb|AI488101|AI488101 EST246423 tomato ovary, TAMU Lycopersicon ... 157 5e-51
 emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 140 7e-51
 emb|AI898581|AI898581 EST268024 tomato ovary, TAMU Lycopersicon ... 161 1e-50
 20 emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 105 2e-50
 emb|AI822907|AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr... 112 5e-50
 emb|AI899156|AI899156 EST268599 tomato ovary, TAMU Lycopersicon ... 161 6e-50
 emb|AI822355|AI822355 L0-804T3 Ice plant Lambda Uni-Zap XR expre... 112 1e-49
 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 136 8e-49
 25 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 128 2e-48
 emb|Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 78 2e-48
 emb|Z18861|BOSRKRPA B.oleracea encoding S-receptor kinase relate... 119 3e-48
 emb|AW034624|AW034624 EST278308 tomato callus, TAMU Lycopersicon... 166 1e-47
 emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 161 1e-47
 30 emb|AW279355|AW279355 sf65g10.y1 Gm-cl013 Glycine max cDNA clone... 115 2e-47
 emb|AW054349|AW054349 L30-1774T3 Ice plant Lambda Uni-Zap XR exp... 112 2e-47
 emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 86 3e-47
 emb|Z18883|BOSRKRPB B.oleracea encoding S-receptor kinase relate... 176 3e-46
 emb|AW706972|AW706972 sk20a03.y1 Gm-cl028 Glycine max cDNA clone... 157 8e-46
 35 emb|AI822347|AI822347 L0-796T3 Ice plant Lambda Uni-Zap XR expre... 107 1e-45
 emb|AI895623|AI895623 EST265066 tomato callus, TAMU Lycopersicon... 185 1e-45
 emb|AB030083|AB030083 Populus nigra PnLPK mRNA for lectin-like p... 86 1e-45
 gb|BE058691|BE058691 sn19e05.y1 Gm-cl016 Glycine max cDNA clone ... 99 2e-45
 emb|AW278186|AW278186 sf40g07.y1 Gm-cl009 Glycine max cDNA clone... 95 4e-45
 40 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 72 8e-45
 gb|U51330|TAU51330 Triticum aestivum leaf rust resistance kinase... 80 5e-44
 emb|Z18862|BOSRKRPD B.oleracea encoding S-receptor kinase protein. 89 1e-43
 emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 78 1e-43
 emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 89 2e-43
 45 gb|U28007|LEU28007 Lycopersicon esculentum Pto kinase interactor... 129 5e-43
 emb|AW982539|AW982539 HVSMEg0003I16f Hordeum vulgare pre-anthesi... 82 5e-43
 emb|AW034993|AW034993 EST279222 tomato callus, TAMU Lycopersicon... 164 6e-43
 emb|AW687052|AW687052 NF005E02RT1F1017 Developing root Medicago ... 175 9e-43
 emb|AW597214|AW597214 si71g06.y1 Gm-cl031 Glycine max cDNA clone... 127 2e-42

50

Query= X74514.2_at 20238_at /id_source genbank /description
 emb|caa52619.1| (x74514) beta-fructofuranosidase [arabidopsis
 thaliana] /blast_score 0 /ec_number ec_3.2.1.26 /family hydrolase
 55 /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x74514|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|x74514|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x74514|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?x74514>
 (1947 letters)

60

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5	Score	E	
	Sequences producing significant alignments:	(bits)	Value
	emb AF000521 AF000521 <i>Fragaria x ananassa</i> cell wall invertase pr...	413	0.0
	emb Z35163 VFCWINV2 <i>V.faba</i> VFCWINV2 mRNA for cell wall invertase...	418	0.0
10	gb M58362 DARBFUC <i>D.carota</i> cell wall beta-fructosidase mRNA, co...	239	0.0
	emb X81792 CRCIN1 <i>C.rubrum</i> CIN1 mRNA for extracellular invertase.	181	0.0
	emb X81834 NTMRNABDF <i>N.tabacum</i> mRNA for beta-fructosidase.	205	0.0
	emb AF030420 AF030420 <i>Triticum aestivum</i> cell wall invertase (IVR...	240	0.0
	emb Y11176 CIFRUCTOS <i>C.intybus</i> mRNA for fructosidase.	144	0.0
15	emb Z21486 STBETFRUA <i>S.tuberosum</i> mRNA for invertase gene encodin...	196	e-180
	emb AJ272305 LPE272305 <i>Lycopersicon pennellii</i> mRNA for beta-fruc...	190	e-170
	emb X85327 PSRNABFRU <i>P.sativum</i> mRNA for beta-fructofuranosidase.	398	e-169
	emb AF063246 AF063246 <i>Pisum sativum</i> cell wall invertase (bfructl...	398	e-169
20	emb AJ272304 LES272304 <i>Lycopersicon esculentum</i> mRNA for beta-fru...	190	e-169
	emb Z22645 STBETFRCA <i>S.tuberosum</i> invertase gene encoding beta-fr...	204	e-166
	emb AF000520 AF000520 <i>Fragaria x ananassa</i> cell wall invertase (I...	210	e-164
	emb AB004558 AB004558 <i>Lycopersicon esculentum</i> mRNA for acid inve...	200	e-164
	emb X69321 DCBFRUCT <i>D.carota</i> (Queen Anne's Lace) Inv*Dc1 gene.	178	e-145
	emb X78424 DCINC1 <i>D.carota</i> (Queen Anne's Lace) Inv*Dc2 gene, 343...	161	e-136
25	emb Z35162 VFCWINV1 <i>V.faba</i> VFCWINV1 mRNA for cell wall invertase I.	207	e-132
	emb AF030421 AF030421 <i>Triticum aestivum</i> cell wall invertase (IVR...	138	e-130
	emb AJ133765 STU133765 <i>Solanum tuberosum</i> invGE and invGF genes.	148	e-128
	gb U87849 CAU87849 <i>Capsicum annuum</i> acid beta-fructosidase mRNA, ...	200	e-126
	emb AJ006067 ACE6067 <i>Allium cepa</i> mRNA for invertase.	210	e-126
30	emb A94218 A94218 Sequence 1 from Patent EP0952222.	176	e-122
	emb AF002656 AF002656 <i>Asparagus officinalis</i> acid invertase mRNA,...	198	e-120
	gb U81520 CIU81520 <i>Cichorium intybus</i> sucrose:sucrose 1-fructosyl...	173	e-120
	emb X75351 DCRNABF <i>D.carota</i> (Nantaise) mRNA for soluble acid bet...	202	e-120
	emb X75353 DCRNASABF <i>D.carota</i> (Nantaise) mRNA for soluble acid b...	203	e-120
35	emb AJ272307 LPE272307 <i>Lycopersicon pennellii</i> lin 5 gene for bet...	145	e-119
	emb X75352 DCRNAABF <i>D.carota</i> (Nantaise) mRNA for soluble acid be...	203	e-119
	emb X78423 DCINUC1 <i>D.carota</i> (Queen Anne's Lace) Inv*Dc3 gene, 44...	160	e-118
	emb A94222 A94222 Sequence 5 from Patent EP0952222.	173	e-117
	emb Y09662 CSSS1FT <i>C.scolymus</i> mRNA for sucrose sucrose 1-fructos...	170	e-117
40	emb A86530 A86530 Sequence 1 from Patent WO9839460.	170	e-117
	emb AJ272306 LES272306 <i>Lycopersicon esculentum</i> lin 5 gene for be...	145	e-116
	emb AJ250634 TOF250634 <i>Taraxacum officinale</i> mRNA for sucrose:suc...	169	e-116
	emb Z49831 VFVCINVMR <i>V.faba</i> VFVCINV mRNA for invertase (beta-fru...	199	e-115
	gb U92438 PVU92438 <i>Phaseolus vulgaris</i> soluble acid invertase mRN...	198	e-114
45	emb AW686881 AW686881 NF003E07RT1F1000 Developing root <i>Medicago</i> ...	413	e-114
	dbj D10265 VIRINVA <i>Vigna radiata</i> mRNA for invertase, complete cds.	194	e-114
	emb AJ009757 HTU9757 <i>Helianthus tuberosus</i> sst-1 gene.	171	e-113
	emb A52468 A52468 Sequence 1 from Patent WO9621023.	171	e-113
	emb X70368 STPAIN1A <i>S.tuberosum</i> PAIN-1 mRNA for beta-fructofuran...	200	e-108
50	emb X67163 DCSBFRU <i>D.carota</i> mRNA for soluble beta-fructosidase.	140	e-107
	gb L29099 POTBFRUASE <i>Solanum tuberosum</i> beta-fructosidase mRNA, c...	198	e-107
	dbj E07108 E07108 cDNA encoding acid invertase.	198	e-106
	dbj D11350 TOMBFSO <i>Tomato</i> mRNA for beta-fructosidase, complete cds.	198	e-106
	emb Z12026 LPBFRUCM <i>L.pimpinellifolium</i> beta-fructosidase mRNA fo...	198	e-106
55	emb Z12025 LEBFRUCM <i>L.esculentum</i> beta-fructosidase mRNA for vacu...	198	e-106
	gb M81081 TOMACIN <i>Tomato</i> acid invertase (TIV1) mRNA, complete cds.	198	e-106
	gb S70040 S70040 acid invertase [<i>Lycopersicon esculentum</i> =tomatoe...	198	e-106
	dbj E16293 E16293 cDNA encoding invertase.	198	e-106
	dbj E08976 E08976 cDNA encoding tomato invertase.	198	e-106
60	emb AF017082 AF017082 <i>Ipomoea batatas</i> beta-fructofuranosidase (S...	141	e-103
	emb Y11124 CIPINVERT <i>C.intybus</i> mRNA for putative invertase.	138	e-102

emb|X97642|TGINV5GEN T.gesneriana mRNA for invertase 5. 180 6e-97
 emb|X95651|TGINV11GN T.gesneriana mRNA for invertase. 186 7e-96
 emb|X97643|TGINV6GEN T.gesneriana mRNA for invertase 6. 186 2e-94
 emb|Y18706|DCA18706 Daucus carota Inv*Dc5 gene. 130 2e-93
 5 emb|Y18707|DCA18707 Daucus carota Inv*Dc4, Inv*Dc4' (partial) ge... 161 2e-93
 emb|AF062735|AF062735 Saccharum officinarum soluble acid inverta... 129 1e-91
 emb|AF062734|AF062734 Saccharum robustum soluble acid invertase ... 129 1e-91
 emb|AF091549|AF091549 Hamamelis virginiana clone 7 beta-fructofu... 331 9e-90
 emb|AJ000481|CSFF1FRUC Cynara scolymus mRNA for fructan fructan ... 162 3e-89
 10 emb|AF091550|AF091550 Hamamelis virginiana clone C beta-fructofu... 330 3e-89
 emb|A94220|A94220 Sequence 3 from Patent EP0952222. 161 1e-88
 emb|AF091548|AF091548 Hamamelis virginiana clone 3 beta-fructofu... 327 1e-88
 gb|U84398|CIU84398 Cichorium intybus fructan-fructan 1-fructosyl... 161 5e-88
 emb|Z12028|LPBFRUCG L.pimpinellifolium gene encoding vacuolar in... 157 6e-88
 15 emb|Z12027|LEBFRUCG L.esculentum gene for vacuolar invertase. 157 6e-88
 emb|AJ009756|HTU9756 Helianthus tuberosus ffr-1 gene. 161 2e-87
 emb|A52470|A52470 Sequence 3 from Patent WO9621023. 161 2e-87
 emb|X81795|BVBIN35 B.vulgaris BIN35 mRNA for extracellular inver... 265 5e-86
 gb|BE055183|BE055183 GA__Ea0035H23f Gossypium arboreum 7-10 dpa ... 203 4e-83
 20 emb|X91392|LELIN8 L.esculentum mRNA for invertase (LIN8). 133 2e-82
 emb|AF091547|AF091547 Hamamelis virginiana clone 1 beta-fructofu... 295 3e-81
 emb|X81793|CRCIN2 C.rubrum CIN2 mRNA for intracellular invertase. 135 2e-80
 emb|X91389|LELIN5 L.esculentum mRNA for invertase (LIN5). 129 1e-78
 emb|X91391|LELIN7 L.esculentum mRNA for invertase (LIN7). 133 5e-78
 25 emb|Y07838|ACY07838 A.cepa mRNA for fructan:fructan 6G-fructosyl... 156 2e-77
 emb|X81796|BVBIN44 B.vulgaris BIN44 mRNA for intracellular inver... 149 5e-77
 emb|AF014925|AF014925 Citrus unshiu acid invertase (CUAI1) gene,... 138 4e-76
 emb|AJ006066|ACE6066 Allium cepa mRNA for sucrose sucrose 1-fruc... 132 2e-75
 emb|AF091545|AF091545 Hamamelis virginiana clone 4 beta-fructofu... 196 2e-75
 30 emb|A48282|A48282 Sequence 3 from Patent WO9601904. 152 4e-75
 emb|AW685050|AW685050 NF024F09NR1F1000 Nodulated root Medicago t... 248 5e-75
 emb|Z83339|PSZ83339 P.sativum mRNA for cell wall invertase II. 280 2e-74
 emb|AF091546|AF091546 Hamamelis virginiana clone 6 beta-fructofu... 193 3e-74
 emb|AV407850|AV407850 AV407850 Lotus japonicus young plants (two... 267 2e-70
 35 emb|A48284|A48284 Sequence 5 from Patent WO9601904. 130 1e-69
 emb|AW666614|AW666614 GA__Ea0005C10 Gossypium arboreum 7-10 dpa ... 207 3e-69
 emb|AW730389|AW730389 GA__Ea0023K22 Gossypium arboreum 7-10 dpa ... 141 2e-68
 emb|A48280|A48280 Sequence 1 from Patent WO9601904. 82 2e-68
 emb|X83233|HVSF6FT Hordeum vulgare mRNA for sucrose:fructan 6-fr... 82 2e-68
 40 emb|AF069309|AF069309 Triticum aestivum vacuolar invertase (WIVR... 127 5e-67
 emb|AW350139|AW350139 GM210007B20F11R Gm-r1021 Glycine max cDNA ... 112 4e-66
 emb|AW618261|AW618261 EST314311 L. pennellii trichome, Cornell U... 248 1e-64
 emb|AW738685|AW738685 EST340112 tomato flower buds, anthesis, Co... 189 3e-64
 emb|X91390|LELIN6 L.esculentum mRNA for invertase (LIN6). 133 5e-64
 45 emb|AI522941|AI522941 sa92d01.y1 Gm-c1004 Glycine max cDNA clone... 201 1e-63
 emb|AW441409|AW441409 EST310805 tomato fruit red ripe, TAMU Lyco... 114 4e-62
 Query= X74514.2_g_at 20239_g_at /id_source genbank /description
 emb|caa52619.1| (x74514) beta-fructofuranosidase [arabidopsis
 thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
 50 /ncgi
 (1947 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

55

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

60

emb|AF000521|AF000521 Fragaria x ananassa cell wall invertase pr... 413 0.0

- emb|Z35163|VFCWINV2 V.faba VFCWINV2 mRNA for cell wall invertase... 418 0.0
gb|M58362|DARBFUC D.carota cell wall beta-fructosidase mRNA, co... 239 0.0
emb|X81792|CRCIN1 C.rubrum CIN1 mRNA for extracellular invertase. 181 0.0
emb|X81834|NTMRNABDF N.tabacum mRNA for beta-fructosidase. 205 0.0
5 emb|AF030420|AF030420 Triticum aestivum cell wall invertase (IVR... 240 0.0
emb|Y11176|CIFRUCTOS C.intybus mRNA for fructosidase. 144 0.0
emb|Z21486|STBETFRUA S.tuberosum mRNA for invertase gene encodin... 196 e-180
emb|AJ272305|LPE272305 Lycopersicon pennellii mRNA for beta-fruc... 190 e-170
emb|X85327|PSRNABFRU P.sativum mRNA for beta-fructofuranosidase. 398 e-169
10 emb|AF063246|AF063246 Pisum sativum cell wall invertase (bfruct1... 398 e-169
emb|AJ272304|LES272304 Lycopersicon esculentum mRNA for beta-fru... 190 e-169
emb|Z22645|STBETFRCA S.tuberosum invertase gene encoding beta-fr... 204 e-166
emb|AF000520|AF000520 Fragaria x ananassa cell wall invertase (I... 210 e-164
emb|AB004558|AB004558 Lycopersicon esculentum mRNA for acid inve... 200 e-164
15 emb|X69321|DCBFRUCT D.carota (Queen Anne's Lace) Inv*Dc1 gene. 178 e-145
emb|X78424|DCINC1 D.carota (Queen Anne's Lace) Inv*Dc2 gene, 343... 161 e-136
emb|Z35162|VFCWINV1 V.faba VFCWINV1 mRNA for cell wall invertase I. 207 e-132
emb|AF030421|AF030421 Triticum aestivum cell wall invertase (IVR... 138 e-130
emb|AJ133765|STU133765 Solanum tuberosum invGE and invGF genes. 148 e-128
20 gb|U87849|CAU87849 Capsicum annuum acid beta-fructosidase mRNA, ... 200 e-126
emb|AJ006067|ACE6067 Allium cepa mRNA for invertase. 210 e-126
emb|A94218|A94218 Sequence 1 from Patent EP0952222. 176 e-122
emb|AF002656|AF002656 Asparagus officinalis acid invertase mRNA,... 198 e-120
gb|U81520|CIU81520 Cichorium intybus sucrose:sucrose 1-fructosyl... 173 e-120
25 emb|X75351|DCRNABF D.carota (Nantaise) mRNA for soluble acid bet... 202 e-120
emb|X75353|DCRNASABF D.carota (Nantaise) mRNA for soluble acid b... 203 e-120
emb|AJ272307|LPE272307 Lycopersicon pennellii lin 5 gene for bet... 145 e-119
emb|X75352|DCRNAABF D.carota (Nantaise) mRNA for soluble acid be... 203 e-119
emb|X78423|DCINUC1 D.carota (Queen Anne's Lace) Inv*Dc3 gene, 44... 160 e-118
30 emb|A94222|A94222 Sequence 5 from Patent EP0952222. 173 e-117
emb|Y09662|CSSS1FT C.scolymus mRNA for sucrose sucrose 1-fructos... 170 e-117
emb|A86530|A86530 Sequence 1 from Patent WO9839460. 170 e-117
emb|AJ272306|LES272306 Lycopersicon esculentum lin 5 gene for be... 145 e-116
emb|AJ250634|TOF250634 Taraxacum officinale mRNA for sucrose:suc... 169 e-116
35 emb|Z49831|VFVCINVMR V.faba VFVCINV mRNA for invertase (beta-fru... 199 e-115
gb|U92438|PVU92438 Phaseolus vulgaris soluble acid invertase mRN... 198 e-114
emb|AW686881|AW686881 NF003E07RT1F1000 Developing root Medicago ... 413 e-114
dbj|D10265|VIRINVA Vigna radiata mRNA for invertase, complete cds. 194 e-114
emb|AJ009757|HTU9757 Helianthus tuberosus sst-1 gene. 171 e-113
40 emb|A52468|A52468 Sequence 1 from Patent WO9621023. 171 e-113
emb|X70368|STPAIN1A S.tuberosum PAIN-1 mRNA for beta-fructofuran... 200 e-108
emb|X67163|DCSBFRU D.carota mRNA for soluble beta-fructosidase. 140 e-107
gb|L29099|POTBFRUASE Solanum tuberosum beta-fructosidase mRNA, c... 198 e-107
dbj|E07108|E07108 cDNA encoding acid invertase. 198 e-106
45 dbj|D11350|TOMBFSO Tomato mRNA for beta-fructosidase, complete cds. 198 e-106
emb|Z12026|LPBFRUCM L.pimpinellifolium beta-fructosidase mRNA fo... 198 e-106
emb|Z12025|LEBFRUCM L.esculentum beta-fructosidase mRNA for vacu... 198 e-106
gb|M81081|TOMACIN Tomato acid invertase (TIV1) mRNA, complete cds. 198 e-106
gb|S70040|S70040 acid invertase [Lycopersicon esculentum=tomatoe... 198 e-106
50 dbj|E16293|E16293 cDNA encoding invertase. 198 e-106
dbj|E08976|E08976 cDNA encoding tomato invertase. 198 e-106
emb|AF017082|AF017082 Ipomoea batatas beta-fructofuranosidase (S... 141 e-103
emb|Y11124|CIPINVERT C.intybus mRNA for putative invertase. 138 e-102
emb|X97642|TGINV5GEN T.gesneriana mRNA for invertase 5. 180 6e-97
55 emb|X95651|TGINV11GN T.gesneriana mRNA for invertase. 186 7e-96
emb|X97643|TGINV6GEN T.gesneriana mRNA for invertase 6. 186 2e-94
emb|Y18706|DCA18706 Daucus carota Inv*Dc5 gene. 130 2e-93
emb|Y18707|DCA18707 Daucus carota Inv*Dc4, Inv*Dc4' (partial) ge... 161 2e-93
emb|AF062735|AF062735 Saccharum officinarum soluble acid inverta... 129 1e-91
60 emb|AF062734|AF062734 Saccharum robustum soluble acid invertase ... 129 1e-91
emb|AF091549|AF091549 Hamamelis virginiana clone 7 beta-fructofu... 331 9e-90

- emb|AJ000481|CSFF1FRUC Cynara scolymus mRNA for fructan fructan ... 162 3e-89
 emb|AF091550|AF091550 Hamamelis virginiana clone C beta-fructofu... 330 3e-89
 emb|A94220|A94220 Sequence 3 from Patent EP0952222. 161 1e-88
 emb|AF091548|AF091548 Hamamelis virginiana clone 3 beta-fructofu... 327 1e-88
 5 gb|U84398|CIU84398 Cichorium intybus fructan-fructan 1-fructosyl... 161 5e-88
 emb|Z12028|LPBFRUCG L.pimpinellifolium gene encoding vacuolar in... 157 6e-88
 emb|Z12027|LEBFRUCG L.esculentum gene for vacuolar invertase. 157 6e-88
 emb|AJ009756|HTU9756 Helianthus tuberosus ffr-1 gene. 161 2e-87
 emb|A52470|A52470 Sequence 3 from Patent WO9621023. 161 2e-87
 10 emb|X81795|BVBIN35 B.vulgaris BIN35 mRNA for extracellular inver... 265 5e-86
 gb|BE055183|BE055183 GA__Ea0035H23f Gossypium arboreum 7-10 dpa ... 203 4e-83
 emb|X91392|LELIN8 L.esculentum mRNA for invertase (LIN8). 133 2e-82
 emb|AF091547|AF091547 Hamamelis virginiana clone 1 beta-fructofu... 295 3e-81
 emb|X81793|CRCIN2 C.rubrum CIN2 mRNA for intracellular invertase. 135 2e-80
 15 emb|X91389|LELIN5 L.esculentum mRNA for invertase (LIN5). 129 1e-78
 emb|X91391|LELIN7 L.esculentum mRNA for invertase (LIN7). 133 5e-78
 emb|Y07838|ACY07838 A.cepa mRNA for fructan:fructan 6G-fructosyl... 156 2e-77
 emb|X81796|BVBIN44 B.vulgaris BIN44 mRNA for intracellular inver... 149 5e-77
 emb|AF014925|AF014925 Citrus unshiu acid invertase (CUAI1) gene,... 138 4e-76
 20 emb|AJ006066|ACE6066 Allium cepa mRNA for sucrose sucrose 1-fruc... 132 2e-75
 emb|AF091545|AF091545 Hamamelis virginiana clone 4 beta-fructofu... 196 2e-75
 emb|A48282|A48282 Sequence 3 from Patent WO9601904. 152 4e-75
 emb|AW685050|AW685050 NF024F09NR1F1000 Nodulated root Medicago t... 248 5e-75
 emb|Z83339|PSZ83339 P.sativum mRNA for cell wall invertase II. 280 2e-74
 25 emb|AF091546|AF091546 Hamamelis virginiana clone 6 beta-fructofu... 193 3e-74
 emb|AV407850|AV407850 AV407850 Lotus japonicus young plants (two... 267 2e-70
 emb|A48284|A48284 Sequence 5 from Patent WO9601904. 130 1e-69
 emb|AW666614|AW666614 GA__Ea0005C10 Gossypium arboreum 7-10 dpa ... 207 3e-69
 emb|AW730389|AW730389 GA__Ea0023K22 Gossypium arboreum 7-10 dpa ... 141 2e-68
 30 emb|A48280|A48280 Sequence 1 from Patent WO9601904. 82 2e-68
 emb|X83233|HVSF6FT Hordeum vulgare mRNA for sucrose:fructan 6-fr... 82 2e-68
 emb|AF069309|AF069309 Triticum aestivum vacuolar invertase (WIVR... 127 5e-67
 emb|AW350139|AW350139 GM210007B20F11R Gm-r1021 Glycine max cDNA ... 112 4e-66
 emb|AW618261|AW618261 EST314311 L. pennellii trichome, Cornell U... 248 1e-64
 35 emb|AW738685|AW738685 EST340112 tomato flower buds, anthesis, Co... 189 3e-64
 emb|X91390|LELIN6 L.esculentum mRNA for invertase (LIN6). 133 5e-64
 emb|AI522941|AI522941 sa92d01.y1 Gm-c1004 Glycine max cDNA clone... 201 1e-63
 emb|AW441409|AW441409 EST310805 tomato fruit red ripe, TAMU Lyco... 114 4e-62
- 40 Query= AC005309.97_s_at20245_s_at /id_source genbank /description
 emb|caa05625.1| (aj002584) atmnp4 [arabidopsis thaliana] thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
 (4551 letters)
- 45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
- Searching.....done
- 50 Score E
 Sequences producing significant alignments: (bits) Value
- emb|Z69369|SPAC3F10 S.pombe chromosome I cosmid c3F10. 314 e-119
 emb|Z48179|SC9302X S.cerevisiae chromosome IV cosmid 9302. 185 e-114
 55 gb|L35237|YSCYCF1MRP Saccharomyces cerevisiae metal resistance p... 184 e-114
 gb|U33010|SPU33010 Schizosaccharomyces pombe cosmids 359, 1198 a... 291 e-112
 emb|AL356012|SPBC359 Schizosaccharomyces pombe cosmid c359. 291 e-112
 emb|AW278374|AW278374 sf43c10.y1 Gm-c1009 Glycine max cDNA clone... 383 e-105
 dbj|D89231|D89231 Schizosaccharomyces pombe mRNA, partial cds, c... 308 e-105
 60 emb|AI781883|AI781883 EST262762 tomato susceptible, Cornell Lyco... 370 e-101
 emb|X91488|SCCEN12RG S.cerevisiae DNA from CEN12 region includin... 159 1e-94

- emb|X97560|SC32KBF *S.cerevisiae* 32kb DNA fragment of chromosome ... 159 1e-94
emb|Z73120|SCYLL015W *S.cerevisiae* chromosome XII reading frame O... 159 1e-94
emb|AW031334|AW031334 EST274788 tomato callus, TAMU Lycopersicon... 315 1e-84
emb|AW441253|AW441253 EST310649 tomato fruit red ripe, TAMU Lyco... 308 2e-82
5 emb|AW686402|AW686402 NF037F01NR1F1000 Nodulated root *Medicago t...* 244 7e-78
emb|AW217265|AW217265 EST295979 tomato callus, TAMU Lycopersicon... 291 3e-77
emb|AW223995|AW223995 EST300806 tomato fruit red ripe, TAMU Lyco... 290 7e-77
emb|AW222948|AW222948 EST299759 tomato fruit red ripe, TAMU Lyco... 285 2e-75
emb|AI437711|AI437711 sa38f05.y1 *Gm-c1004* Glycine max cDNA clone... 276 7e-73
10 emb|AW476771|AW476771 ga37g03.y1 Moss EST library PPU Physcomitr... 275 1e-72
emb|AW100468|AW100468 sd55e07.y1 *Gm-c1016* Glycine max cDNA clone... 272 2e-71
emb|AI487304|AI487304 EST245626 tomato ovary, TAMU Lycopersicon ... 268 2e-70
emb|AI896472|AI896472 EST265903 tomato callus, TAMU Lycopersicon... 267 6e-70
emb|AW100453|AW100453 sd55c07.y1 *Gm-c1016* Glycine max cDNA clone... 266 1e-69
15 emb|AW034253|AW034253 EST277824 tomato callus, TAMU Lycopersicon... 265 2e-69
emb|AW216929|AW216929 EST295643 tomato callus, TAMU Lycopersicon... 259 1e-67
emb|AW759237|AW759237 sl38f09.y1 *Gm-c1027* Glycine max cDNA clone... 259 1e-67
emb|X94332|SCCHVIRA *S.cerevisiae* DNA for fragment from chromoso... 171 2e-67
emb|Z73066|SCYGR281W *S.cerevisiae* chromosome VII reading frame O... 171 2e-67
20 dbj|E12376|E12376 Nucleotide sequence of scaur2 gene. 170 2e-67
emb|AW092564|AW092564 EST285744 tomato mixed elicitor, BTI Lycop... 249 1e-64
emb|AF110027|AF110027 *Candida albicans* ATP-dependent transporter... 150 5e-64
emb|AI779714|AI779714 EST260593 tomato susceptible, Cornell Lyco... 246 9e-64
emb|AI900368|AI900368 sc04g04.y1 *Gm-c1012* Glycine max cDNA clone... 243 6e-63
25 emb|AW037624|AW037624 EST279082 tomato mixed elicitor, BTI Lycop... 242 1e-62
emb|AF110147|AF110147 *Cryptosporidium parvum* ATP-binding cassett... 242 2e-62
emb|Z73153|SCYLL048C *S.cerevisiae* chromosome XII reading frame O... 142 4e-62
emb|AL114698|CNS01BUA *Botrytis cinerea* strain T4 cDNA library un... 238 7e-62
emb|Z28329|SCYKR104W *S.cerevisiae* chromosome XI reading frame OR... 129 7e-61
30 emb|AI895676|AI895676 EST265119 tomato callus, TAMU Lycopersicon... 234 4e-60
emb|AL115672|CNS01CLC *Botrytis cinerea* strain T4 cDNA library un... 185 1e-58
emb|AW737284|AW737284 EST338711 tomato flower buds, anthesis, Co... 229 2e-58
emb|X17154|LTHCPG *Leishmania tarentolae* H circle borne ltpgpA ge... 197 2e-57
gb|L29484|LEIPGLYA *Leishmania tarentolae* P-glycoprotein related ... 181 2e-57
35 emb|AI729186|AI729186 BNLGHi12864 Six-day Cotton fiber *Gossypium...* 210 3e-57
gb|U11583|YSCH9196 *Saccharomyces cerevisiae* chromosome VIII cosm... 136 6e-57
gb|L29485|LEIPGLYB *Leishmania tarentolae* P-glycoprotein related ... 171 6e-57
emb|AI489515|AI489515 EST247854 tomato ovary, TAMU Lycopersicon ... 222 2e-56
emb|AL135898|LMFL673 *Leishmania major* Friedlin chromosome 23 cos... 176 2e-56
40 emb|AW459613|AW459613 sh89d10.y1 *Gm-c1016* Glycine max cDNA clone... 219 1e-55
emb|AB009972|AB009972 *Aspergillus oryzae* gene for beta-1,4-xylos... 122 2e-53
emb|AW757110|AW757110 sl29c06.y1 *Gm-c1027* Glycine max cDNA clone... 208 3e-52
gb|BE021265|BE021265 sm56g10.y1 *Gm-c1028* Glycine max cDNA clone ... 206 9e-52
emb|AW761593|AW761593 sl69g02.y1 *Gm-c1027* Glycine max cDNA clone... 205 2e-51
45 emb|Z99262|SPAC9E9 *S.pombe* chromosome I cosmid c9E9. 129 2e-51
emb|Y09354|SPABC1 *S.pombe* ABC1 gene. 129 2e-51
emb|AL136538|SPAC30 *S.pombe* chromosome I cosmid c30. 144 1e-48
emb|AI974480|AI974480 T110430e KV0 *Medicago truncatula* cDNA clon... 196 1e-48
emb|AI495498|AI495498 sa98g09.y1 *Gm-c1004* Glycine max cDNA clone... 194 4e-48
50 emb|AW736468|AW736468 EST332482 KV3 *Medicago truncatula* cDNA clo... 191 3e-47
emb|AW677202|AW677202 DG1_6_D10.b1_A002 Dark Grown 1 (DG1) *Sorgh...* 191 5e-47
gb|BE022474|BE022474 sm74d06.y1 *Gm-c1015* Glycine max cDNA clone ... 188 3e-46
emb|Z49222|TCPGP2 *T.cruzi* gene for P-glycoprotein. 140 9e-45
emb|AI437929|AI437929 sa41e03.y1 *Gm-c1004* Glycine max cDNA clone... 153 2e-44
55 emb|AI777095|AI777095 EST258060 tomato resistant, Cornell Lycop... 177 6e-43
emb|AQ935847|AQ935847 CpG2684B CpIOWAgDNA1 *Cryptosporidium parvu...* 175 3e-42
gb|U95956|TCU95956 *Trypanosoma cruzi* P-glycoprotein (tcpgp1A) ge... 130 9e-42
emb|AW830202|AW830202 sm24a04.y1 *Gm-c1028* Glycine max cDNA clone... 172 2e-41
emb|AL113101|CNS01ALX *Botrytis cinerea* strain T4 cDNA library un... 138 4e-41
60 emb|AW155943|AW155943 ga22b09.y1 Moss EST library PPU Physcomitr... 167 7e-40
emb|AW202254|AW202254 sf12h06.y1 *Gm-c1027* Glycine max cDNA clone... 166 9e-40

- emb|AW759534|AW759534 sl44f02.y1 Gm-c1027 Glycine max cDNA clone... 166 9e-40
 emb|AW223508|AW223508 EST300319 tomato fruit red ripe, TAMU Lyco... 165 2e-39
 emb|AW219577|AW219577 EST302059 tomato root during/after fruit s... 164 5e-39
 emb|AW775340|AW775340 EST334405 DSIL Medicago truncatula cDNA cl... 161 3e-38
 5 emb|Z28328|SCYKR103W S.cerevisiae chromosome XI reading frame OR... 122 6e-38
 emb|AW039256|AW039256 EST281513 tomato mixed elicitor, BTI Lycop... 159 2e-37
 emb|AJ388890|AJ388890 AJ388890 Medicago truncatula R108 Medicago... 159 2e-37
 emb|AQ849029|AQ849029 LMAJFV1_lm45c02.x1 Leishmania major FV1 ra... 112 2e-37
 gb|U55381|LTU55381 Leishmania tropica P-glycoprotein E gene, com... 114 4e-37
 10 emb|AW350529|AW350529 GM210009A10F6R Gm-r1021 Glycine max cDNA 3... 157 7e-37
 emb|AQ950989|AQ950989 Sheared DNA-52G21.TF Sheared DNA Trypanoso... 154 5e-36
 emb|AF034608|AF034608 Candida albicans YOR1 homolog gene, partia... 153 9e-36
 emb|AW775084|AW775084 EST334235 KV3 Medicago truncatula cDNA clo... 153 1e-35
 emb|AQ911544|AQ911544 LMAJFV1_lm86e04.y1 Leishmania major FV1 ra... 127 1e-35
 15 emb|AW781305|AW781305 sk68b06.y1 Gm-c1016 Glycine max cDNA clone... 152 2e-35
 emb|AW441948|AW441948 EST311344 tomato fruit red ripe, TAMU Lyco... 114 2e-35
 emb|AW350905|AW350905 GM210009B10G8R Gm-r1021 Glycine max cDNA 3... 151 3e-35
 emb|AQ849904|AQ849904 LMAJFV1_lm51d04.x1 Leishmania major FV1 ra... 118 3e-35
 20 emb|AB013851|AB013851 Aspergillus oryzae gene for beta-xylosidas... 122 5e-35
 emb|AW775168|AW775168 EST334319 KV3 Medicago truncatula cDNA clo... 150 6e-35
 emb|AJ278038|BFU278038 Botryotinia fuckeliana BcatrG gene for MR... 148 4e-34
 gb|U62929|FNU62929 Filobasidiella neoformans multidrug resistanc... 93 1e-32
 emb|AQ946563|AQ946563 Sheared DNA-49C19.TR Sheared DNA Trypanoso... 142 2e-32
 25 emb|AQ646228|AQ646228 RPCI93-DpnII-30J14.TV RPCI93-DpnII Trypano... 141 5e-32
 gb|U62931|AFU62931 Aspergillus flavus multidrug resistance prote... 88 1e-31
 emb|AW756083|AW756083 sl13f12.y1 Gm-c1036 Glycine max cDNA clone... 135 2e-30
 emb|AI676508|AI676508 etmEST0269 EtH1 Eimeria tenella cDNA clone... 135 2e-30
 emb|AQ640396|AQ640396 927P1-5E2.TP 927P1 Trypanosoma brucei geno... 105 4e-30
 30 emb|AI782195|AI782195 EST263074 tomato susceptible, Cornell Lyco... 134 4e-30
 emb|AW033521|AW033521 EST277092 tomato callus, TAMU Lycopersicon... 134 6e-30

Query= AF084037.3_s_at 20246_s_at /id_source genbank /description

- 35 gb|aac95354.1| (af084037) receptor-like protein kinase [arabidopsis
 thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
 /ncgi

(2055 letters)

Database: plantfungal

- 40 661,018 sequences; 426,114,510 total letters

Searching.....done

- 45 Score E
 Sequences producing significant alignments: (bits) Value

- emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 356 e-115
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 318 e-100
 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 322 e-99
 50 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 312 9e-99
 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 313 1e-97
 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase... 315 2e-97
 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 323 3e-97
 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 307 4e-95
 55 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 308 1e-93
 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 313 2e-93
 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 312 1e-92
 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 310 3e-92
 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 309 7e-92
 60 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 266 1e-90
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 182 6e-90

- dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 260 1e-89
emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 286 2e-89
emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 262 4e-89
dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 258 3e-87
5 gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 197 4e-84
emb|Y12530|BOARLKGEN B.oleraceae gene encoding serine/threonine ... 111 1e-83
gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 268 4e-82
emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 302 6e-81
emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 302 8e-81
10 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 232 1e-80
emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 105 3e-80
gb|BE057261|BE057261 sm99f12.y1 Gm-c1015 Glycine max cDNA clone ... 289 4e-77
emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 117 7e-75
emb|AW760240|AW760240 sl59g07.y1 Gm-c1027 Glycine max cDNA clone... 261 1e-68
15 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 107 2e-68
emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 109 2e-65
emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 105 3e-65
dbj|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 104 1e-64
emb|AI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 247 2e-64
20 emb|AB024422|AB024422S2 Brassica oleracea SRK13-b gene, exon 2, ... 105 5e-64
emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 105 7e-64
emb|AW442344|AW442344 EST311740 tomato fruit red ripe, TAMU Lyco... 190 1e-63
emb|AI486193|AI486193 EST244514 tomato ovary, TAMU Lycopersicon ... 181 5e-63
emb|AW831390|AW831390 sm22a06.y1 Gm-c1028 Glycine max cDNA clone... 183 6e-63
25 emb|AW620957|AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone... 202 1e-62
emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 109 2e-62
emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 104 2e-62
gb|BE034949|BE034949 ML07F03 ML Mesembryanthemum crystallinum cD... 239 7e-62
emb|X79432|BOSRK3 B.oleracea SRK3 gene. 108 8e-62
30 emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 99 7e-61
emb|AI896155|AI896155 EST265598 tomato callus, TAMU Lycopersicon... 158 3e-59
emb|AW203661|AW203661 sf36g06.y1 Gm-c1028 Glycine max cDNA clone... 187 1e-58
emb|AW309544|AW309544 sf20h08.x1 Gm-c1028 Glycine max cDNA clone... 227 2e-58
emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 226 3e-58
35 emb|AW033458|AW033458 EST277029 tomato callus, TAMU Lycopersicon... 215 7e-55
emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 215 1e-54
emb|AI967314|AI967314 Ljirmp00-017 Ljirmp Lambda HybriZap two... 117 3e-54
emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 212 9e-54
emb|AW220677|AW220677 EST297146 tomato fruit mature green, TAMU ... 211 2e-53
40 emb|AW666141|AW666141 sk32f11.y1 Gm-c1028 Glycine max cDNA clone... 166 5e-53
emb|AW667985|AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ... 119 1e-52
emb|AI822907|AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr... 119 1e-51
emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 104 1e-51
emb|AI822355|AI822355 L0-804T3 Ice plant Lambda Uni-Zap XR expre... 119 4e-51
45 emb|AI899009|AI899009 EST268452 tomato ovary, TAMU Lycopersicon ... 161 7e-51
emb|AI897876|AI897876 EST267319 tomato ovary, TAMU Lycopersicon ... 146 2e-50
emb|AI771857|AI771857 EST252957 tomato ovary, TAMU Lycopersicon ... 157 9e-50
emb|AI488101|AI488101 EST246423 tomato ovary, TAMU Lycopersicon ... 157 9e-50
emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 84 2e-49
50 emb|Y16999|TCA16999 Theobroma cacao microsatellite DNA, clone mT... 106 2e-49
emb|AI486584|AI486584 EST244905 tomato ovary, TAMU Lycopersicon ... 146 6e-49
emb|AI901283|AI901283 sc31d08.y1 Gm-c1014 Glycine max cDNA clone... 152 8e-49
emb|AI898581|AI898581 EST268024 tomato ovary, TAMU Lycopersicon ... 161 8e-49
emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 119 2e-48
55 emb|AW054349|AW054349 L30-1774T3 Ice plant Lambda Uni-Zap XR exp... 119 3e-48
emb|AI899156|AI899156 EST268599 tomato ovary, TAMU Lycopersicon ... 161 4e-48
emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 119 5e-48
emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 141 1e-47
gb|U51330|TAU51330 Triticum aestivum leaf rust resistance kinase... 77 6e-47
60 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 118 8e-47
emb|AI822347|AI822347 L0-796T3 Ice plant Lambda Uni-Zap XR expre... 106 4e-46

- emb|X81833|BOSLR31 *B.oleracea* mRNA for SLR3-1 protein. 85 5e-46
 emb|AI938169|AI938169 sc40d07.y1 *Gm-c1014* Glycine max cDNA clone... 185 9e-46
 emb|Z18884|BOSRKRPC *B.oleracea* encoding S-receptor kinase relate... 109 1e-45
 emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 161 2e-45
 5 emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 99 2e-45
 emb|AI896953|AI896953 EST266396 tomato callus, TAMU Lycopersicon... 158 1e-44
 emb|AF085164|AF085164 *Hordeum vulgare* receptor-like kinase LRK10... 77 3e-44
 emb|AW039406|AW039406 EST281663 tomato mixed elicitor, BTI Lycop... 112 5e-44
 emb|AF142596|AF142596 *Nicotiana tabacum* LRR receptor-like protei... 65 7e-44
 10 emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 178 1e-43
 emb|AW034993|AW034993 EST279222 tomato callus, TAMU Lycopersicon... 166 1e-42
 emb|A67797|A67797 Sequence 2 from Patent WO9743427. 62 2e-42
 gb|U93048|DCU93048 *Daucus carota* somatic embryogenesis receptor-... 62 2e-42
 emb|AW706972|AW706972 sk20a03.y1 *Gm-c1028* Glycine max cDNA clone... 174 2e-42
 15 emb|AW034624|AW034624 EST278308 tomato callus, TAMU Lycopersicon... 174 2e-42
 emb|AI895623|AI895623 EST265066 tomato callus, TAMU Lycopersicon... 173 5e-42
 emb|AW687052|AW687052 NF005E02RT1F1017 Developing root Medicago ... 170 3e-41
 emb|AW775756|AW775756 EST334821 DSIL Medicago truncatula cDNA cl... 137 5e-41
 emb|AF085168|AF085168 *Triticum aestivum* receptor-like protein ki... 68 6e-41
 20 emb|AW597214|AW597214 si71g06.y1 *Gm-c1031* Glycine max cDNA clone... 116 1e-40
 emb|AI772117|AI772117 EST253217 tomato resistant, Cornell Lycop... 127 2e-40
 emb|AF220603|AF220603 *Lycopersicon esculentum* VFNT Cherry Pto lo... 96 2e-40
 gb|U59316|LEU59316 *Lycopersicon esculentum* serine/threonine prot... 96 2e-40
 emb|Y14600|SBRLK1 *Sorghum bicolor* mRNA for protein serine/threon... 61 4e-40

25 Query= AC002387.237_at 20269_at /id_source genbank /description
 gb|aab82640.1| (ac002387) putative pectinesterase [arabidopsis
 thaliana] /blast_score 0 /ec_number /family pectinesterase /chip nova
 /gb_link [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002387|/ncgi)
 30 [post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002387|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002387|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac002387>
 (1533 letters)

Database: plantfungal
 35 661,018 sequences; 426,114,510 total letters

Searching.....done

- | | Score | E |
|----|---|--------------|
| 40 | Sequences producing significant alignments: | (bits) Value |
| | gb U82977 CSU82977 <i>Citrus sinensis</i> pectinesterase mRNA, complete... | 483 0.0 |
| | gb U82976 CSU82976 <i>Citrus sinensis</i> pectinesterase mRNA, complete... | 218 e-119 |
| | gb U82975 CSU82975 <i>Citrus sinensis</i> pectinesterase (PECS-2.1) gen... | 421 e-116 |
| 45 | emb AF152172 AF152172 <i>Solanum tuberosum</i> cultivar Desiree pectin ... | 208 e-111 |
| | emb AF229849 AF229849 <i>Vigna radiata</i> pectin methylesterase isoform... | 208 e-107 |
| | gb U49330 SLU49330 <i>Solanum lycopersicum</i> pectin methylesterase (P... | 205 e-106 |
| | emb Z71752 NPPME2MR <i>N.plumbaginifolia</i> mRNA for pectin methyleste... | 177 e-104 |
| | emb Z71753 NPPME3MR <i>N.plumbaginifolia</i> mRNA for pectin methyleste... | 177 e-103 |
| 50 | emb X94443 VRPECMEST <i>V.radiata</i> mRNA for pectinmethylesterase. | 175 e-100 |
| | gb U82973 CSU82973 <i>Citrus sinensis</i> pectinesterase (PECS-1.1) gen... | 218 8e-97 |
| | emb AF056493 AF056493 <i>Pisum sativum</i> pectin methylesterase mRNA, ... | 163 3e-95 |
| | emb AF152171 AF152171 <i>Solanum tuberosum</i> cultivar Desiree pectin ... | 190 2e-94 |
| | emb AJ249786 NTA249786 <i>Nicotiana tabacum</i> partial mRNA for pectin... | 192 4e-94 |
| 55 | emb A17011 A17011 tomato fruit pectin esterase with pPel DNA seq... | 190 5e-94 |
| | emb A17010 A17010 tomato fruit pectin esterase seq ID no1. | 190 9e-94 |
| | emb X74638 LEPEC1 <i>L.esculentum</i> mRNA for pectin esterase. | 190 9e-94 |
| | emb X74639 LEPEC2 <i>L.esculentum</i> mRNA for pectin esterase clone. | 188 3e-93 |
| | gb U50986 SLU50986 <i>Solanum lycopersicum</i> pectin methylesterase PM... | 188 6e-93 |
| 60 | gb S66607 S66607 <i>Lycopersicon esculentum</i> pectinmethylesterase-li... | 190 8e-93 |
| | emb X07910 LEPECES Tomato mRNA for pectin esterase. | 190 1e-92 |

- emb|A15983|A15983 *L.esculentum* mRNA for pectin esterase. 190 1e-92
gb|U50985|SLU50985 *Solanum lycopersicum* pectin methylesterase PM... 185 2e-92
emb|Z71754|NPPME4MR *N.plumbaginifolia* mRNA for pectin methyleste... 177 2e-92
emb|X95991|PPPECESTR *P.persica* mRNA for pectin esterase. 161 3e-92
5 emb|A24196|A24196 *L.esculentum* pectin esterase clone pPE1. 188 7e-92
emb|AF081457|AF081457 *Pisum sativum* pectin methylesterase (rcpme... 136 4e-90
emb|X67425|PSPMEAG *Pisum sativum* pmeA gene for pectinesterase. 136 4e-90
emb|AW650699|AW650699 EST329153 tomato germinating seedlings, TA... 271 2e-86
emb|AW696177|AW696177 NF103C11ST1F1085 Developing stem *Medicago* ... 193 4e-83
10 emb|AB029461|AB029461 *Salix gilgiana* SgPME1 mRNA for pectin meth... 144 1e-82
emb|AW257370|AW257370 EST305507 KV2 *Medicago truncatula* cDNA clo... 232 7e-81
emb|AI166540|AI166540 xylem.est.362 *Poplar* xylem Lambda ZAPII li... 167 4e-79
emb|X85216|PVRNAPE *P.vulgaris* mRNA for pectinesterase. 170 2e-78
gb|U70676|LEU70676 *Lycopersicon esculentum* pectin methylesteras... 188 1e-77
15 gb|U70677|LEU70677 *Lycopersicon esculentum* (LePME1) gene, partia... 188 4e-77
gb|U70675|LEU70675 *Lycopersicon esculentum* fruit-specific pectin... 189 1e-76
emb|AW429110|AW429110 EST306566 tomato flower buds 0-3 mm, Corne... 187 1e-75
emb|AW429158|AW429158 EST306614 tomato flower buds 0-3 mm, Corne... 160 3e-74
emb|AW349192|AW349192 GM210004A21F6R *Gm-r1021* *Glycine max* cDNA 3... 129 1e-72
20 emb|AW930691|AW930691 EST356534 tomato fruit mature green, TAMU ... 168 1e-70
emb|AW559494|AW559494 EST314542 DSIR *Medicago truncatula* cDNA cl... 141 2e-70
emb|AW774488|AW774488 EST333639 KV3 *Medicago truncatula* cDNA clo... 141 2e-70
emb|AW687047|AW687047 NF005D06RT1F1057 Developing root *Medicago* ... 132 6e-70
emb|AW784073|AW784073 NXNV_117_D06_F Nsf Xylem Normal wood Verti... 153 6e-70
25 gb|BE020131|BE020131 sm41e11.y1 *Gm-c1028* *Glycine max* cDNA clone ... 246 2e-69
emb|Y07899|CPSPE1 *C.papaya* mRNA for pectinesterase. 155 6e-69
emb|AI897776|AI897776 EST267219 tomato ovary, TAMU *Lycopersicon* ... 198 1e-68
emb|AW220185|AW220185 EST302668 tomato root during/after fruit s... 172 2e-68
emb|AW666622|AW666622 GA_Ea0005C20 *Gossypium arboreum* 7-10 dpa ... 177 1e-67
30 emb|AW760550|AW760550 sl51g07.y1 *Gm-c1027* *Glycine max* cDNA clone... 155 2e-67
emb|AW329215|AW329215 N200427e rootphos(-) *Medicago truncatula* c... 149 3e-67
emb|X68029|PVVPE2 *P.vulgaris* PvVPE2 mRNA for pectin esterase. 149 2e-66
emb|AW774605|AW774605 EST333756 KV3 *Medicago truncatula* cDNA clo... 141 4e-66
emb|AW299038|AW299038 EST305712 KV2 *Medicago truncatula* cDNA clo... 141 4e-66
35 emb|AW649176|AW649176 EST327630 tomato germinating seedlings, TA... 180 7e-65
emb|AI782839|AI782839 EST263718 tomato susceptible, Cornell Lyco... 156 5e-64
gb|U28148|MSU28148 *Medicago sativa* putative pectinesterase mRNA,... 134 5e-64
emb|X97762|STBPE1 *S.tuberosum* mRNA BPE1 for pectin methylesterase. 165 1e-63
emb|AI440753|AI440753 sa53f07.y1 *Gm-c1004* *Glycine max* cDNA clone... 161 1e-63
40 emb|AW774519|AW774519 EST333670 KV3 *Medicago truncatula* cDNA clo... 137 3e-63
emb|AW706153|AW706153 sj52e04.y1 *Gm-c1033* *Glycine max* cDNA clone... 242 5e-63
emb|AW649290|AW649290 EST327744 tomato germinating seedlings, TA... 196 8e-63
emb|AW257345|AW257345 EST305482 KV2 *Medicago truncatula* cDNA clo... 167 9e-63
emb|AW616248|AW616248 EST307287 *L. hirsutum* trichome, Cornell Un... 173 1e-62
45 emb|AW758821|AW758821 NXNV_091_A04_F Nsf Xylem Normal wood Verti... 160 8e-62
emb|AW398150|AW398150 EST298033 *L. pennellii* trichome, Cornell U... 173 1e-61
gb|L27101|PETPPE1A *Petunia inflata* pectinesterase (PPE1) gene, c... 134 2e-61
emb|AI781139|AI781139 EST262018 tomato susceptible, Cornell Lyco... 205 2e-61
emb|AW932254|AW932254 EST358097 tomato fruit mature green, TAMU ... 148 4e-61
50 gb|U82974|CSU82974 *Citrus sinensis* pectinesterase (PECS-1.2) gen... 216 6e-60
emb|AW221911|AW221911 EST298722 tomato fruit red ripe, TAMU Lyco... 155 6e-60
emb|AW424141|AW424141 sh61d11.y1 *Gm-c1015* *Glycine max* cDNA clone... 146 2e-59
emb|AW289642|AW289642 NXNV003F09F Nsf Xylem Normal wood Vertical... 160 2e-59
emb|AW888107|AW888107 NXNV_129_C06_F Nsf Xylem Normal wood Verti... 141 6e-59
55 emb|AW620942|AW620942 sj95g05.y1 *Gm-c1023* *Glycine max* cDNA clone... 164 1e-58
emb|AW154926|AW154926 EST290291 tomato root deficiency, Cornell ... 190 2e-58
emb|AW623570|AW623570 EST321515 tomato flower buds 3-8 mm, Corne... 135 2e-58
emb|AI780635|AI780635 EST261610 tomato susceptible, Cornell Lyco... 196 2e-58
emb|AW616681|AW616681 EST323092 *L. hirsutum* trichome, Cornell Un... 177 5e-58
60 emb|AW041247|AW041247 EST284111 tomato mixed elicitor, BTI Lycop... 135 7e-58
emb|AW221863|AW221863 EST298674 tomato fruit red ripe, TAMU Lyco... 190 1e-57

emb|AW774676|AW774676 EST333827 KV3 Medicago truncatula cDNA clo... 113 1e-57
 emb|AW287387|AW287387 LG1_303_C07.b1_A002 Light Grown 1 (LG1) So... 222 6e-57
 emb|AW930330|AW930330 EST340883 tomato fruit mature green, TAMU ... 122 9e-57
 5 emb|AW458218|AW458218 sh79h10.y1 Gm-cl016 Glycine max cDNA clone... 120 1e-56
 gb|L48178|BNAPECT Brassica campestris pectinesterase mRNA, 3' en... 110 1e-56
 emb|AW616155|AW616155 EST296925 L. hirsutum trichome, Cornell Un... 177 3e-56
 emb|AW221834|AW221834 EST298645 tomato fruit red ripe, TAMU Lyco... 155 3e-56
 emb|AW617508|AW617508 EST323919 L. hirsutum trichome, Cornell Un... 177 3e-56
 emb|AW617079|AW617079 EST323490 L. hirsutum trichome, Cornell Un... 177 3e-56
 10 emb|AW616977|AW616977 EST323388 L. hirsutum trichome, Cornell Un... 173 9e-56
 emb|AW623150|AW623150 EST321095 tomato flower buds 3-8 mm, Corne... 150 1e-55
 emb|AW934244|AW934244 EST360087 tomato fruit mature green, TAMU ... 155 2e-55
 emb|X68028|PVPPE3 P.vulgaris PvVPE3 mRNA for pectin esterase. 170 3e-55
 emb|AW616290|AW616290 EST307330 L. hirsutum trichome, Cornell Un... 173 4e-55
 15 emb|AW617047|AW617047 EST323458 L. hirsutum trichome, Cornell Un... 173 4e-55
 emb|AW220280|AW220280 EST302763 tomato root during/after fruit s... 186 6e-55
 emb|X97763|STBPE2 S.tuberosum mRNA BPE2 for pectin methylesterase. 156 6e-55
 emb|AI441604|AI441604 sa68e03.y1 Gm-cl004 Glycine max cDNA clone... 155 5e-54
 emb|AI731654|AI731654 BNLGHi10367 Six-day Cotton fiber Gossypium... 152 1e-53

20

Query= Y14590.5_at 20287_at /id_source genbank /description
 emb|caa74930.1| (y14590) class iv chitinase [arabidopsis thaliana]
 /blast_score 1.00e-166 /ec_number /family chitinase /chip nova
 25 /gb_link [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|y14590|/ncgi)
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|y14590|/ncgi
<http://www.ncgr.org/cgi-bin/ff?y14590>
 (825 letters)

30 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

35 Score E
 Sequences producing significant alignments: (bits) Value

emb|X57187|PVCHITIN P.vulgaris mRNA for chitinase. 238 e-123
 gb|U97522|VVU97522 Vitis vinifera class IV endochitinase (VvChi4... 248 e-112
 40 emb|X88803|VURNACHI4 V.unguiculata mRNA for chitinase clase 4 (p... 201 e-107
 gb|U97521|VVU97521 Vitis vinifera class IV endochitinase (VvChi4... 247 1e-97
 dbj|D45183|D45183 Chenopodium amaranticolor mRNA for chitinase, ... 197 8e-96
 dbj|D45182|D45182 Chenopodium amaranticolor mRNA for chitinase, ... 136 6e-95
 dbj|D45181|D45181 Chenopodium amaranticolor mRNA for chitinase, ... 136 4e-94
 45 emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 227 5e-91
 gb|U52845|DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... 143 5e-91
 emb|AI897733|AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... 164 1e-90
 gb|U52848|DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3... 137 3e-90
 gb|U52846|DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP... 142 4e-90
 50 emb|AI897843|AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... 158 2e-89
 gb|U52847|DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP... 133 4e-89
 emb|X61488|BNCHITIN B.napus mRNA for chitinase. 181 5e-85
 emb|Z46948|SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re... 166 2e-84
 emb|AI897217|AI897217 EST266756 tomato ovary, TAMU Lycopersicon ... 164 2e-84
 55 gb|L25826|BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. 185 9e-83
 emb|X75945|BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. 127 8e-80
 emb|A23392|A23392 B.vulgaris mRNA for chitinase 4 (B15). 127 8e-80
 emb|AI898279|AI898279 EST267722 tomato ovary, TAMU Lycopersicon ... 126 2e-78
 gb|BE034166|BE034166 MG05H02 MG Mesembryanthemum crystallinum cD... 167 4e-78
 60 emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem Medicago ... 131 5e-78
 emb|AW030814|AW030814 EST274069 tomato callus, TAMU Lycopersicon... 126 1e-77

- emb|AW035013|AW035013 EST279284 tomato callus, TAMU Lycopersicon... 126 2e-77
 emb|AI485982|AI485982 EST244303 tomato ovary, TAMU Lycopersicon ... 126 2e-77
 gb|BE034428|BE034428 MH04G02 MH Mesembryanthemum crystallinum cD... 170 3e-77
 dbj|D45184|D45184 Chenopodium amaranticolor mRNA for chitinase, ... 136 2e-76
 5 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 156 7e-75
 emb|AF090336|AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA... 215 1e-74
 gb|BE034976|BE034976 ML07H11 ML Mesembryanthemum crystallinum cD... 160 1e-74
 emb|AI776153|AI776153 EST257241 tomato resistant, Cornell Lycop... 164 1e-74
 emb|Z46950|SNCHJET19 S.nigra mRNA chitinase class II, pathogenes... 139 1e-74
 10 emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 126 2e-74
 gb|L42467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 104 3e-74
 emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 156 4e-72
 emb|X74919|PVGEC9 P.vulgaris gene for endochitinase. 238 6e-71
 emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 126 2e-70
 15 gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 132 2e-68
 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 126 3e-68
 gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 114 2e-67
 emb|AF112963|AF112963 Triticum aestivum chitinase II precursor (... 154 1e-66
 emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root Medicago t... 122 5e-66
 20 emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 215 5e-65
 gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 79 2e-64
 gb|BE035287|BE035287 MM04H04 MM Mesembryanthemum crystallinum cD... 208 6e-63
 emb|AW680953|AW680953 WS1_9_A06.b1_A002 Water-stressed 1 (WS1) S... 224 7e-63
 emb|AI729668|AI729668 BNLGHi13889 Six-day Cotton fiber Gossypium... 121 1e-61
 25 emb|AI055037|AI055037 coau0002N18 Cotton Boll Abscission Zone cD... 111 3e-60
 gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 101 3e-60
 gb|BE033502|BE033502 ME03F10 ME Mesembryanthemum crystallinum cD... 100 4e-59
 emb|AW924422|AW924422 WS1_69_C06.b1_A002 Water-stressed 1 (WS1) ... 171 4e-59
 emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 108 2e-58
 30 emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 224 6e-58
 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 224 6e-58
 gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 108 2e-57
 gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 208 2e-57
 emb|AI488583|AI488583 EST246922 tomato ovary, TAMU Lycopersicon ... 126 3e-57
 35 emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 118 4e-57
 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 221 4e-57
 emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 111 1e-56
 emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 111 1e-56
 emb|AI897391|AI897391 EST266834 tomato ovary, TAMU Lycopersicon ... 126 1e-56
 40 emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 110 7e-56
 emb|AW924229|AW924229 WS1_51_H04.b1_A002 Water-stressed 1 (WS1) ... 215 3e-55
 emb|AW676775|AW676775 DG1_14_C09.g1_A002 Dark Grown 1 (DG1) Sorg... 215 3e-55
 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 105 4e-55
 emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 109 6e-55
 45 emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed 1 (WS1) ... 214 7e-55
 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 108 2e-54
 emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 110 2e-54
 gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 107 5e-54
 emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 110 6e-54
 50 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 110 7e-54
 gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 105 1e-53
 gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 105 1e-53
 emb|AF043247|AF043247 Solanum tuberosum class I chitinase (ChtC1... 105 1e-53
 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 104 2e-53
 55 gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 110 6e-53
 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 112 9e-53
 emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 112 9e-53
 emb|AW029730|AW029730 EST272985 tomato callus, TAMU Lycopersicon... 125 1e-52
 gb|BE033398|BE033398 ME01A01 ME Mesembryanthemum crystallinum cD... 205 3e-52
 60 emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 114 1e-51
 gb|BE034447|BE034447 MH05A08 MH Mesembryanthemum crystallinum cD... 83 1e-51

emb|AF034566|AF034566 *Gossypium hirsutum* class I chitinase mRNA,... 108 2e-51
 emb|AF043248|AF043248 *Solanum tuberosum* class I chitinase (ChtC2... 100 3e-51
 gb|U83592|MSU83592 *Medicago sativa* class I chitinase mRNA, compl... 112 4e-51
 gb|U83591|MSU83591 *Medicago sativa* class I chitinase mRNA, compl... 112 4e-51
 5 emb|Z54234|VVCHIT1MR *V. vinifera* mRNA for chitinase. 102 7e-51
 gb|U02608|STU02608 *Solanum tuberosum* chitinase (chtB4) mRNA, par... 107 1e-50
 emb|X88800|VURNACHI1 *V. unguiculata* mRNA for chitinase clase 1 (p... 107 2e-50
 emb|AF000964|AF000964 *Poa pratensis* chitinase (Chi1) gene, compl... 100 2e-50
 gb|U78888|GHU78888 *Gossypium hirsutum* class I endochitinase mRNA... 103 4e-50
 10 emb|X63899|PSCHITIN *P. sativum* mRNA for chitinase. 94 1e-49
 emb|AB015655|AB015655 *Cucurbita* sp. mRNA for chitinase, complete... 100 7e-49
 gb|BE034450|BE034450 MH05B01 MH *Mesembryanthemum crystallinum* cD... 84 1e-48
 gb|U02287|HVVU02287 *Hordeum vulgare* cultivar NK1558 chitinase gen... 111 3e-48
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 108 6e-48
 15 gb|M15173|TOBECH Tobacco (*N. tabacum*) endochitinase mRNA, partial... 108 6e-48

Query= Y14590.5_g_at 20288_g_at /id_source genbank /description
 emb|caa74930.1| (y14590) class iv chitinase [*arabidopsis thaliana*]
 20 /blast_score 1.00e-166 /ec_number /family /chip nova /gb_link /ncgi

(825 letters)

Database: plantfungal
 25 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 30 Sequences producing significant alignments: (bits) Value

emb|X57187|PVCHITIN *P. vulgaris* mRNA for chitinase. 238 e-123
 gb|U97522|VVU97522 *Vitis vinifera* class IV endochitinase (VvChi4... 248 e-112
 emb|X88803|VURNACHI4 *V. unguiculata* mRNA for chitinase clase 4 (p... 201 e-107
 35 gb|U97521|VVU97521 *Vitis vinifera* class IV endochitinase (VvChi4... 247 1e-97
 dbj|D45183|D45183 *Chenopodium amaranticolor* mRNA for chitinase, ... 197 8e-96
 dbj|D45182|D45182 *Chenopodium amaranticolor* mRNA for chitinase, ... 136 6e-95
 dbj|D45181|D45181 *Chenopodium amaranticolor* mRNA for chitinase, ... 136 4e-94
 emb|AF112966|AF112966 *Triticum aestivum* chitinase IV precursor (... 227 5e-91
 40 gb|U52845|DCU52845 *Daucus carota* class IV chitinase EP3-1/H5 (EP... 143 5e-91
 emb|AI897733|AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... 164 1e-90
 gb|U52848|DCU52848 *Daucus carota* class IV chitinase EP3B/E6 (EP3... 137 3e-90
 gb|U52846|DCU52846 *Daucus carota* class IV chitinase EP3-2/H1 (EP... 142 4e-90
 emb|AI897843|AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... 158 2e-89
 45 gb|U52847|DCU52847 *Daucus carota* class IV chitinase EP3-3/E7 (EP... 133 4e-89
 emb|X61488|BNCHITIN *B. napus* mRNA for chitinase. 181 5e-85
 emb|Z46948|SNCHJET15 *S. nigra* mRNA for chitinase, pathogenesis-re... 166 2e-84
 emb|AI897217|AI897217 EST266756 tomato ovary, TAMU Lycopersicon ... 164 2e-84
 gb|L25826|BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. 185 9e-83
 50 emb|X75945|BVCH4RNA *B. vulgaris* Ch4 mRNA for chitinase. 127 8e-80
 emb|A23392|A23392 *B. vulgaris* mRNA for chitinase 4 (B15). 127 8e-80
 emb|AI898279|AI898279 EST267722 tomato ovary, TAMU Lycopersicon ... 126 2e-78
 gb|BE034166|BE034166 MG05H02 MG *Mesembryanthemum crystallinum* cD... 167 4e-78
 emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem *Medicago* ... 131 5e-78
 55 emb|AW030814|AW030814 EST274069 tomato callus, TAMU Lycopersicon... 126 1e-77
 emb|AW035013|AW035013 EST279284 tomato callus, TAMU Lycopersicon... 126 2e-77
 emb|AI485982|AI485982 EST244303 tomato ovary, TAMU Lycopersicon ... 126 2e-77
 gb|BE034428|BE034428 MH04G02 MH *Mesembryanthemum crystallinum* cD... 170 3e-77
 dbj|D45184|D45184 *Chenopodium amaranticolor* mRNA for chitinase, ... 136 2e-76
 60 gb|BE034975|BE034975 ML07H10 ML *Mesembryanthemum crystallinum* cD... 156 7e-75
 emb|AF090336|AF090336 *Citrus sinensis* chitinase CHI1 (chi1) mRNA... 215 1e-74

- gb|BE034976|BE034976 ML07H11 ML Mesembryanthemum crystallinum cD... 160 1e-74
emb|AI776153|AI776153 EST257241 tomato resistant, Cornell Lycopersicon... 164 1e-74
emb|Z46950|SNCHJET19 S.nigra mRNA chitinase class II, pathogenes... 139 1e-74
emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 126 2e-74
5 gb|L42467|PLACHI Picea glauca chitinase (chi) mRNA, complete cds. 104 3e-74
emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 156 4e-72
emb|X74919|PVGEC9 P.vulgaris gene for endochitinase. 238 6e-71
emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 126 2e-70
gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 132 2e-68
10 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 126 3e-68
gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 114 2e-67
emb|AF112963|AF112963 Triticum aestivum chitinase II precursor (... 154 1e-66
emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root Medicago t... 122 5e-66
emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 215 5e-65
15 gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 79 2e-64
gb|BE035287|BE035287 MM04H04 MM Mesembryanthemum crystallinum cD... 208 6e-63
emb|AW680953|AW680953 WS1_9_A06.b1_A002 Water-stressed 1 (WS1) S... 224 7e-63
emb|AI729668|AI729668 BNLGHI13889 Six-day Cotton fiber Gossypium... 121 1e-61
emb|AI055037|AI055037 coau0002N18 Cotton Boll Abcission Zone cD... 111 3e-60
20 gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 101 3e-60
gb|BE033502|BE033502 ME03F10 ME Mesembryanthemum crystallinum cD... 100 4e-59
emb|AW924422|AW924422 WS1_69_C06.b1_A002 Water-stressed 1 (WS1) ... 171 4e-59
emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 108 2e-58
emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 224 6e-58
25 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 224 6e-58
gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 108 2e-57
gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 208 2e-57
emb|AI488583|AI488583 EST246922 tomato ovary, TAMU Lycopersicon ... 126 3e-57
emb|Z78202|PACHII Persea americana mRNA for endochitinase. 118 4e-57
30 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 221 4e-57
emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 111 1e-56
emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 111 1e-56
emb|AI897391|AI897391 EST266834 tomato ovary, TAMU Lycopersicon... 126 1e-56
emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 110 7e-56
35 emb|AW924229|AW924229 WS1_51_H04.b1_A002 Water-stressed 1 (WS1) ... 215 3e-55
emb|AW676775|AW676775 DG1_14_C09.g1_A002 Dark Grown 1 (DG1) Sorg... 215 3e-55
emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 105 4e-55
emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 109 6e-55
emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed 1 (WS1) ... 214 7e-55
40 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 108 2e-54
emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 110 2e-54
gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 107 5e-54
emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 110 6e-54
gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 110 7e-54
45 gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 105 1e-53
gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 105 1e-53
emb|AF043247|AF043247 Solanum tuberosum class I chitinase (ChtC1... 105 1e-53
gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 104 2e-53
gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 110 6e-53
50 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 112 9e-53
emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 112 9e-53
emb|AW029730|AW029730 EST272985 tomato callus, TAMU Lycopersicon... 125 1e-52
gb|BE033398|BE033398 ME01A01 ME Mesembryanthemum crystallinum cD... 205 3e-52
emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 114 1e-51
55 gb|BE034447|BE034447 MH05A08 MH Mesembryanthemum crystallinum cD... 83 1e-51
emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 108 2e-51
emb|AF043248|AF043248 Solanum tuberosum class I chitinase (ChtC2... 100 3e-51
gb|U83592|MSU83592 Medicago sativa class I chitinase mRNA, compl... 112 4e-51
gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 112 4e-51
60 emb|Z54234|VVCHITIMR V.vinifera mRNA for chitinase. 102 7e-51
gb|U02608|STU02608 Solanum tuberosum chitinase (chtB4) mRNA, par... 107 1e-50

emb[X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 107 2e-50
 emb|AF000964|AF000964 Poa pratensis chitinase (Chi1) gene, compl... 100 2e-50
 gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 103 4e-50
 emb[X63899|PSCHITIN P.sativum mRNA for chitinase. 94 1e-49
 5 emb|AB015655|AB015655 Cucurbita sp. mRNA for chitinase, complete... 100 7e-49
 gb|BE034450|BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 84 1e-48
 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 111 3e-48
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 108 6e-48
 gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 108 6e-48
 10

Query= M92353.4_s_at 20291_s_at /id_source genbank /description
 gb|aaa32738.1| (m92353) anthranilate synthase alpha subunit
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 15 /gb_link /ncgi
 (1788 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters
 20

Searching.....done

	Score	E
Sequences producing significant alignments:	(bits)	Value
25 gb L34344 RTAANTSYNB Ruta graveolens anthranilate synthase alpha...	772	0.0
gb L34343 RTAANTSYNB Ruta graveolens anthranilate synthase alpha...	467	0.0
emb AF079168 AF079168 Nicotiana tabacum feedback-insensitive ant...	365	0.0
emb AW931942 AW931942 EST357785 tomato fruit mature green, TAMU ...	356	3e-97
30 emb AW218352 AW218352 EST303535 tomato radicle, 5 d post-imbibit...	210	1e-73
emb AL031966 SPCC1442 S.pombe chromosome III cosmid c1442.	209	6e-69
emb AW651095 AW651095 EST329549 tomato germinating seedlings, TA...	222	2e-64
dbj D89256 D89256 Schizosaccharomyces pombe mRNA, partial cds, c...	205	5e-64
emb AW982499 AW982499 HVSMEg0003G22f Hordeum vulgare pre-anthesi...	215	2e-58
35 emb AW460005 AW460005 si07d11.y1 Gm-c1029 Glycine max cDNA clone...	116	1e-57
gb U18839 SCE9747 Saccharomyces cerevisiae chromosome V cosmids ...	123	4e-48
emb X68327 SCTRP2 S.cerevisiae TRP2 gene for anthranilate syntha...	123	4e-48
emb AW719463 AW719463 LjNEST5b1r Lotus japonicus nodule library,...	184	1e-45
emb AI736775 AI736775 sb33d01.y1 Gm-c1012 Glycine max cDNA clone...	104	2e-40
40 gb K01388 YSCTRP2 Yeast (S.cerevisiae) TRP2 gene coding for anth...	122	4e-38
emb AL032684 SPBP8B7 S.pombe chromosome II p1 p8B7.	95	6e-25
emb AW509018 AW509018 si39b01.y1 Gm-r1030 Glycine max cDNA clone...	113	5e-24
gb T14852 T14852 crs299 lambdaZAPST Ricinus communis cDNA clone ...	107	2e-22
emb AW223881 AW223881 EST300692 tomato fruit red ripe, TAMU Lyco...	103	4e-21
45 emb AF119554 AF119554 Plasmodium falciparum para-aminobenzoic ac...	67	6e-10
emb AL111470 CNS019CM Botrytis cinerea strain T4 cDNA library un...	45	2e-05
emb AI329873 AI329873 b9g02ne.r1 Neurospora crassa evening cDNA ...	48	3e-04
emb AW224247 AW224247 EST300974 tomato fruit red ripe, TAMU Lyco...	46	7e-04
emb AF149719 AF149719 Aspergillus fumigatus para aminobenzoic ac...	42	0.012
50 emb AQ448372 AQ448372 mgxb0020C12f CUGI Rice Blast BAC Library P...	39	0.15
emb AQ324360 AQ324360 mgxb0018K01r CUGI Rice Blast BAC Library P...	39	0.15
emb AQ160089 AQ160089 mgxb0003G09r CUGI Rice Blast BAC Library P...	39	0.15
emb AW599019 AW599019 gb01b03.y1 Moss EST library PPN Physcomitr...	37	0.38
emb AW599000 AW599000 ga99h03.y1 Moss EST library PPN Physcomitr...	37	0.38
55 emb AW678847 AW678847 WS1_1_A04.g1_A002 Water-stressed 1 (WS1) S...	35	0.88
emb AW680390 AW680390 WS1_52_D12.g1_A002 Water-stressed 1 (WS1) ...	35	0.89
emb AW678385 AW678385 WS1_15_H06.g1_A002 Water-stressed 1 (WS1) ...	35	0.89
emb AW747146 AW747146 WS1_66_E07.b1_A002 Water-stressed 1 (WS1) ...	35	0.89
emb AW678361 AW678361 WS1_15_H06.b1_A002 Water-stressed 1 (WS1) ...	35	0.90
60 emb AW745749 AW745749 WS1_37_D12.b1_A002 Water-stressed 1 (WS1) ...	35	0.90
emb AW747427 AW747427 WS1_68_B09.b1_A002 Water-stressed 1 (WS1) ...	35	0.90

	emb AW678071 AW678071 WS1_13_E01.b1_A002 Water-stressed 1 (WS1) ...	35	0.90
	emb AW747468 AW747468 WS1_68_B09.g1_A002 Water-stressed 1 (WS1) ...	35	0.90
	emb AW672427 AW672427 LG1_359_A06.g1_A002 Light Grown 1 (LG1) So...	35	0.90
	emb AW744836 AW744836 LG1_384_E07.g1_A002 Light Grown 1 (LG1) So...	35	0.90
5	emb AW746170 AW746170 WS1_39_B05.g1_A002 Water-stressed 1 (WS1) ...	35	0.90
	emb AW922317 AW922317 DG1_17_E06.g1_A002 Dark Grown 1 (DG1) Sorg...	35	0.91
	emb AQ648582 AQ648582 RPCI93-EcoRI-1M22.TP RPCI93-EcoRI Trypanos...	36	0.99
	emb AQ643551 AQ643551 RPCI93-EcoRI-3I24.TJ RPCI93-EcoRI Trypanos...	36	0.99
	emb AI443370 AI443370 sa31b05.x1 Gm-cl004 Glycine max cDNA clone...	35	1.4
10	emb AW101313 AW101313 sd77d08.y1 Gm-cl009 Glycine max cDNA clone...	35	1.4
	emb AW678030 AW678030 WS1_12_B10.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
	emb AW349006 AW349006 GM210004A12H10R Gm-r1021 Glycine max cDNA ...	35	1.4
	emb AW309961 AW309961 sf27b12.x1 Gm-cl028 Glycine max cDNA clone...	35	1.4
	emb AW678582 AW678582 WS1_16_E09.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
15	emb AW317198 AW317198 sf38f03.x1 Gm-cl028 Glycine max cDNA clone...	35	1.4
	emb AW678305 AW678305 WS1_14_G05.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
	emb AW680905 AW680905 WS1_8_A08.b1_A002 Water-stressed 1 (WS1) S...	35	1.4
	emb AW679666 AW679666 WS1_30_B11.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
	emb AL031746 PFMAL1P3 Plasmodium falciparum MAL1P3, complete seq...	35	1.9
20	emb AI959816 AI959816 sc94f02.y1 Gm-cl019 Glycine max cDNA clone...	35	1.9
	emb AW924277 AW924277 WS1_52_D12.b1_A002 Water-stressed 1 (WS1) ...	35	1.9
	gb J03998 PFAGAR Plasmodium falciparum glutamic acid-rich protei...	35	1.9
	emb AW696796 AW696796 NF109A07ST1F1052 Developing stem Medicago ...	35	1.9
	emb AW396753 AW396753 sf37c11.x1 Gm-cl028 Glycine max cDNA clone...	35	2.6
25	gb M98871 SOYCHS7A Glycine max chalcone synthase (chs7) gene, co...	35	2.6
	emb AI460797 AI460797 sa69d02.y1 Gm-cl004 Glycine max cDNA clone...	35	2.6
	emb AW348617 AW348617 GM210002B22G1R Gm-r1021 Glycine max cDNA 3...	35	2.6
	emb AW310362 AW310362 sf35a09.x1 Gm-cl028 Glycine max cDNA clone...	35	2.6
	emb AI437832 AI437832 sa40c07.y1 Gm-cl004 Glycine max cDNA clone...	35	2.6
30	gb BE023927 BE023927 sm94c05.y1 Gm-cl015 Glycine max cDNA clone ...	35	2.6
	emb AW424189 AW424189 sh62b04.y1 Gm-cl015 Glycine max cDNA clone...	35	2.6
	emb AW102370 AW102370 sd86h01.y1 Gm-cl009 Glycine max cDNA clone...	35	2.6
	emb AW101907 AW101907 sd72d01.y1 Gm-cl008 Glycine max cDNA clone...	35	2.6
	emb AW309356 AW309356 sf16d02.x1 Gm-cl028 Glycine max cDNA clone...	35	2.6
35	emb AL355932 NCB5O22 Neurospora crassa DNA linkage group II BAC ...	34	3.5
	emb AQ652663 AQ652663 Sheared DNA-20A9.TR Sheared DNA Trypanosom...	34	3.5
	emb Z98056 SPAC5D6 S.pombe chromosome I cosmid c5D6.	34	3.5
	emb AW348286 AW348286 GM210001B23B6R Gm-r1021 Glycine max cDNA 3...	34	4.9
	emb AB018422 AB018422 Pisum sativum mRNA for DNA binding zinc fi...	34	4.9
40	emb AW734949 AW734949 sk93b10.y1 Gm-cl035 Glycine max cDNA clone...	34	4.9
	emb AW679089 AW679089 WS1_22_A07.g1_A002 Water-stressed 1 (WS1) ...	34	4.9
	emb AW306776 AW306776 sf48c12.y1 Gm-cl009 Glycine max cDNA clone...	34	4.9
	gb M36941 BLYHORDCA Hordeum vulgare C-hordein gene, complete cds.	29	5.3
	gb BE034677 BE034677 ML01H08 ML Mesembryanthemum crystallinum cD...	33	6.7
45	emb Z26877 SCDCHR11 S.cerevisiae (S288C) 36.2kb DNA fragment fro...	33	6.7
	emb AW267708 AW267708 EST305836 DSIR Medicago truncatula cDNA cl...	33	6.7
	emb Z28162 SCYKL162C S.cerevisiae chromosome XI reading frame OR...	33	6.7
	emb AW980990 AW980990 EST392143 GVN Medicago truncatula cDNA clo...	33	6.7
	gb BE037412 BE037412 MP20G03 MP Mesembryanthemum crystallinum cD...	33	6.7
50	emb Z28161 SCYKL161C S.cerevisiae chromosome XI reading frame OR...	33	6.7
	emb AI726247 AI726247 BNLGHi5399 Six-day Cotton fiber Gossypium ...	33	6.7
	emb AE001401 AE001401 Plasmodium falciparum chromosome 2, sectio...	33	6.7
	emb AW573801 AW573801 EST316392 GVN Medicago truncatula cDNA clo...	33	6.7
	emb Z98547 PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque...	33	9.2
55	emb AQ659747 AQ659747 Sheared DNA-16J5.TR Sheared DNA Trypanosom...	33	9.2
	gb BE021269 BE021269 sm56h04.y1 Gm-cl028 Glycine max cDNA clone ...	33	9.2
	emb AW222457 AW222457 EST299268 tomato fruit red ripe, TAMU Lyco...	33	9.2
	emb AB012116 AB012116 Vigna mungo UFGlyT mRNA for UDP-glycose:fl...	33	9.2
	emb AW725836 AW725836 GA_Ea0019N24 Gossypium arboreum 7-10 dpa ...	33	9.2
60	emb AQ324451 AQ324451 mgxb0018L23r CUGI Rice Blast BAC Library P...	33	9.2
	gb M73492 LEIHSP90 Leishmania donovani heat shock protein 90 mRN...	33	9.2

emb|AW132634|AW132634 se06h07.y1 Gm-cl013 Glycine max cDNA clone... 33 9.2
 emb|AI166186|AI166186 a032p32u Hybrid aspen plasmid library Popu... 33 9.2
 gb|BE053953|BE053953 GA__Ea0031D23f Gossypium arboreum 7-10 dpa ... 33 9.2

5 Query= AC007168.86_at20331_at /id_source genbank /description
 gb|aad23617.1|ac007168_8 (ac007168) putative aspartate
 aminotransferase [arabidopsis thaliana] /blast_score 0 /ec_number
 /family aminotransferase /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 10 post/entrez/query?db=n&form=6&dopt=g&cuid=gb|ac007168|/ncgi
 http://www.ncgr.org/cgi-bin/ff?ac007168
 (1342 letters)

Database: plantfungal
 15 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 20 Sequences producing significant alignments: (bits) Value

emb|AI729480|AI729480 BNLGHi13474 Six-day Cotton fiber Gossypium... 365 e-116
 emb|AW032260|AW032260 EST275714 tomato callus, TAMU Lycopersicon... 336 2e-91
 emb|AW719468|AW719468 LjNEST5c2r Lotus japonicus nodule library,... 297 2e-79
 25 emb|AW729492|AW729492 GA__Ea0025C18 Gossypium arboreum 7-10 dpa ... 291 8e-78
 emb|AW924000|AW924000 WS1_32_E10.b1_A002 Water-stressed 1 (WS1) ... 277 1e-73
 emb|AW042762|AW042762 ST25B02 Pine TriplEx shoot tip library Pin... 268 2e-72
 emb|AW755778|AW755778 sl09c05.y1 Gm-cl036 Glycine max cDNA clone... 248 1e-64
 emb|AW737762|AW737762 EST339189 tomato flower buds, anthesis, Co... 169 1e-60
 30 emb|AW621695|AW621695 EST312493 tomato root during/after fruit s... 206 3e-52
 emb|AW350933|AW350933 GM210010B10D11R Gm-r1021 Glycine max cDNA ... 203 3e-51
 emb|AI166669|AI166669 xylem.est.479 Poplar xylem Lambda ZAPII li... 144 3e-50
 emb|AI496468|AI496468 sb08a12.y1 Gm-cl004 Glycine max cDNA clone... 197 2e-49
 35 emb|AI774565|AI774565 EST255665 tomato resistant, Cornell Lycop... 192 7e-48
 emb|AW907026|AW907026 EST343253 potato stolon, Cornell Universit... 186 4e-46
 emb|AW423906|AW423906 sh57f06.y1 Gm-cl015 Glycine max cDNA clone... 173 2e-42
 emb|AW458923|AW458923 sh16f03.y1 Gm-cl016 Glycine max cDNA clone... 171 8e-42
 gb|BE057095|BE057095 sm97d03.y1 Gm-cl015 Glycine max cDNA clone ... 164 2e-39
 40 emb|AW704991|AW704991 sk41b08.y1 Gm-cl019 Glycine max cDNA clone... 161 8e-39
 emb|AW034075|AW034075 EST277570 tomato callus, TAMU Lycopersicon... 150 2e-35
 emb|AI166457|AI166457 xylem.est.288 Poplar xylem Lambda ZAPII li... 145 7e-35
 emb|AW738611|AW738611 EST340038 tomato flower buds, anthesis, Co... 131 1e-29
 emb|AW679816|AW679816 WS1_32_E10.g1_A002 Water-stressed 1 (WS1) ... 126 5e-28
 45 emb|AW599717|AW599717 ga92a09.y1 Moss EST library PPN Physcomitr... 126 5e-28
 emb|AW704716|AW704716 sk39f03.y1 Gm-cl028 Glycine max cDNA clone... 100 5e-20
 emb|Z98531|SPAC6B12 S.pombe chromosome I cosmid c6B12. 50 1e-13
 emb|AW268000|AW268000 EST306222 DSIR Medicago truncatula cDNA cl... 58 1e-13
 emb|AW684914|AW684914 NF023A07NR1F1000 Nodulated root Medicago t... 58 1e-13
 50 emb|AW191292|AW191292 T113595e KV2 Medicago truncatula cDNA clon... 58 1e-13
 emb|AW040370|AW040370 EST283234 tomato mixed elicitor, BTI Lycop... 56 5e-13
 emb|AI440588|AI440588 sa68b05.y1 Gm-cl004 Glycine max cDNA clone... 57 2e-12
 emb|AW831752|AW831752 sm16f02.y1 Gm-cl027 Glycine max cDNA clone... 60 8e-12
 emb|AW906615|AW906615 EST342737 potato stolon, Cornell Universit... 56 1e-11
 55 gb|L00673|TRBANTA Trypanosoma cruzi antigen tyrosine aminotransf... 40 7e-10
 emb|AI773775|AI773775 EST254875 tomato resistant, Cornell Lycop... 63 5e-09
 emb|AW691076|AW691076 NF041A07ST1F1000 Developing stem Medicago ... 61 2e-08
 emb|AW477177|AW477177 ga42h10.y1 Moss EST library PPU Physcomitr... 61 3e-08
 emb|AI900082|AI900082 sb98f05.y1 Gm-cl012 Glycine max cDNA clone... 45 2e-07
 60 gb|BE022324|BE022324 sm73d10.y1 Gm-cl028 Glycine max cDNA clone ... 45 2e-07
 emb|AW690226|AW690226 NF030F01ST1F1000 Developing stem Medicago ... 40 3e-07

	emb AI736990 AI736990 sb36c06.y1 Gm-c1013 Glycine max cDNA clone...	57	4e-07
	emb AV409052 AV409052 AV409052 Lotus japonicus young plants (two...	56	6e-07
	gb BE020537 BE020537 sm44h11.y1 Gm-c1028 Glycine max cDNA clone ...	42	2e-06
	emb Z49335 SCYJL060W S.cerevisiae chromosome X reading frame ORF...	54	2e-06
5	emb AF074932 AF074932 Sinapis arvensis 1-aminocyclopropane-1-car...	36	2e-05
	emb AW727211 AW727211 GA_Ea0023N19 Gossypium arboreum 7-10 dpa ...	51	3e-05
	emb AI562691 AI562691 TENS2678 T. cruzi epimastigote normalized ...	37	3e-05
	emb AI460900 AI460900 sa70f07.y1 Gm-c1004 Glycine max cDNA clone...	50	5e-05
	emb AB015494 AB015494 Passiflora edulis PE-ACS1 mRNA for ACC syn...	36	5e-05
10	emb AI483496 AI483496 EST249317 tomato ovary, TAMU Lycopersicon ...	38	5e-05
	gb M34289 TOMACS Tomato 1-aminocyclopropane-1-carboxylate syntha...	36	1e-04
	gb L20634 POTACCSYN Solanum tuberosum 1-aminocyclopropane-1-carb...	36	1e-04
	emb X62536 LEACC L.esculentum mRNA for ACC synthase.	36	1e-04
	emb AI487017 AI487017 EST245339 tomato ovary, TAMU Lycopersicon ...	36	1e-04
15	emb X59145 LEACC2MR Lycopersicon esculentum LE-ASCC2 mRNA (ptACC...	35	2e-04
	emb AW568631 AW568631 si60b11.y1 Gm-r1030 Glycine max cDNA clone...	47	3e-04
	dbj D88273 D88273 Hordeum vulgare naat-A mRNA for nicotianamine ...	36	8e-04
	emb AB005788 AB005788 Hordeum vulgare mRNA for nicotianamine ami...	35	0.001
	emb AV390505 AV390505 AV390505 Chlamydomonas reinhardtii C9 Chla...	35	0.002
20	emb AV414385 AV414385 AV414385 Lotus japonicus young plants (two...	44	0.002
	emb AI054518 AI054518 coau0001D13 Cotton Boll Abscission Zone cD...	35	0.003
	emb Z18953 PHAMCRBSY P.hybrida mRNA for 1-aminocyclopropane 1-ca...	37	0.004
	emb AB007639 AB007639 Pyrus pyrifolia mRNA for 1-aminocyclopropana...	33	0.007
	emb AI941267 AI941267 sb86g03.y1 Gm-c1010 Glycine max cDNA clone...	31	0.007
25	emb AB033502 AB033502 Populus euphratica peacs-1 mRNA for 1-amin...	42	0.008
	gb U73816 MDU73816 Malus domestica ACC synthase (MdACS-3) mRNA, ...	32	0.009
	emb AI773174 AI773174 EST254274 tomato resistant, Cornell Lycope...	32	0.010
	emb X82273 BOACCS B.oleracea mRNA for ACC synthase.	42	0.012
	emb AJ012550 CSI012550 Citrus sinensis acs1 gene, exons 1-4.	41	0.016
30	emb Z11613 VRACCSYNM V.radiata mRNA for ACC synthase.	41	0.016
	emb Z18952 DCAMCRBSY D.caryophyllus mRNA for 1-aminocyclopropane...	41	0.016
	emb Z11562 VRACCSYN V.radiata mRNA for 1-aminocyclopropane-1-car...	41	0.016
	gb U68216 CPU68216 Carica papaya ACC synthase mRNA, complete cds.	41	0.022
	emb AF178076 AF178076 Carica papaya 1-aminocyclopropane-1-carbox...	41	0.022
35	emb AF048753 AF048753 Citrus X paradisi 1-aminocyclopropane-1-ca...	41	0.022
	emb AW925529 AW925529 HVSMEg0002F12 Hordeum vulgare pre-anthesis...	41	0.022
	emb AW030650 AW030650 EST273905 tomato callus, TAMU Lycopersicon...	41	0.022
	emb AJ012577 CPA012577 Carica papaya mRNA for 1-aminocyclopropan...	41	0.022
	emb AJ012551 CSI012551 Citrus sinensis mRNA for ACC synthase.	41	0.022
40	emb AI440609 AI440609 sa68d05.y1 Gm-c1004 Glycine max cDNA clone...	41	0.022
	emb AW928458 AW928458 EST337246 tomato flower buds 8 mm to pre-a...	41	0.022
	emb AJ276295 CSI276295 Citrus sinensis partial mRNA for ACC synt...	40	0.030
	gb U17231 PHU17231 Pelargonium hortorum clone pGAC-2 1-aminocycl...	40	0.030
	emb AF177769 AF177769 Carica papaya 1-aminocyclopropane-1-carbox...	40	0.030
45	gb U88971 PHU88971 Pelargonium hortorum 1-aminocyclopropane-1-ca...	40	0.030
	emb AF170705 AF170705 Mangifera indica 1-aminocyclopropane-1-car...	40	0.041
	gb BE020529 BE020529 sm44h02.y1 Gm-c1028 Glycine max cDNA clone ...	40	0.057
	emb AW100199 AW100199 sd26h06.y1 Gm-c1012 Glycine max cDNA clone...	40	0.057
	emb X67100 GMCACCS1 G.max mRNA for ACC synthase.	40	0.057
50	emb AI487927 AI487927 EST246249 tomato ovary, TAMU Lycopersicon ...	40	0.057
	emb AF239987 AF239987 Prunus persica ACC synthase ACS1 mRNA, par...	40	0.057
	emb AW221912 AW221912 EST298723 tomato fruit red ripe, TAMU Lyco...	40	0.057
	emb AW774036 AW774036 EST333022 KV3 Medicago truncatula cDNA clo...	40	0.057
	emb AI165890 AI165890 B003P14U Hybrid aspen plasmid library Popu...	40	0.057
55	emb AJ277160 CPA277160 Carica papaya partial paccs1A gene for 1-...	39	0.078
	emb AW703931 AW703931 sk25h05.y1 Gm-c1028 Glycine max cDNA clone...	39	0.078
	emb AW928492 AW928492 EST337280 tomato flower buds 8 mm to pre-a...	39	0.078
	emb AW043088 AW043088 ST29B11 Pine TriplEx shoot tip library Pin...	39	0.078
	emb Y09204 NTHPA N.tabacum mRNA for histidinol-phosphate aminotr...	30	0.10
60	emb AF083814 AF083814 Antirrhinum majus ACC synthase 1 (ACS1) mR...	39	0.11
	gb U17230 PHU17230 Pelargonium hortorum clone pGAC-2G 1-aminocyc...	39	0.11

Query= AC005850.19_s_at 20365_s_at /id_source genbank /description
 gb|aad25552.1|ac005850_9 (ac005850) highly similar to mlo proteins
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 5 /gb_link /ncgi
 (1752 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

10 Searching.....done

	Score	E	
	(bits)		Value
15	Sequences producing significant alignments:		
	emb A92838 A92838	Sequence 12 from Patent WO9804586.	258 e-123
	emb Z83834 HVMLO	H.vulgare mRNA for Mlo protein.	261 e-116
	emb A92833 A92833	Sequence 7 from Patent WO9804586.	261 e-116
	emb A92828 A92828	Sequence 2 from Patent WO9804586.	261 e-116
20	emb AW216578 AW216578	EST295292 tomato callus, TAMU Lycopersicon...	165 6e-78
	emb AJ005341 LUAJ5341	Linum usitatissimum mRNA for MLO-like prot...	287 2e-76
	emb AW934153 AW934153	EST359996 tomato fruit mature green, TAMU ...	235 4e-74
	emb AW132264 AW132264	sd98f11.y1 Gm-c1013 Glycine max cDNA clone...	128 2e-60
	emb AI779924 AI779924	EST260803 tomato susceptible, Cornell Lyco...	228 8e-59
25	gb BE020055 BE020055	sm38e01.y1 Gm-c1028 Glycine max cDNA clone ...	199 2e-58
	emb AW132268 AW132268	sd98g11.y1 Gm-c1013 Glycine max cDNA clone...	124 5e-58
	emb AI729603 AI729603	BNLGHi13760 Six-day Cotton fiber Gossypium...	202 8e-51
	emb AI054629 AI054629	coau0001J02 Cotton Boll Abscission Zone cD...	133 2e-44
	emb AV426381 AV426381	AV426381 Lotus japonicus young plants (two...	145 3e-43
30	emb AI729043 AI729043	BNLGHi12416 Six-day Cotton fiber Gossypium...	142 6e-42
	emb Y14573 HVCH4H	Hordeum vulgare DNA for chromosome 4H.	107 7e-41
	emb A92831 A92831	Sequence 5 from Patent WO9804586.	107 7e-41
	emb AI731933 AI731933	BNLGHi11440 Six-day Cotton fiber Gossypium...	136 3e-40
	emb AI440563 AI440563	sa84c07.y1 Gm-c1004 Glycine max cDNA clone...	155 1e-36
35	emb AI166945 AI166945	xylem.est.727 Poplar xylem Lambda ZAPII li...	149 4e-35
	emb A92829 A92829	Sequence 3 from Patent WO9804586.	107 4e-34
	gb BE059771 BE059771	sm36h06.y1 Gm-c1016 Glycine max cDNA clone ...	137 2e-31
	emb AB011444 AB011444	Triticum aestivum WESR3 mRNA, partial cds.	137 2e-31
	emb AW350270 AW350270	GM210007B20B6R Gm-r1021 Glycine max cDNA 3...	127 7e-31
40	emb AI778500 AI778500	EST259379 tomato susceptible, Cornell Lyco...	76 3e-30
	emb AW299018 AW299018	EST305692 KV2 Medicago truncatula cDNA clo...	125 1e-27
	emb AW442776 AW442776	EST307706 tomato mixed elicitor, BTI Lycop...	117 2e-25
	emb AW719459 AW719459	LjNEST4h6r Lotus japonicus nodule library,...	85 4e-25
	emb AW087034 AW087034	gal1ld07.y1 Moss EST library CPU Ceratodon ...	83 5e-25
45	emb AW672144 AW672144	LG1_357_A11.b1_A002 Light Grown 1 (LG1) So...	108 1e-22
	emb AT000894 AT000894	AT000894 Brassica rapa guard cell Brassica...	108 2e-22
	emb AW906979 AW906979	EST343206 potato stolon, Cornell Universit...	98 2e-19
	emb Z95496 HVMLOH1	H.vulgare Mlo-h1 gene.	98 2e-19
	emb A92836 A92836	Sequence 10 from Patent WO9804586.	98 2e-19
50	emb A92832 A92832	Sequence 6 from Patent WO9804586.	98 2e-19
	emb AW570038 AW570038	si85h06.y1 Gm-c1031 Glycine max cDNA clone...	96 6e-19
	emb AA660856 AA660856	00751 MtRHE Medicago truncatula cDNA 5', m...	90 4e-17
	emb AT000630 AT000630	AT000630 Brassica rapa guard cell Brassica...	87 5e-16
	gb BE022484 BE022484	sm74e08.y1 Gm-c1015 Glycine max cDNA clone ...	84 3e-15
55	emb AW672173 AW672173	LG1_357_A11.g1_A002 Light Grown 1 (LG1) So...	80 4e-14
	emb AI443125 AI443125	sa84f05.y1 Gm-c1004 Glycine max cDNA clone...	78 3e-13
	emb AW870276 AW870276	NXNV_128_G07_F Nsf Xylem Normal wood Verti...	77 4e-13
	emb AW726816 AW726816	GA_Ea0022N04 Gossypium arboreum 7-10 dpa ...	50 6e-13
	emb AI960937 AI960937	sc92h06.y1 Gm-c1019 Glycine max cDNA clone...	76 1e-12
60	emb AW569990 AW569990	si85c05.y1 Gm-c1031 Glycine max cDNA clone...	75 1e-12
	emb AI484886 AI484886	EST243149 tomato ovary, TAMU Lycopersicon ...	73 7e-12

	emb AW285009 AW285009 LG1_297_B09.g1_A002 Light Grown 1 (LG1) So...	72	1e-11
	emb AW203816 AW203816 sf38e09.y1 Gm-c1028 Glycine max cDNA clone...	62	2e-08
	emb AW719871 AW719871 LjNEST11d10r Lotus japonicus nodule librar...	51	8e-08
	emb AW757069 AW757069 sl02g02.y1 Gm-c1036 Glycine max cDNA clone...	59	9e-08
5	emb AW567653 AW567653 si77b05.y1 Gm-c1031 Glycine max cDNA clone...	55	2e-06
	emb AT000874 AT000874 AT000874 Brassica rapa guard cell Brassica...	46	7e-04
	emb AI563090 AI563090 EST00214 watermelon lambda zap library Cit...	37	0.010
	emb Z74921 BOK8A2 B.oleracea mRNA (unknown).	31	0.26
	emb AZ221382 AZ221382 Gm_UMb001_002_A13R UMN Soybean BAC Library...	33	0.65
10	gb BE035329 BE035329 MM06C12 MM Mesembryanthemum crystallinum cD...	36	0.71
	emb AW186503 AW186503 se68f07.y1 Gm-c1019 Glycine max cDNA clone...	36	0.97
	emb AW218260 AW218260 EST303441 tomato radicle, 5 d post-imbibit...	35	1.3
	emb AW693662 AW693662 NF067A11ST1F1084 Developing stem Medicago ...	35	1.3
	emb AW688978 AW688978 NF014A05ST1F1000 Developing stem Medicago ...	35	1.3
15	emb AI374173 AI374173 T6346 MVAT4 bloodstream form of serodeme W...	35	1.3
	emb AW689953 AW689953 NF027B09ST1F1000 Developing stem Medicago ...	35	1.3
	emb AW218259 AW218259 EST303440 tomato radicle, 5 d post-imbibit...	35	1.3
	emb X96770 SCLACHXVI S.cerevisiae chromosome XVI, left arm DNA.	35	1.8
	emb X05498 SCSNR17B Yeast SNR17B gene for U3 small nuclear RNA.	35	1.8
20	emb Z73500 SCYPL144W S.cerevisiae chromosome XVI reading frame O...	35	1.8
	gb U43703 SCU43703 Saccharomyces cerevisiae chromosome XVI cosmi...	35	1.8
	emb Z73499 SCYPL143W S.cerevisiae chromosome XVI reading frame O...	35	1.8
	emb AJ242498 CCL242498 Candida cloacae mRNA for long chain fatty...	35	1.8
	emb AQ949106 AQ949106 Sheared DNA-49L9.TR Sheared DNA Trypanosom...	35	2.5
25	emb AQ650344 AQ650344 Sheared DNA-28J12.TF Sheared DNA Trypanoso...	35	2.5
	emb AQ657515 AQ657515 Sheared DNA-3K7.TR Sheared DNA Trypanosoma...	35	2.5
	emb Z74965 SCYOR057W S.cerevisiae chromosome XV reading frame OR...	34	3.5
	emb AC007061 AC007061 Leishmania major chromosome 3 clone L1559 ...	34	3.5
	emb AQ642037 AQ642037 RPCI93-DpnII-29K3.TJ RPCI93-DpnII Trypanos...	34	3.5
30	emb AQ445280 AQ445280 GSSTc01558 Trypanosoma cruzi random genomi...	34	3.5
	emb Z70678 SCXV55KB S.cerevisiae chromosome XV DNA, 54.7 kb region.	34	3.5
	emb AQ659145 AQ659145 Sheared DNA-16H2.TF Sheared DNA Trypanosom...	34	3.5
	gb U88830 SCU88830 Saccharomyces cerevisiae Sgt1p (SGT1) gene, c...	34	3.5
	emb AC005927 AC005927 Leishmania major chromosome 3 clone L3561 ...	34	3.5
35	emb AQ637975 AQ637975 927P1-6A12.TV 927P1 Trypanosoma brucei gen...	34	3.5
	emb AL031744 PFMALIP1 Plasmodium falciparum chromosome 1 strain ...	29	4.5
	emb AF091345 AF091345 Schizosaccharomyces pombe N-terminal serin...	34	4.7
	emb AC013353 AC013353 Trypanosoma brucei chromosome VI clone RPC...	34	4.7
	emb AQ948416 AQ948416 Sheared DNA-38M22.TR Sheared DNA Trypanoso...	34	4.7
40	emb AW257222 AW257222 EST305359 KV2 Medicago truncatula cDNA clo...	34	4.7
	emb Y13973 CACIP1 Candida sp. CIP1 gene.	34	4.7
	emb AL031263 SPBC17F3 S.pombe chromosome II cosmid c17F3.	34	4.7
	emb AF152552 AF152552 Sorghum bicolor chalcone synthase 5 (CHS5)...	34	4.7
	emb AQ655690 AQ655690 Sheared DNA-9G1.TR Sheared DNA Trypanosoma...	34	4.7
45	emb AZ212373 AZ212373 Sheared DNA-101E1.TF Sheared DNA Trypanoso...	34	4.7
	emb AJ250726 TBR250726 Trypanosoma brucei HSP100 gene, GPI-PLC g...	34	4.7
	gb M17420 YSTHEP Saccharomyces cerevisiae heptapeptide repeat re...	33	6.5
	emb AI730517 AI730517 BNLGHi6942 Six-day Cotton fiber Gossypium ...	33	6.5
	emb Z49511 SCYJR011C S.cerevisiae chromosome X reading frame ORF...	33	6.5
50	gb U59312 HVU59312 Hordeum vulgare (1,4)-beta-xylan endohydrolas...	33	6.5
	emb Z74188 SCYDL140C S.cerevisiae chromosome IV reading frame OR...	33	6.5
	emb X87611 SCXCOSM83 S.cerevisiae chromosome X DNA (cosmid 83).	33	6.5
	emb AA003500 AA003500 T3189 MVAT4 bloodstream form of serodeme W...	33	6.5
	emb AQ951709 AQ951709 Sheared DNA-51E22.TF Sheared DNA Trypanoso...	33	6.5

55

Query= AC005314.38_at 20368_at /id_source genbank /description
gb|aac36163.1| (ac005314) putative serpin [arabidopsis thaliana]
/blast_score 0 /ec_number /family /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005314|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005314|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005314|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac005314>

60

(1125 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5

Searching.....done

		Score	E	
	Sequences producing significant alignments:	(bits)	Value	
10	emb Y11486 TASERPIN T.aestivum mRNA for serpin WZS3.	112	2e-68	
	emb AJ245879 TAE245879 Triticum aestivum mRNA for serpin (WSZ2a ...	113	7e-66	
	emb AJ245878 TAE245878 Triticum aestivum mRNA for serpin (WSZ1c ...	116	2e-65	
	emb Y11485 TAESERPIN T.aestivum mRNA for serpin WZS2.	116	2e-62	
15	emb Z49890 TAWZCISPIN T.aestivum WZCI mRNA for serpin.	109	3e-60	
	emb X95277 HVSEH H.vulgare mRNA for serpin.	98	6e-58	
	emb AW458573 AW458573 sh10h03.y1 Gm-cl016 Glycine max cDNA clone...	115	6e-55	
	emb X97636 HVSERP H.vulgare mRNA for serpin.	96	2e-44	
	emb AW598408 AW598408 sj91a11.y1 Gm-cl023 Glycine max cDNA clone...	144	2e-43	
20	gb BE058355 BE058355 sn15a03.y1 Gm-cl016 Glycine max cDNA clone ...	134	3e-40	
	emb AW688254 AW688254 NF005C03ST1F1000 Developing stem Medicago ...	127	7e-38	
	emb Z15116 HVPAXXG H.vulgare pazx gene encoding protein zx.	80	6e-32	
	emb AF118560 AF118560 Avena fatua barley protein Z homolog mRNA,...	73	7e-32	
	emb AW394511 AW394511 sh33b01.y1 Gm-cl017 Glycine max cDNA clone...	81	2e-31	
25	emb AI730301 AI730301 BNLGHi6607 Six-day Cotton fiber Gossypium ...	77	8e-31	
	emb AI725411 AI725411 BNLGHi11751 Six-day Cotton fiber Gossypium...	55	9e-30	
	emb AV420945 AV420945 AV420945 Lotus japonicus young plants (two...	126	4e-28	
	emb AI772215 AI772215 EST253315 tomato resistant, Cornell Lycopersicon...	116	6e-27	
	emb X51726 HVPZ1 Barley Paz1 gene for protein Z.	76	3e-26	
30	emb AW219573 AW219573 EST302055 tomato root during/after fruit s...	83	4e-26	
	emb AI726323 AI726323 BNLGHi5614 Six-day Cotton fiber Gossypium ...	112	8e-26	
	emb AW926241 AW926241 HVSMEg0006L04 Hordeum vulgare pre-anthesis...	117	2e-25	
	emb AW729167 AW729167 GA__Ea0024E14 Gossypium arboreum 7-10 dpa ...	73	6e-24	
	emb AW725528 AW725528 GA__Ea0018H14 Gossypium arboreum 7-10 dpa ...	73	6e-24	
35	emb AV408545 AV408545 AV408545 Lotus japonicus young plants (two...	68	9e-22	
	gb BE036749 BE036749 MP04H03 MP Mesembryanthemum crystallinum cD...	48	1e-21	
	emb AW983183 AW983183 HVSMEg0008J04f Hordeum vulgare pre-anthesi...	64	2e-21	
	emb AW728267 AW728267 GA__Ea0016C18 Gossypium arboreum 7-10 dpa ...	102	4e-21	
	emb AW099940 AW099940 sd18f07.y2 Gm-cl012 Glycine max cDNA clone...	57	5e-18	
40	emb AW720162 AW720162 LjNEST16a4r Lotus japonicus nodule library...	84	1e-15	
	emb AW598800 AW598800 ga88d04.y1 Moss EST library PPU Physcomittr...	84	3e-15	
	gb BE058596 BE058596 sn18b11.y1 Gm-cl016 Glycine max cDNA clone ...	48	7e-14	
	gb BE051905 BE051905 GA__Ea0023M15f Gossypium arboreum 7-10 dpa ...	56	4e-13	
	emb AV428665 AV428665 AV428665 Lotus japonicus young plants (two...	70	3e-11	
45	emb AV418072 AV418072 AV418072 Lotus japonicus young plants (two...	70	4e-11	
	emb AW428704 AW428704 Ljirnp22-785-g1 Ljirnp Lambda HybriZap ...	70	4e-11	
	emb AW560154 AW560154 EST315202 DSIR Medicago truncatula cDNA cl...	69	5e-11	
	emb AQ917127 AQ917127 T233156b Medicago truncatula BAC library M...	47	3e-09	
	emb AW306929 AW306929 sf50e08.y1 Gm-cl009 Glycine max cDNA clone...	56	4e-08	
50	emb AW010023 AW010023 ST01E04 Pine TriplEx shoot tip library Pin...	41	1e-07	
	emb X51727 HVPZPSE Barley DNA for pseudogene PAZ.	51	3e-07	
	gb BE022668 BE022668 sm75h09.y1 Gm-cl015 Glycine max cDNA clone ...	56	7e-07	
	emb X05902 HVPROTZ Barley mRNA fragment for protein Z.	46	8e-07	
	emb AW102228 AW102228 sd85a05.y1 Gm-cl009 Glycine max cDNA clone...	48	7e-06	
55	emb AI779352 AI779352 EST260231 tomato susceptible, Cornell Lyco...	51	1e-05	
	emb AI779351 AI779351 EST260230 tomato susceptible, Cornell Lyco...	51	1e-05	
	emb AV420150 AV420150 AV420150 Lotus japonicus young plants (two...	50	3e-05	
	emb AW599056 AW599056 gb01e09.y1 Moss EST library PPN Physcomittr...	50	3e-05	
	emb AV414917 AV414917 AV414917 Lotus japonicus young plants (two...	50	3e-05	
60	emb AW738877 AW738877 gb03f10.y1 Moss EST library PPN Physcomittr...	42	0.002	
	emb AW693477 AW693477 NF065F09ST1F1000 Developing stem Medicago ...	42	0.010	

emb|AW905918|AW905918 EST342091 potato stolon, Cornell Universit... 35 0.81
 emb|Z49939|SC9959 S.cerevisiae chromosome XIII cosmid 9959. 35 1.5
 gb|BE059186|BE059186 sn27d04.y1 Gm-c1016 Glycine max cDNA clone ... 35 1.5
 emb|AW119311|AW119311 A57 Neospora caninum Lambda Zap cDNA libra... 34 2.1
 5 emb|AL114606|CNS01BRQ Botrytis cinerea strain T4 cDNA library un... 34 2.1
 emb|AL114185|CNS01BGI Botrytis cinerea strain T4 cDNA library un... 34 2.1
 emb|AL114991|CNS01C2F Botrytis cinerea strain T4 cDNA library un... 34 2.1
 emb|AQ367717|AQ367717 toxb0002L20r CUGI Tomato BAC Library Lycop... 34 2.1
 emb|AL114160|CNS01BFC Botrytis cinerea strain T4 cDNA library un... 34 2.1
 10 emb|AL115273|CNS01CA9 Botrytis cinerea strain T4 cDNA library un... 34 2.1
 emb|AL113815|CNS01B5R Botrytis cinerea strain T4 cDNA library un... 34 2.1
 emb|AI490380|AI490380 EST248706 tomato ovary, TAMU Lycopersicon ... 34 2.9
 emb|AL116919|CNS01DJZ Botrytis cinerea strain T4 cDNA library un... 34 2.9
 gb|U68716|BFU68716 Botryotinia fuckeliana endopolygalacturonase ... 33 4.0
 15 gb|L25681|HYBRG18S Hydnora africana Thunb. 18S ribosomal RNA (18... 33 4.0
 emb|AI165169|AI165169 A077P18U Hybrid aspen plasmid library Popu... 33 4.0
 gb|BE020501|BE020501 sm44e08.y1 Gm-c1028 Glycine max cDNA clone ... 33 5.5
 gb|M55639|AURRR16S Aureobasidium pullulans 16S-like ribosomal RN... 33 5.5
 emb|AQ953266|AQ953266 Sheared DNA-39D4.TF Sheared DNA Trypanosom... 33 5.5
 20 emb|AI494738|AI494738 sb14f02.y1 Gm-c1004 Glycine max cDNA clone... 33 5.5
 gb|M35065|BLYPROZ Barley protein Z mRNA, partial cds. 33 5.5
 emb|AV409233|AV409233 AV409233 Lotus japonicus young plants (two... 26 6.2
 emb|AJ273043|AJ273043 AJ273043 Metarhizium anisopliae ARSEF 2575... 32 7.5
 emb|AF106529|AF106529 Monacrosporium leptosporum 18S small subun... 32 7.5
 25 emb|AW569360|AW569360 si86a11.y1 Gm-c1031 Glycine max cDNA clone... 32 7.5
 emb|X51599|NTCHN50 Tobacco CHN50 gene for endochitinase. 32 7.5
 emb|AL356192|NCB24B19 Neurospora crassa DNA linkage group II BAC... 32 7.5
 emb|AF123288|AF123288 Lagynion scherffellii small subunit ribosom... 32 7.5
 emb|AW180275|AW180275 MgA0367f MgA Library Mycosphaerella gramin... 32 7.5
 30 emb|AL356172|NCB23L21 Neurospora crassa DNA linkage group II BAC... 32 7.5
 emb|AI779615|AI779615 EST260494 tomato susceptible, Cornell Lyco... 32 7.5
 emb|X64519|NTCHN50G N.tabacum chitinase gene 50 for class I chit... 32 7.5
 emb|AF123299|AF123299 Chrysosphaera parvula small subunit riboso... 32 7.5
 emb|AQ398442|AQ398442 mgxb0015C20f CUGI Rice Blast BAC Library P... 32 7.5

35
 Query= AL024486.131_at 20420_at /id_source genbank /description
 emb|caa19698.1| (al024486) putative chitinase [arabidopsis thaliana]
 /blast_score 0 /ec_number /family chitinase /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 40 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al024486| /ncgi
 http://www.ncgr.org/cgi-bin/ff?al024486
 (1140 letters)

Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E
50 Sequences producing significant alignments:	(bits)	Value
emb X78325 NTSNNPZ N.tabacum (Samsun NN) Pz mRNA.	317	e-139
emb A72838 A72838 Sequence 1 from Patent WO9505467.	314	e-138
emb X77110 NTCHIVR N.tabacum chi-V mRNA for chitinase class V.	312	e-137
55 emb AF088885 AF088885 Nicotiana tabacum receptor-like kinase CHR...	189	3e-84
emb X77111 NTCHIVD N.tabacum chi-V gene.	204	1e-69
emb A72844 A72844 Sequence 7 from Patent WO9505467.	204	7e-69
emb AW690230 AW690230 NF030F05ST1F1000 Developing stem Medicago ...	139	4e-66
emb AF108893 AF108893 AF108893 Capsicum annuum root 1st-branched...	201	7e-51
60 emb AW032116 AW032116 EST275570 tomato callus, TAMU Lycopersicon...	186	2e-46
emb AW560415 AW560415 EST315463 DSIR Medicago truncatula cDNA cl...	169	3e-41

- emb|AW351251|AW351251 GM210011A20A4R Gm-r1021 Glycine max cDNA 3... 145 6e-34
- emb|AV423067|AV423067 AV423067 Lotus japonicus young plants (two... 129 2e-32
- emb|AV412385|AV412385 AV412385 Lotus japonicus young plants (two... 129 4e-29
- 5 emb|AV411642|AV411642 AV411642 Lotus japonicus young plants (two... 84 3e-28
- emb|AI495953|AI495953 sb18c04.y1 Gm-c1004 Glycine max cDNA clone... 111 1e-23
- emb|AV422006|AV422006 AV422006 Lotus japonicus young plants (two... 75 3e-21
- emb|AF188932|AF188932 Hypocrea rufa strain Hy9 42 kDa endochitin... 68 1e-20
- emb|AF188921|AF188921 Trichoderma atroviride strain DAOM 165782 ... 70 3e-20
- 10 gb|U49455|THU49455 Trichoderma harzianum endochitinase (chi1) mR... 69 3e-20
- emb|AF188918|AF188918 Hypocrea koningii 42 kDa endochitinase gen... 71 3e-20
- emb|AF188930|AF188930 Trichoderma asperellum strain CBS 361.97, ... 68 6e-20
- emb|AF188926|AF188926 Trichoderma asperellum strain GJS 90-14 42... 68 6e-20
- emb|AF188923|AF188923 Hypocrea rufa strain GJS 89-142 42 kDa end... 68 8e-20
- 15 emb|X79381|THECH42 T.harzianum (IMI 206040) ech-42 gene. 68 9e-20
- gb|L14614|TRRENDOCHI Trichoderma harzianum endochitinase mRNA, c... 68 9e-20
- emb|AF188920|AF188920 Trichoderma atroviride strain DAOM 165779 ... 68 9e-20
- emb|AF188929|AF188929 Trichoderma asperellum strain CBS 433.97, ... 68 9e-20
- emb|AF188933|AF188933 Trichoderma asperellum strain BBA 68646R 4... 68 9e-20
- 20 gb|S78423|S78423 chit42=endochitinase [Trichoderma harzianum, mR... 67 9e-20
- gb|U88560|THU88560 Trichoderma hamatum endochitinase gene, compl... 68 1e-19
- emb|AF188931|AF188931 Hypocrea vinosa 42 kDa endochitinase gene,... 68 1e-19
- emb|AF188927|AF188927 Trichoderma viride strain GJS 90-20 42 kDa... 68 2e-19
- gb|U33265|CIU33265 Coccidioides immitis complement fixation/chit... 60 2e-19
- 25 gb|U60807|CIU60807 Coccidioides immitis complement fixation-chit... 60 3e-19
- emb|AF188924|AF188924 Trichoderma viride strain ATCC 32630, syno... 68 4e-19
- emb|AF188928|AF188928 Trichoderma viride strain BBA 66069R 42 kD... 68 4e-19
- emb|AF188925|AF188925 Trichoderma viride strain Tr6 42 kDa endoc... 68 4e-19
- emb|AF188919|AF188919 Trichoderma viride strain ATCC 18652, syno... 66 2e-18
- 30 emb|AF188922|AF188922 Hypocrea rufa strain GJS 89-127 42 kDa end... 66 3e-18
- emb|AF050098|AF050098 Trichoderma virens chitinase gene, complet... 65 2e-17
- emb|X64104|AACHI1A A.album chi1 gene for chitinase. 65 3e-17
- emb|AJ243014|MFL243014 Metarhizium flavoviride mRNA for chitinas... 62 8e-17
- emb|AF027498|AF027498 Metarhizium anisopliae chitinase CHIT42 (C... 60 9e-16
- 35 emb|AF027497|AF027497 Metarhizium anisopliae chitinase CHIT42 (C... 60 9e-16
- emb|AI967677|AI967677 Ljimpest08-687-g4 Ljirnp Lambda HybriZap ... 72 5e-14
- emb|AV421624|AV421624 AV421624 Lotus japonicus young plants (two... 63 2e-13
- emb|AI899627|AI899627 EST269070 tomato susceptible, Cornell Lyco... 75 1e-12
- dbj|D87894|D87894 Rhizopus oligosporus DNA for chitinase, comple... 59 2e-10
- 40 emb|AV407063|AV407063 AV407063 Lotus japonicus young plants (two... 68 2e-10
- emb|AF009354|AF009354 Leishmania donovani chitinase (Chi-1) gene... 57 4e-09
- emb|AA786967|AA786967 m7d11a1.r1 Aspergillus nidulans 24hr asexu... 54 5e-09
- emb|AA966331|AA966331 w4a12a1.r1 Aspergillus nidulans 24hr asexu... 54 5e-09
- emb|AI212420|AI212420 x5f11a1.r1 Aspergillus nidulans 24hr asexu... 43 6e-08
- 45 emb|AI210660|AI210660 k0b03a1.r1 Aspergillus nidulans 24hr asexu... 53 1e-07
- emb|AA785435|AA785435 g7d04a1.r1 Aspergillus nidulans 24hr asexu... 54 2e-07
- emb|AA787768|AA787768 r1d06a1.r1 Aspergillus nidulans 24hr asexu... 46 2e-06
- emb|AA784794|AA784794 g2d07a1.r1 Aspergillus nidulans 24hr asexu... 43 2e-06
- gb|L41663|COICTS1CHI Coccidioides immitis chitinase (cts1) gene,... 44 5e-06
- 50 gb|U51271|CIU51271 Coccidioides immitis complement-fixation anti... 44 5e-06
- gb|U60806|CIU60806 Coccidioides immitis complement-fixation chit... 44 5e-06
- emb|AI213337|AI213337 z1b11a1.r1 Aspergillus nidulans 24hr asexu... 50 7e-06
- emb|AI211269|AI211269 o0h07a1.r1 Aspergillus nidulans 24hr asexu... 43 1e-05
- emb|AW334147|AW334147 S31A10 AGS-1 Pneumocystis carinii f. sp. c... 51 1e-05
- 55 emb|Z71415|THENDOCHS T.hamatum endochitinase gene. 50 3e-05
- emb|AA786295|AA786295 l3d02a1.r1 Aspergillus nidulans 24hr asexu... 31 6e-05
- emb|AI209456|AI209456 a0h06a1.r1 Aspergillus nidulans 24hr asexu... 43 6e-05
- gb|M11815|YSKGKL1A Plasmid pGKL1 from killer yeast (K.lactis), c... 39 1e-04
- emb|X01095|KLKILL1L Yeast DNA killer plasmid pGKL1. 39 1e-04
- 60 emb|X00762|KLKILL05 Kluyveromyces lactis (killer strain) plasmid... 39 1e-04
- emb|X07127|KLK1P Kluyveromyces lactis killer plasmid k1 DNA. 39 1e-04

emb|X89212|MADNACHIA M.anisopliae DNA for ChiA gene. 48 1e-04
 emb|A86212|A86212 Sequence 871 from Patent EP0866129. 48 2e-04
 emb|AA787160|AA787160 m8b03a1.r1 Aspergillus nidulans 24hr asexu... 46 8e-04
 gb|U28373|YSCD9481 Saccharomyces cerevisiae chromosome IV cosmid... 45 0.001
 5 emb|AA966303|AA966303 v7h11a1.r1 Aspergillus nidulans 24hr asexu... 43 0.005
 emb|AA788389|AA788389 r7f09a1.r1 Aspergillus nidulans 24hr asexu... 30 0.039
 emb|AI210224|AI210224 h0g10a1.r1 Aspergillus nidulans 24hr asexu... 32 0.13
 dbj|D87063|D87063 Aspergillus nidulans chiB gene for chitinase, ... 31 0.15
 emb|AA787747|AA787747 r1b07a1.r1 Aspergillus nidulans 24hr asexu... 31 0.17
 10 emb|AA783278|AA783278 c3h07a1.r1 Aspergillus nidulans 24hr asexu... 31 0.17
 emb|AA785323|AA785323 g6e04a1.r1 Aspergillus nidulans 24hr asexu... 31 0.17
 emb|AW335048|AW335048 S42E2 AGS-1 Pneumocystis carinii f. sp. ca... 37 0.23
 emb|AW333489|AW333489 S22D2 AGS-1 Pneumocystis carinii f. sp. ca... 36 0.44
 emb|AI210899|AI210899 m0b11a1.r1 Aspergillus nidulans 24hr asexu... 29 0.57
 15 emb|AW310633|AW310633 sg22d12.x1 Gm-c1024 Glycine max cDNA clone... 36 0.60
 emb|AA785309|AA785309 g6d06a1.r1 Aspergillus nidulans 24hr asexu... 31 0.77
 gb|L19093|PEARHOGTPP Pisum sativum rho (ras-related) GTP-binding... 35 1.6
 gb|BE053716|BE053716 GA__Ea0002M02f Gossypium arboreum 7-10 dpa ... 34 2.1
 emb|AQ162416|AQ162416 mgxb0012N01r CUGI Rice Blast BAC Library P... 34 2.1
 20 emb|AW108998|AW108998 gate0002M02f Gossypium arboreum 7-10 dpa f... 34 2.1
 emb|AI727383|AI727383 BNLGHi7901 Six-day Cotton fiber Gossypium ... 34 2.1
 emb|AL353817|NC1A9 Neurospora crassa DNA linkage group V Cosmid ... 34 2.9
 emb|AI730373|AI730373 BNLGHi6756 Six-day Cotton fiber Gossypium ... 34 2.9
 emb|AJ273533|AJ273533 AJ273533 Metarhizium anisopliae ARSEF 2575... 33 4.0
 25 gb|BE054457|BE054457 GA__Ea0034I24f Gossypium arboreum 7-10 dpa ... 33 4.0
 emb|AJ274366|AJ274366 AJ274366 Metarhizium anisopliae ARSEF 2575... 33 4.0
 emb|AJ274146|AJ274146 AJ274146 Metarhizium anisopliae ARSEF 2575... 33 4.0
 emb|AF006311|AF006311 Cookeina tricholoma 18S ribosomal RNA gene... 32 4.2
 emb|AW625979|AW625979 EST319874 tomato radicle, 5 d post-imbibit... 33 5.5
 30 emb|AB027528|AB027528 Physcomitrella patens ppCRY1 mRNA for blue... 33 5.5

Query= Z97336.167_s_at 20429_s_at /id_source genbank /description
 emb|cab10219.1| (z97336) hypothetical protei [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
 35 (2034 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

45 emb|AI894928|AI894928 EST264371 tomato callus, TAMU Lycopersicon... 59 4e-11
 emb|AW621748|AW621748 EST312546 tomato root during/after fruit s... 62 1e-08
 emb|AW991081|AW991081 SsS0293 Suaeda salsa ZAP cDNA library Suae... 58 3e-07
 emb|AI896054|AI896054 EST265497 tomato callus, TAMU Lycopersicon... 55 2e-06
 emb|AW932874|AW932874 EST358717 tomato fruit mature green, TAMU ... 54 3e-06
 50 emb|AW035961|AW035961 EST282820 tomato callus, TAMU Lycopersicon... 53 5e-06
 emb|AW217271|AW217271 EST295985 tomato callus, TAMU Lycopersicon... 51 3e-05
 emb|AI736949|AI736949 sb35a01.y1 Gm-c1013 Glycine max cDNA clone... 45 6e-05
 emb|AI729969|AI729969 BNLGHi5823 Six-day Cotton fiber Gossypium ... 41 8e-05
 gb|BE033853|BE033853 MG01B02 MG Mesembryanthemum crystallinum cD... 49 1e-04
 55 emb|AZ124241|AZ124241 T223105b Medicago truncatula BAC library M... 47 4e-04
 emb|AI729861|AI729861 BNLGHi5428 Six-day Cotton fiber Gossypium ... 44 0.005
 emb|AW623353|AW623353 EST321298 tomato flower buds 3-8 mm, Come... 44 0.005
 emb|AZ124239|AZ124239 T223103b Medicago truncatula BAC library M... 44 0.005
 emb|AI166315|AI166315 xylem.est.16 Poplar xylem Lambda ZAPII lib... 42 0.013
 60 emb|AW219421|AW219421 EST301999 tomato root during/after fruit s... 42 0.013
 emb|AI974296|AI974296 T110298e KV0 Medicago truncatula cDNA clon... 42 0.013

	emb AI054990 AI054990 coau0002L09 Cotton Boll Abscission Zone cD...	40	0.037
	emb AW929405 AW929405 EST338193 tomato flower buds 8 mm to pre-a...	39	0.17
	emb AW649475 AW649475 EST327929 tomato germinating seedlings, TA...	39	0.17
	emb AW222512 AW222512 EST299323 tomato fruit red ripe, TAMU Lyco...	38	0.23
5	emb AW222518 AW222518 EST299329 tomato fruit red ripe, TAMU Lyco...	38	0.23
	emb AI781303 AI781303 EST262182 tomato susceptible, Cornell Lyco...	38	0.23
	emb AI779448 AI779448 EST260327 tomato susceptible, Cornell Lyco...	38	0.23
	emb AW053754 AW053754 L30-1647T3 Ice plant Lambda Uni-Zap XR exp...	38	0.23
	emb AF141013 AF141013 Vigna unguiculata clone KINE12 disease res...	32	0.32
10	emb AW164678 AW164678 se76b06.y1 Gm-cl023 Glycine max cDNA clone...	38	0.32
	emb AW736367 AW736367 EST332286 KV3 Medicago truncatula cDNA clo...	37	0.42
	emb Z67751 SC38KCXVI S.cerevisiae DNA (chromosome XVI; 38 kb).	34	0.77
	emb AV420300 AV420300 AV420300 Lotus japonicus young plants (two...	36	0.82
	emb AW424334 AW424334 sh64b12.y1 Gm-cl015 Glycine max cDNA clone...	36	0.82
15	emb Z73595 SCYPL239W S.cerevisiae chromosome XVI reading frame O...	34	0.94
	gb U34385 SCU34385 Saccharomyces cerevisiae ankyrin repeat prote...	34	0.98
	emb AQ522032 AQ522032 CpG0990A CpIOWAgDNA1 Cryptosporidium parvu...	36	1.1
	emb AQ083671 AQ083671 CpG0567A CpIOWAgDNA1 Cryptosporidium parvu...	36	1.1
	emb AF141012 AF141012 Vigna unguiculata clone KIND12 disease res...	30	1.4
20	emb AW283124 AW283124 LG1_224_H10.g1_A002 Light Grown 1 (LG1) So...	35	1.6
	emb AI054715 AI054715 coau0001M19 Cotton Boll Abscission Zone cD...	35	1.6
	emb Y10579 VFPOTCHAN V.faba mRNA for potassium channel.	29	1.7
	emb AQ935638 AQ935638 CpG2573A CpIOWAgDNA1 Cryptosporidium parvu...	35	2.1
	emb AW040703 AW040703 EST283567 tomato mixed elicitor, BTI Lycop...	35	2.1
25	emb X73850 BNPNL3 B.napus (pNL3) mRNA for acyl-ACP-thioesterase.	35	2.9
	emb AL096797 SPBC146 S.pombe chromosome II cosmid c146.	35	2.9
	emb X87842 BNDNAFATA B.napus Fata gene.	35	2.9
	emb AF073683 073693S155 Tinguarra sicula internal transcribed sp...	35	2.9
	dbj D30788 YSPCUT3B Schizosaccharomyces pombe gene for cut3 prot...	35	2.9
30	gb BE035556 BE035556 MO09B06 MO Mesembryanthemum crystallinum cD...	35	2.9
	gb M21813 YSCELF2B S.cerevisiae SUI3 gene encoding translation i...	35	2.9
	gb BE036920 BE036920 MP09B06 MP Mesembryanthemum crystallinum cD...	35	2.9
	gb BE035567 BE035567 MO09C08 MO Mesembryanthemum crystallinum cD...	27	3.2
	emb AW923857 AW923857 DG1_60_G12.g1_A002 Dark Grown 1 (DG1) Sorg...	30	3.4
35	emb AA680502 AA680502 T3691 Bloodstream form of serodeme ILTat1...	34	4.0
	emb AW691484 AW691484 NF041F05ST1F1000 Developing stem Medicago ...	34	4.0
	emb AJ055156 AJ055156 coau0003D05 Cotton Boll Abscission Zone cD...	34	4.0
	emb AL356815 NCB24H17 Neurospora crassa DNA linkage group II BAC...	30	4.2
	emb AF181702 AF181702 Leptosphaeria contecta 18S ribosomal RNA g...	34	5.5
40	emb AW145916 AW145916 ga35g12.y1 Moss EST library PPN Physcomitr...	34	5.5
	emb AW617253 AW617253 EST323664 L. hirsutum trichome, Cornell Un...	34	5.5
	emb AW615864 AW615864 EST325362 tomato flower buds 0-3 mm, Corne...	34	5.5
	emb AW691785 AW691785 NF044B05ST1F1000 Developing stem Medicago ...	34	5.5
	dbj D38256 YSCSCT1 Yeast gene for suppressor of ctr mutation.	34	5.5
45	gb U26175 LDU26175 Leishmania donovani lipophosphoglycan biosynt...	34	5.5
	emb AB029613 AB029613 Aspergillus terreus TOP2 gene for type II ...	34	5.5
	emb AW696259 AW696259 NF104F08ST1F1074 Developing stem Medicago ...	34	5.5
	emb AC004710 AC004710 Plasmodium falciparum chromosome 12, *** S...	33	7.6
	emb AV421315 AV421315 AV421315 Lotus japonicus young plants (two...	33	7.6
50	emb AW599293 AW599293 gb13a06.y1 Moss EST library PPN Physcomitr...	33	7.6
	emb AC005507 AC005507 Plasmodium falciparum chromosome 12 clone ...	33	7.6
	gb U16862 PFU16862 Plasmodium falciparum HSP70-like protein gene...	33	7.6
	emb AI213448 AI213448 z2a11a1.fl Aspergillus nidulans 24hr asexu...	33	7.6
	emb X73849 BNPNL2 B.napus (pNL2) mRNA for acyl-ACP-thioesterase.	33	7.6
55	emb AW694856 AW694856 NF080G09ST1F1071 Developing stem Medicago ...	33	7.6
	emb AV408901 AV408901 AV408901 Lotus japonicus young plants (two...	33	7.6
	emb AV412721 AV412721 AV412721 Lotus japonicus young plants (two...	33	7.6
	emb AI759851 AI759851 sb65b08.y1 Gm-cl017 Glycine max cDNA clone...	33	7.6
	emb AZ124240 AZ124240 T223104b Medicago truncatula BAC library M...	33	7.6
60	emb Y08926 PFAARP1PR P.falciparum mRNA for AARP1 protein, partial.	33	7.6
	emb AV410224 AV410224 AV410224 Lotus japonicus young plants (two...	33	7.6

	emb AQ849926 AQ849926 LMAJFV1_lm51f05.x1 Leishmania major FV1 ra...	33	7.6
	emb AL034557 PFMAL4P1 Plasmodium falciparum chromosome 4:strain ...	27	8.3
	emb AQ944606 AQ944606 Sheared DNA-48P15.TR Sheared DNA Trypanoso...	28	8.4
	emb AF099095 AF099095 Samanea saman pulvinus inward-rectifying c...	26	9.8
5	Query= AC005896.161_g_at 20620_g_at /id_source genbank /description gb aac98070.1 (ac005896) putative c2h2-type zinc finger protein [arabidopsis thaliana] /blast_score 8.00e-92 /ec_number /family /chip nova /gb_link /ncgi (864 letters)		
10	Database: plantfungal 661,018 sequences; 426,114,510 total letters		
15	Searching.....done		
	Score E		
	Sequences producing significant alignments:	(bits)	Value
20	emb AB006600 AB006600 Petunia x hybrida mRNA for ZPT2-13, comple...	86	1e-30
	emb AB000451 AB000451 Petunia hybrida mRNA for PETHy;ZPT2-5, com...	74	5e-29
	emb AW685937 AW685937 NF031H10NR1F1000 Nodulated root Medicago t...	76	9e-29
	emb AB006599 AB006599 Petunia x hybrida mRNA for ZPT2-12, comple...	77	1e-28
	emb AB006601 AB006601 Petunia x hybrida mRNA for ZPT2-14, comple...	72	2e-26
25	emb AI898309 AI898309 EST267752 tomato ovary, TAMU Lycopersicon ...	68	3e-26
	emb AI485362 AI485362 EST243683 tomato ovary, TAMU Lycopersicon ...	67	1e-25
	emb AI483886 AI483886 EST249757 tomato ovary, TAMU Lycopersicon ...	68	1e-25
	emb AW030869 AW030869 EST274159 tomato callus, TAMU Lycopersicon...	68	5e-24
	emb AI966235 AI966235 sc35g05.y1 Gm-c1014 Glycine max cDNA clone...	72	3e-23
30	emb AB006603 AB006603 Petunia x hybrida mRNA for ZPT2-8, complet...	65	1e-22
	emb AI486627 AI486627 EST244948 tomato ovary, TAMU Lycopersicon ...	61	1e-22
	emb AI485555 AI485555 EST243876 tomato ovary, TAMU Lycopersicon ...	61	1e-22
	emb AI488341 AI488341 EST246663 tomato ovary, TAMU Lycopersicon ...	61	1e-22
	emb AI486228 AI486228 EST244549 tomato ovary, TAMU Lycopersicon ...	61	1e-22
35	emb AI959966 AI959966 sc35g05.x1 Gm-c1014 Glycine max cDNA clone...	69	2e-22
	emb AI771123 AI771123 EST252223 tomato ovary, TAMU Lycopersicon ...	61	3e-22
	emb AI897376 AI897376 EST266819 tomato ovary, TAMU Lycopersicon ...	68	5e-22
	emb AI894711 AI894711 EST264154 tomato callus, TAMU Lycopersicon...	68	6e-22
	emb AV422177 AV422177 AV422177 Lotus japonicus young plants (two...	103	2e-21
40	emb AB006602 AB006602 Petunia x hybrida mRNA for ZPT2-7, complet...	66	6e-21
	emb AI485123 AI485123 EST243427 tomato ovary, TAMU Lycopersicon ...	68	6e-21
	emb AW216442 AW216442 EST295072 tomato callus, TAMU Lycopersicon...	68	8e-21
	emb AW687462 AW687462 NF009H03RT1F1031 Developing root Medicago ...	70	2e-20
	emb AI771824 AI771824 EST252924 tomato ovary, TAMU Lycopersicon ...	68	2e-20
45	emb AW034640 AW034640 EST278324 tomato callus, TAMU Lycopersicon...	68	7e-20
	emb AW033868 AW033868 EST277439 tomato callus, TAMU Lycopersicon...	72	1e-19
	emb AI487993 AI487993 EST246315 tomato ovary, TAMU Lycopersicon ...	68	1e-18
	emb AW684455 AW684455 NF017B06NR1F1000 Nodulated root Medicago t...	68	2e-18
	emb X60700 PHEPF1 P.hybrida EPF1 gene for DNA-binding protein.	61	2e-18
50	emb AB006604 AB006604 Petunia x hybrida mRNA for ZPT2-9, complet...	59	5e-18
	emb AI489727 AI489727 EST248066 tomato ovary, TAMU Lycopersicon ...	50	1e-16
	emb AW034622 AW034622 EST278306 tomato callus, TAMU Lycopersicon...	87	2e-16
	emb AB035132 AB035132 Petunia x hybrida gene for C2H2 zinc-finge...	57	1e-15
	emb AB006597 AB006597 Petunia x hybrida mRNA for ZPT2-10, comple...	57	1e-15
55	emb AB035133 AB035133 Petunia x hybrida gene for C2H2 zinc-finge...	56	2e-15
	emb AB006605 AB006605 Petunia x hybrida mRNA for ZPT3-3, complet...	56	2e-15
	emb AW777036 AW777036 M111167e DSIR Medicago truncatula cDNA clo...	74	2e-15
	emb AI488445 AI488445 EST246784 tomato ovary, TAMU Lycopersicon ...	50	4e-15
	emb AF119050 AF119050 Datisca glomerata zinc-finger protein 1 (z...	53	7e-15
60	emb AB000455 AB000455 Petunia hybrida mRNA for PETHy;ZPT4-1, com...	55	9e-15
	emb AI988657 AI988657 sd06b03.y1 Gm-cl020 Glycine max cDNA clone...	51	1e-14

- emb|AW781249|AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone... 51 1e-14
gb|L46574|L46574 BNAF1975 Mustard flower buds Brassica rapa cDNA... 59 1e-14
emb|Y16131|Y16131 Y16131 young root nodules Medicago sativa subs... 51 2e-14
dbj|D26085|PETZFDB3 Petunia zinc-finger DNA binding protein gene. 50 2e-14
5 dbj|D16415|WHTWZF1A Wheat gene for WZF1, complete cds. 53 2e-14
emb|AB000453|AB000453 Petunia hybrida mRNA for PETHy;ZPT3-1, com... 55 2e-14
dbj|D16416|WHTWZF1B Wheat mRNA for WZF1, complete cds. 53 2e-14
dbj|D26084|PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro... 52 3e-14
emb|Y18788|MSY18788 Medicago sativa mRNA for putative TFIIIA (or... 51 3e-14
10 emb|AW560934|AW560934 EST315982 DSIR Medicago truncatula cDNA cl... 51 3e-14
emb|AI988290|AI988290 sc98f10.y1 Gm-c1020 Glycine max cDNA clone... 52 3e-14
emb|AW706944|AW706944 sk08e10.y1 Gm-c1023 Glycine max cDNA clone... 50 5e-14
dbj|D26083|PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin... 52 6e-14
emb|AF053077|AF053077 Nicotiana tabacum osmotic stress-induced z... 51 6e-14
15 emb|AW729218|AW729218 GA_Ea0024G18 Gossypium arboreum 7-10 dpa ... 51 1e-13
emb|AW102472|AW102472 sd88f02.y1 Gm-c1009 Glycine max cDNA clone... 52 1e-13
emb|AW680050|AW680050 WS1_3_G12.g1_A002 Water-stressed 1 (WS1) S... 50 2e-13
gb|BE095284|BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two-... 53 2e-13
emb|AW033574|AW033574 EST277145 tomato callus, TAMU Lycopersicon... 49 2e-13
20 gb|U76555|BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA... 52 2e-13
gb|U76554|BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR... 52 2e-13
emb|AW775559|AW775559 EST334624 DSIL Medicago truncatula cDNA cl... 50 2e-13
gb|BE123920|BE123920 EST394045 DSIL Medicago truncatula cDNA clo... 50 2e-13
gb|U68763|GMU68763 Glycine max putative transcription factor SCO... 48 3e-13
25 gb|BE059872|BE059872 sn38c04.y1 Gm-c1016 Glycine max cDNA clone ... 48 3e-13
emb|AW153229|AW153229 se37f05.y1 Gm-c1015 Glycine max cDNA clone... 48 3e-13
emb|AI896031|AI896031 EST265474 tomato callus, TAMU Lycopersicon... 48 4e-13
emb|AW030876|AW030876 EST274166 tomato callus, TAMU Lycopersicon... 48 4e-13
emb|AW033257|AW033257 EST276828 tomato callus, TAMU Lycopersicon... 48 4e-13
30 emb|AI771191|AI771191 EST252387 tomato ovary, TAMU Lycopersicon ... 48 4e-13
emb|AW032357|AW032357 EST275811 tomato callus, TAMU Lycopersicon... 48 4e-13
emb|AW279005|AW279005 sg04d04.y1 Gm-c1019 Glycine max cDNA clone... 48 6e-13
emb|AW164639|AW164639 se74f02.y1 Gm-c1023 Glycine max cDNA clone... 48 6e-13
emb|AW030858|AW030858 EST274148 tomato callus, TAMU Lycopersicon... 48 1e-12
35 emb|AW278572|AW278572 sf46c03.y1 Gm-c1009 Glycine max cDNA clone... 48 1e-12
dbj|D26086|PETZFP4 Petunia zinc-finger protein gene. 49 3e-12
emb|AW616587|AW616587 EST322998 L. hirsutum trichome, Cornell Un... 47 9e-12
emb|AW924420|AW924420 WS1_69_C08.b1_A002 Water-stressed 1 (WS1) ... 50 9e-12
emb|AI778714|AI778714 EST259593 tomato susceptible, Cornell Lyco... 46 1e-11
40 emb|AI487287|AI487287 EST245609 tomato ovary, TAMU Lycopersicon ... 46 1e-11
emb|AW037956|AW037956 EST279600 tomato mixed elicitor, BTI Lycop... 46 1e-11
emb|AI485651|AI485651 EST243972 tomato ovary, TAMU Lycopersicon ... 46 2e-11
emb|AB006606|AB006606 Petunia x hybrida mRNA for ZPT4-4, complet... 53 2e-11
emb|AW035987|AW035987 EST282846 tomato callus, TAMU Lycopersicon... 48 2e-11
45 emb|X87374|PSZINCFIN P.sativum putative zinc finger protein. 64 3e-11
emb|AW625323|AW625323 EST319146 tomato radicle, 5 d post-imbibit... 46 6e-11
emb|AI894812|AI894812 EST264255 tomato callus, TAMU Lycopersicon... 68 7e-11
emb|AI966679|AI966679 sc55a11.y1 Gm-c1015 Glycine max cDNA clone... 52 1e-10
emb|AW219517|AW219517 EST301915 tomato root during/after fruit s... 46 2e-10
50 gb|BE058334|BE058334 sn14g01.y1 Gm-c1016 Glycine max cDNA clone ... 48 3e-10
emb|AI488218|AI488218 EST246540 tomato ovary, TAMU Lycopersicon ... 46 3e-10
emb|AI771385|AI771385 EST252485 tomato ovary, TAMU Lycopersicon ... 66 3e-10
emb|AV426673|AV426673 AV426673 Lotus japonicus young plants (two... 47 5e-10
emb|AW032112|AW032112 EST275566 tomato callus, TAMU Lycopersicon... 45 5e-10
55 emb|AB006598|AB006598 Petunia x hybrida mRNA for ZPT2-11, comple... 64 7e-10
emb|AW219736|AW219736 EST302218 tomato root during/after fruit s... 46 7e-10
emb|AW924443|AW924443 WS1_69_C08.g1_A002 Water-stressed 1 (WS1) ... 48 9e-10
emb|AB000452|AB000452 Petunia hybrida mRNA for PETHy;ZPT2-6, com... 64 1e-09
- 60 Query= AL049658.102_at 20625_at /id_source genbank /description
emb|cab41131.1| (al049658) hypothetical protein [arabidopsis thaliana]

/blast_score 0 /ec_number /family /chip nova /gb_link
<http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al049658|/ncgi>
<http://www.ncgr.org/cgi-bin/ff?al049658>
 5 (1890 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

10 Searching.....done

		Score	E	
	Sequences producing significant alignments:			(bits) Value
15	emb AW559251 AW559251 EST306087 DSIR Medicago truncatula cDNA cl...	169	3e-49	
	emb AW032676 AW032676 EST276235 tomato callus, TAMU Lycopersicon...	181	1e-44	
	emb AI778594 AI778594 EST259473 tomato susceptible, Cornell Lyco...	181	1e-44	
	emb AW774727 AW774727 EST333878 KV3 Medicago truncatula cDNA clo...	169	6e-41	
	emb AV423915 AV423915 AV423915 Lotus japonicus young plants (two...	163	3e-39	
20	emb AW559836 AW559836 EST314884 DSIR Medicago truncatula cDNA cl...	131	6e-37	
	emb AW349142 AW349142 GM210003B22H5R Gm-r1021 Glycine max cDNA 3...	107	3e-23	
	emb AW560074 AW560074 EST315122 DSIR Medicago truncatula cDNA cl...	84	6e-23	
	emb AI855891 AI855891 sc30h08.y1 Gm-cl014 Glycine max cDNA clone...	100	4e-21	
25	emb AW560073 AW560073 EST315121 DSIR Medicago truncatula cDNA cl...	77	5e-21	
	emb AW225676 AW225676 ST70B12 Pine TriplEx shoot tip library Pin...	91	3e-17	
	emb AW870069 AW870069 NXNV_123_G03_F Nsf Xylem Normal wood Verti...	68	3e-17	
	emb AW587665 AW587665 ST63B10 Pine TriplEx shoot tip library Pin...	87	4e-17	
	emb AW011208 AW011208 ST18A05 Pine TriplEx shoot tip library Pin...	89	1e-16	
30	emb AW438038 AW438038 ST83G07 Pine TriplEx shoot tip library Pin...	84	5e-15	
	emb AV417662 AV417662 AV417662 Lotus japonicus young plants (two...	54	7e-15	
	emb AI920196 AI920196 1726 Pine Lambda Zap Xylem library Pinus t...	54	2e-14	
	emb AW981483 AW981483 EST392636 DSIL Medicago truncatula cDNA cl...	70	5e-13	
	emb AW689240 AW689240 NF017A06ST1F1000 Developing stem Medicago ...	76	8e-13	
35	emb AW684289 AW684289 NF015A11NR1F1000 Nodulated root Medicago t...	70	1e-12	
	emb AW933515 AW933515 EST359274 tomato fruit mature green, TAMU ...	48	3e-12	
	emb AW685948 AW685948 NF036G07NR1F1000 Nodulated root Medicago t...	58	8e-12	
	emb AW687095 AW687095 NF005H11RT1F1095 Developing root Medicago ...	72	1e-11	
	emb AW686129 AW686129 NF033H12NR1F1000 Nodulated root Medicago t...	47	1e-11	
40	emb AI894750 AI894750 EST264193 tomato callus, TAMU Lycopersicon...	59	3e-11	
	emb AW698315 AW698315 NXNV_071_G01_F Nsf Xylem Normal wood Verti...	71	3e-11	
	emb AW290408 AW290408 NXNV019H08F Nsf Xylem Normal wood Vertical...	67	4e-11	
	emb AW065112 AW065112 ST39G09 Pine TriplEx shoot tip library Pin...	51	5e-11	
	emb AW560897 AW560897 EST315945 DSIR Medicago truncatula cDNA cl...	55	7e-11	
45	emb AW257406 AW257406 EST305543 KV2 Medicago truncatula cDNA clo...	55	7e-11	
	emb AW217058 AW217058 EST295772 tomato callus, TAMU Lycopersicon...	51	5e-10	
	emb AV407304 AV407304 AV407304 Lotus japonicus young plants (two...	65	2e-09	
	gb BE049795 BE049795 NXNV_144_C08_F Nsf Xylem Normal wood Vertic...	53	7e-09	
	emb AW746848 AW746848 WS1_55_B02.g1_A002 Water-stressed 1 (WS1)...	57	5e-07	
50	emb AW888098 AW888098 NXNV_108_F09_F Nsf Xylem Normal wood Verti...	56	1e-06	
	emb AW032082 AW032082 EST275536 tomato callus, TAMU Lycopersicon...	51	2e-06	
	emb AW032864 AW032864 EST276423 tomato callus, TAMU Lycopersicon...	46	2e-06	
	emb AW736866 AW736866 NXNV_083_H05_F Nsf Xylem Normal wood Verti...	52	2e-05	
	emb AW775153 AW775153 EST334304 KV3 Medicago truncatula cDNA clo...	51	4e-05	
55	emb AV411498 AV411498 AV411498 Lotus japonicus young plants (two...	47	5e-04	
	emb AW934555 AW934555 EST353447 tomato flower buds 0-3 mm, Corne...	36	9e-04	
	emb AW010126 AW010126 ST02C06 Pine TriplEx shoot tip library Pin...	46	0.001	
	emb AW031593 AW031593 EST275047 tomato callus, TAMU Lycopersicon...	31	0.001	
	emb AW746715 AW746715 WS1_55_B02.b1_A002 Water-stressed 1 (WS1) ...	39	0.001	
60	emb AW720513 AW720513 LjNEST18e1r Lotus japonicus nodule library...	46	0.001	
	emb AW773847 AW773847 EST332833 KV3 Medicago truncatula cDNA clo...	35	0.004	

	emb AZ051219 AZ051219 Gm_UMb001_062_F16R UMN Soybean BAC Library...	38	0.006
	emb AW684275 AW684275 NF014H05NR1F1000 Nodulated root Medicago t...	43	0.007
	emb AW043221 AW043221 ST30G04 Pine TriplEx shoot tip library Pin...	43	0.007
	emb AW687647 AW687647 NF011F10RT1F1090 Developing root Medicago ...	35	0.019
5	emb AW560122 AW560122 EST315170 DSIR Medicago truncatula cDNA cl...	35	0.019
	emb AW687408 AW687408 NF009C08RT1F1065 Developing root Medicago ...	35	0.019
	emb AW980840 AW980840 EST391993 GVN Medicago truncatula cDNA clo...	35	0.019
	emb AW560121 AW560121 EST315169 DSIR Medicago truncatula cDNA cl...	35	0.019
	gb BE123705 BE123705 NXNV_151_H02_F Nsf Xylem Normal wood Vertic...	41	0.032
10	emb AI781175 AI781175 EST262054 tomato susceptible, Cornell Lyco...	40	0.060
	emb AW616497 AW616497 EST322908 L. hirsutum trichome, Cornell Un...	31	0.063
	emb AZ214029 AZ214029 Sheared DNA-77H12.TF Sheared DNA Trypanoso...	40	0.083
	emb AW693887 AW693887 NF070B08ST1F1064 Developing stem Medicago ...	40	0.083
	emb AZ214023 AZ214023 Sheared DNA-77H11.TF Sheared DNA Trypanoso...	38	0.22
15	emb AI487450 AI487450 EST245772 tomato ovary, TAMU Lycopersicon ...	37	0.41
	emb AI780239 AI780239 EST261118 tomato susceptible, Cornell Lyco...	37	0.41
	emb AI485040 AI485040 EST243320 tomato ovary, TAMU Lycopersicon ...	37	0.41
	emb AW618666 AW618666 EST320652 L. pennellii trichome, Cornell U...	28	0.52
	emb AZ213147 AZ213147 Sheared DNA-96E11.TR Sheared DNA Trypanoso...	35	0.53
20	emb AW698283 AW698283 NXNV_071_C12_F Nsf Xylem Normal wood Verti...	33	0.53
	emb AW690496 AW690496 NF035B12ST1F1000 Developing stem Medicago ...	37	0.56
	emb AW693913 AW693913 NF070E02ST1F1017 Developing stem Medicago ...	37	0.56
	emb AW686233 AW686233 NF035E09NR1F1000 Nodulated root Medicago t...	37	0.56
	emb AW257090 AW257090 EST305227 KV2 Medicago truncatula cDNA clo...	37	0.56
25	emb AW573732 AW573732 EST316323 GVN Medicago truncatula cDNA clo...	37	0.56
	emb AW559393 AW559393 EST314441 DSIR Medicago truncatula cDNA cl...	37	0.56
	emb AW329638 AW329638 N200899e rootphos(-) Medicago truncatula c...	36	0.77
	gb BE123796 BE123796 NXNV_156_E06_F Nsf Xylem Normal wood Vertic...	27	0.96
	emb AW257266 AW257266 EST305403 KV2 Medicago truncatula cDNA clo...	36	1.1
30	emb AW317531 AW317531 sg51e11.y1 Gm-c1025 Glycine max cDNA clone...	33	1.3
	emb AC009259 AC009259 Trypanosoma brucei chromosome VI clone RPC...	35	1.4
	emb AW702888 AW702888 TgESTzz91a12.y1 TgRH*-Tachyzoite cDNA Toxo...	35	1.4
	emb AF013339 AF013339 Cucurbita moschata clone 3 internal transc...	35	1.4
	emb AW704685 AW704685 sk39c02.y1 Gm-c1028 Glycine max cDNA clone...	35	1.4
35	emb AQ650196 AQ650196 Sheared DNA-18B3.TF Sheared DNA Trypanosom...	35	1.4
	emb AW685575 AW685575 NF029B05NR1F1000 Nodulated root Medicago t...	35	2.0
	emb AW773999 AW773999 EST332985 KV3 Medicago truncatula cDNA clo...	35	2.0
	emb Z38060 SC5610 S.cerevisiae chromosome IX sequence derived fr...	35	2.0
	emb AW033298 AW033298 EST276869 tomato callus, TAMU Lycopersicon...	35	2.0
40	gb L36822 SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas...	35	2.0
	emb AQ952285 AQ952285 Sheared DNA-39M20.TF Sheared DNA Trypanoso...	35	2.0
	emb AI812757 AI812757 18G10 Pine Lambda Zap Xylem library Pinus ...	30	2.3
	emb AI441832 AI441832 sa47h09.y1 Gm-c1004 Glycine max cDNA clone...	35	2.7
	emb AW694970 AW694970 NF082B02ST1F1015 Developing stem Medicago ...	31	3.1
45	emb AW685287 AW685287 NF027B11NR1F1000 Nodulated root Medicago t...	31	3.1
	emb AW932856 AW932856 EST358699 tomato fruit mature green, TAMU ...	34	3.8
	emb AF013320 AF013320 Cucurbita fraterna clone 2 internal transc...	34	3.8
	emb AW719424 AW719424 LjNEST4d11r Lotus japonicus nodule library...	29	4.2
	emb X90770 LEMSREPRG L.esculentum microsatellite repeat DNA region.	34	5.2
50	emb AW133354 AW133354 se17h02.y1 Gm-c1013 Glycine max cDNA clone...	34	5.2
	emb AI967637 AI967637 Ljirnp08-639-b9 Ljirnp Lambda HybriZap ...	34	5.2
	emb AW156054 AW156054 ga24c05.y1 Moss EST library PPU Physcomitr...	34	5.2
	emb AF053127 AF053127 Malus domestica leucine-rich receptor-like...	34	5.2
	emb AB000394 AB000394 Ipomoea purpurea DNA, LTR retrotransposon ...	34	5.2
55	Query= X91919.1_at 20641_at /id_source genbank /description		
	"emb caa63012.1 (x91919) lea76 homologue type1 [arabidopsis thaliana]		
	arabidopsis thaliana. ests gb n97082, gb z27056 and gb z29902 come		
	from this gene." /blast_score 9.00e-78 /ec_number /family /chip nova		
60	/gb_link http://www3.ncbi.nlm.nih.gov/htbin-		
	post/entrez/query?db=n&form=6&dopt=g&uid=gb x91919 /ncgi		

<http://www.ncgr.org/cgi-bin/ff?x91919>
(762 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	(bits)	Value
10	Sequences producing significant alignments:			
	emb AJ224519 CAR224519 Cicer arietinum mRNA for LEA protein (clo...	148	6e-35	
	emb X15348 BNLEA76 Brassica napus LEA76 mRNA for late embryogene...	135	4e-31	
	emb AF117884 AF117884 Glycine max seed maturation protein PM30 (...	88	1e-30	
15	emb AJ224518 CAR224518 Cicer arietinum mRNA for LEA protein (clo...	126	2e-28	
	emb AW472097 AW472097 si20a05.y1 Gm-c1029 Glycine max cDNA clone...	86	9e-27	
	emb AW395529 AW395529 sg72c09.y1 Gm-c1007 Glycine max cDNA clone...	88	7e-24	
	emb AW507599 AW507599 si53h08.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24	
	emb AW318205 AW318205 sg62d04.y1 Gm-c1007 Glycine max cDNA clone...	88	7e-24	
20	emb AW568476 AW568476 si59c06.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24	
	emb AW567816 AW567816 si66b10.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24	
	emb AW706800 AW706800 sk03e03.y1 Gm-c1023 Glycine max cDNA clone...	88	1e-23	
	emb AW509384 AW509384 si22d10.y1 Gm-c1029 Glycine max cDNA clone...	86	2e-23	
	emb AW746690 AW746690 WS1_54_F07.g1_A002 Water-stressed 1 (WS1) ...	106	2e-22	
25	emb AW096396 AW096396 EST289576 tomato mixed elicitor, BTI Lycop...	103	1e-21	
	emb X78205 HVHVA1 H.vulgare (Himalaya) HVA1 gene.	77	1e-20	
	emb X13498 HVABAIP Barley pHVA1 mRNA for an ABA-inducible protein.	77	1e-20	
	gb M36000 BLYABA Barley abscisic acid (ABA) mRNA, complete cds.	77	1e-20	
	emb AW680076 AW680076 WS1_3_C03.g1_A002 Water-stressed 1 (WS1) S...	100	2e-20	
30	emb AW397921 AW397921 sg69h06.y1 Gm-c1007 Glycine max cDNA clone...	57	3e-20	
	emb AW747095 AW747095 WS1_65_C09.g1_A002 Water-stressed 1 (WS1) ...	95	4e-19	
	gb BE034388 BE034388 MH04B06 MH Mesembryanthemum crystallinum cD...	73	1e-18	
	emb X13201 GHLEA7 Cotton set 5A Lea gene for seed protein D-7.	61	1e-18	
	emb X15086 GHLEA29R Cotton set 5A Lea mRNA for seed protein D-29.	61	1e-18	
35	emb X56882 TA3LEA Wheat mRNA for a group 3 late embryogenesis ab...	75	1e-18	
	emb AW746385 AW746385 WS1_49_G03.g1_A002 Water-stressed 1 (WS1) ...	93	2e-18	
	emb AW680063 AW680063 WS1_3_B02.g1_A002 Water-stressed 1 (WS1) S...	91	1e-17	
	emb AF255052 AF255052 Triticum aestivum cold-responsive LEA/RAB-...	85	6e-17	
	emb AF139915 AF139915 Triticum aestivum ABA-inducible protein WR...	85	6e-17	
40	emb AW164114 AW164114 Ljirnp20-575-b9 Ljirnp Lambda HybriZap ...	88	7e-17	
	emb Y10779 SSY10779 S.stapfianus pSD.42 mRNA.	86	3e-16	
	emb AW569002 AW569002 si62c03.y1 Gm-r1030 Glycine max cDNA clone...	62	4e-16	
	emb AW508284 AW508284 si52b01.y1 Gm-r1030 Glycine max cDNA clone...	62	4e-16	
	gb BE034389 BE034389 MH04B07 MH Mesembryanthemum crystallinum cD...	72	7e-16	
45	emb AW681055 AW681055 WS1_8_F06.b1_A002 Water-stressed 1 (WS1) S...	75	7e-13	
	emb AW746839 AW746839 WS1_55_D06.g1_A002 Water-stressed 1 (WS1) ...	75	7e-13	
	emb AW678335 AW678335 WS1_14_F02.g1_A002 Water-stressed 1 (WS1) ...	75	7e-13	
	emb AW678291 AW678291 WS1_14_D10.g1_A002 Water-stressed 1 (WS1) ...	74	1e-12	
	emb AW679525 AW679525 WS1_29_F04.g1_A002 Water-stressed 1 (WS1) ...	74	1e-12	
50	emb Z18891 BPBP8GEN Betula pendula BP8 gene.	74	1e-12	
	emb AW432699 AW432699 sh85b12.y1 Gm-c1016 Glycine max cDNA clone...	74	1e-12	
	emb AW678194 AW678194 WS1_13_E06.g1_A002 Water-stressed 1 (WS1) ...	72	5e-12	
	emb AW459847 AW459847 sh96a04.y1 Gm-c1016 Glycine max cDNA clone...	70	2e-11	
	emb X13203 GHLEA29 Cotton set 5A Lea gene for seed protein D-29.	62	5e-09	
55	emb Z49713 PMDORORF6 P.menziesii mRNA (open reading frame) (DF77B).	59	3e-08	
	emb Z49712 PMDORORF5 P.menziesii mRNA (open reading frame) (DF77A).	59	3e-08	
	emb AJ225460 AJ225460 AJ225460 Abscisic acid-treated protonemata...	59	5e-08	
	emb X89041 RFLASPPRO R.fluitans mRNA for landform specific protein.	58	6e-08	
	gb M80664 SOYLEAB Soybean late embryogenesis abundant (LEA) prot...	58	9e-08	
60	emb AF166485 AF166485 Glycine max maturation protein pPM32 (PM32...	57	2e-07	
	gb M19388 COTSPG G.hirsutum (cotton) storage protein (late embry...	57	2e-07	

- gb|U47096|DCU47096 *Daucus carota* LEA protein mRNA, somatic embryo... 57 2e-07
 gb|U02966|GMU02966 *Glycine max* Shi-shi 51 kDa seed maturation pr... 56 3e-07
 emb|Z49715|PMDORORF8 *P. menziesii* mRNA (open reading frame) (DF77D). 56 4e-07
 gb|L47932|L47932 BNAF1873 Mustard flower buds *Brassica rapa* cDNA... 56 4e-07
 5 emb|Z49714|PMDORORF7 *P. menziesii* mRNA (open reading frame) (DF77C). 55 8e-07
 emb|AW746616|AW746616 WS1_54_F07.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW678229|AW678229 WS1_14_F02.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW924822|AW924822 WS1_72_A12.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW924712|AW924712 WS1_71_A12.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 10 emb|AW679366|AW679366 WS1_24_E04.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW746766|AW746766 WS1_55_D06.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW678206|AW678206 WS1_14_D10.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW747038|AW747038 WS1_65_C09.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW678115|AW678115 WS1_13_E06.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 15 emb|AW679354|AW679354 WS1_24_G08.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AI305014|AI305014 EST00119 mRNP Lambda ZapII Express Library... 51 8e-06
 emb|AF009953|AF009953 *Glycine max* 35 kDa seed maturation protein... 51 8e-06
 emb|Z22872|GMLEAPROA *G. max* Lea protein mRNA, complete CDS. 51 1e-05
 emb|X92955|BOPC15 *B. oleracea* mRNA for pollen coat protein. 51 1e-05
 20 emb|AW680922|AW680922 WS1_8_F06.g1_A002 Water-stressed 1 (WS1) S... 51 1e-05
 emb|AW678045|AW678045 WS1_13_A03.b1_A002 Water-stressed 1 (WS1) ... 50 2e-05
 gb|L33614|L33614 BNAESTF503 Mustard flower buds *Brassica rapa* cD... 50 2e-05
 emb|X79466|HVES2A *H. vulgare* (Dbg 567) ES2A mRNA. 39 4e-05
 emb|AJ000100|HVAJ100 *Hordeum vulgare* mRNA for cold-regulated pro... 39 4e-05
 25 emb|AJ130888|FSY130888 *Fagus sylvatica* mRNA for ABA-inducible pr... 49 4e-05
 emb|AW703962|AW703962 sk14e10.y1 Gm-c1023 *Glycine max* cDNA clone... 49 5e-05
 emb|AW509514|AW509514 ga73a10.y1 Moss EST library PPU Physcomitr... 49 5e-05
 emb|AW679440|AW679440 WS1_24_C05.g1_A002 Water-stressed 1 (WS1) ... 48 1e-04
 gb|L46517|L46517 BNAF1718 Mustard flower buds *Brassica rapa* cDNA... 47 1e-04
 30 emb|AW185164|AW185164 se87g01.y1 Gm-c1023 *Glycine max* cDNA clone... 38 2e-04
 emb|AW679430|AW679430 WS1_24_G08.g1_A002 Water-stressed 1 (WS1) ... 46 5e-04
 emb|X16131|DCDC8 *D. carota* DC8 gene for an embryonic-specific 66... 41 8e-04
 emb|AW754854|AW754854 PC06D01 Pine TriplEx pollen cone library P... 45 9e-04
 emb|AW679001|AW679001 WS1_21_C11.g1_A002 Water-stressed 1 (WS1) ... 44 0.002
 35 emb|AW679463|AW679463 WS1_24_E04.g1_A002 Water-stressed 1 (WS1) ... 44 0.002
 emb|AW981579|AW981579 PC14C08 Pine TriplEx pollen cone library P... 43 0.002
 emb|AF255053|AF255053 *Triticum aestivum* cold-responsive LEA/RAB-... 39 0.004
 emb|AW680686|AW680686 WS1_6_H05.g1_A002 Water-stressed 1 (WS1) S... 42 0.004
 emb|AW747334|AW747334 WS1_67_C01.g1_A002 Water-stressed 1 (WS1) ... 42 0.004
 40 emb|AW747282|AW747282 WS1_67_C01.b1_A002 Water-stressed 1 (WS1) ... 42 0.004
 emb|AW983308|AW983308 HVSMEg0010C18f *Hordeum vulgare* pre-anthesi... 35 0.005
 emb|AW679087|AW679087 WS1_22_A07.b1_A002 Water-stressed 1 (WS1) ... 42 0.006
 emb|AW981621|AW981621 PC14G04 Pine TriplEx pollen cone library P... 42 0.006
 emb|AJ225515|AJ225515 AJ225515 Absciscic acid-treated protonemata... 37 0.017
 45 emb|AW754577|AW754577 PC03H06 Pine TriplEx pollen cone library P... 40 0.021
 emb|AW458460|AW458460 sh09e04.y1 Gm-c1016 *Glycine max* cDNA clone... 39 0.040
 emb|AW981729|AW981729 PC18A04 Pine TriplEx pollen cone library P... 39 0.055
 gb|BE033848|BE033848 MG01A05 *Mesembryanthemum crystallinum* cD... 38 0.076
 emb|AI068981|AI068981 mgae0004dH11f *Magnaporthe grisea* Appressor... 38 0.076
 50 emb|AW679089|AW679089 WS1_22_A07.g1_A002 Water-stressed 1 (WS1) ... 38 0.10

Query= Z99708.249_at 12007_at /id_source genbank /description
 emb|cab16829.1| (z99708) putative protein [arabidopsis thaliana]
 /blast_score 1.00e-168 /ec_number /family /chip nova /gb_link
 55 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|z99708|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|z99708|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|z99708|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?z99708>
 (885 letters)

- 60 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	(bits)	Value
5	Sequences producing significant alignments:			
	emb AI486681 AI486681	EST245003	tomato ovary, TAMU Lycopersicon ...	414 e-115
	emb AI488706 AI488706	EST247045	tomato ovary, TAMU Lycopersicon ...	373 e-102
	emb AW185116 AW185116	se87a08.y1	Gm-cl023 Glycine max cDNA clone...	364 e-100
10	emb AW776370 AW776370	EST335435	DSIL Medicago truncatula cDNA cl...	316 1e-85
	emb AW441466 AW441466	EST310862	tomato fruit red ripe, TAMU Lyco...	311 4e-84
	emb AW775237 AW775237	EST331959	GVN Medicago truncatula cDNA clo...	278 4e-74
	emb AW564397 AW564397	LG1_292_F08.b1_A002	Light Grown 1 (LG1) So...	275 2e-73
	emb AW648604 AW648604	EST327154	tomato germinating seedlings, TA...	275 3e-73
15	emb AW309188 AW309188	sg05d07.y1	Gm-cl019 Glycine max cDNA clone...	274 8e-73
	emb AW329561 AW329561	N200812e	rootphos(-) Medicago truncatula c...	204 3e-69
	emb AI897460 AI897460	EST266903	tomato ovary, TAMU Lycopersicon ...	158 7e-67
	emb AI775112 AI775112	EST256212	tomato resistant, Cornell Lycope...	248 4e-65
	emb AI898201 AI898201	EST267644	tomato ovary, TAMU Lycopersicon ...	118 1e-51
20	emb AW011189 AW011189	ST17G07	Pine TripleX shoot tip library Pin...	172 4e-48
	emb AW622515 AW622515	EST313315	tomato root during/after fruit s...	189 3e-47
	emb AW933718 AW933718	EST359561	tomato fruit mature green, TAMU ...	188 7e-47
	emb AI897919 AI897919	EST267362	tomato ovary, TAMU Lycopersicon ...	102 6e-45
	emb AW623431 AW623431	EST321376	tomato flower buds 3-8 mm, Corne...	179 2e-44
25	emb AI967352 AI967352	Ljirnp01-065-f5	Ljirnp Lambda HybriZap ...	167 5e-44
	emb AW496876 AW496876	ga49e04.y1	Moss EST library PPU Physcomitr...	175 5e-43
	emb AW616498 AW616498	EST322909	L. hirsutum trichome, Cornell Un...	174 1e-42
	emb AW687128 AW687128	NF006C08RT1F1065	Developing root Medicago ...	156 1e-41
	emb AW191300 AW191300	T113619e	KV2 Medicago truncatula cDNA clon...	167 1e-40
30	emb AW257178 AW257178	EST305315	KV2 Medicago truncatula cDNA clo...	144 7e-34
	emb AW699388 AW699388	gb07g07.y1	Moss EST library PPN Physcomitr...	139 2e-32
	emb AV421449 AV421449	AV421449	Lotus japonicus young plants (two...	132 4e-30
	emb AW626193 AW626193	EST320100	tomato radicle, 5 d post-imbibit...	132 5e-30
	emb AL109608 SPCC23B6	S.pombe	chromosome III cosmid c23B6.	99 3e-28
35	emb AV426790 AV426790	AV426790	Lotus japonicus young plants (two...	123 2e-27
	emb AI778049 AI778049	EST258928	tomato susceptible, Cornell Lyco...	116 2e-25
	emb AW626687 AW626687	NXNV068E07	Nsf Xylem Normal wood Vertical ...	114 1e-24
	emb AW929355 AW929355	EST338143	tomato flower buds 8 mm to pre-a...	106 2e-22
	emb AW719259 AW719259	LjNEST1h10r	Lotus japonicus nodule library...	105 4e-22
40	emb Z69381 SCCXIV39K	S.cerevisiae	38,855 bp segment of chromosom...	60 1e-17
	emb Z71507 SCYNL231C	S.cerevisiae	chromosome XIV reading frame O...	60 1e-17
	emb AB001995 AB001995	Schizosaccharomyces pombe	gene for Tellp, ...	82 6e-17
	emb AI442227 AI442227	sa49c11.y1	Gm-cl1004 Glycine max cDNA clone...	85 8e-16
	emb AI725484 AI725484	BNLGH112268	Six-day Cotton fiber Gossypium...	54 2e-15
45	emb X92494 SCBNI1	S.cerevisiae	BNI1, N0647, APL1, N0665, N0670, ...	46 5e-13
	emb Z71540 SCYNL264C	S.cerevisiae	chromosome XIV reading frame O...	46 5e-13
	emb AI731920 AI731920	BNLGH111386	Six-day Cotton fiber Gossypium...	44 2e-12
	emb AI729569 AI729569	BNLGH113678	Six-day Cotton fiber Gossypium...	44 6e-11
	emb AI728685 AI728685	BNLGH111318	Six-day Cotton fiber Gossypium...	45 3e-10
50	emb AI725979 AI725979	BNLGH113788	Six-day Cotton fiber Gossypium...	45 6e-10
	emb AJ273110 AJ273110	AJ273110	Metarhizium anisopliae ARSEF 2575...	52 6e-09
	emb AQ655616 AQ655616	Sheared DNA-2J3	TR Sheared DNA Trypanosoma...	61 1e-08
	emb AQ501933 AQ501933	V11E10 mTn-3xHA/lacZ	Insertion Library Sac...	60 2e-08
	emb X97320 CGSEC14GN	C.glabrata	SEC14 gene.	55 7e-08
55	emb Z49259 SC9582X	S.cerevisiae	chromosome XIII cosmid 9582.	55 9e-08
	emb X15483 SCSEC14G	Yeast	SEC14 gene for cytosolic factor.	55 9e-08
	gb BE053932 BE053932	GA_Ea0031D10f	Gossypium arboreum 7-10 dpa ...	46 6e-07
	emb AQ023632 AQ023632	CpGR0082A	Cryptosporidium parvum genomic r...	55 7e-07
	emb AQ449556 AQ449556	500001H03.x1	CpLOWAM13mp18gDNA1 Cryptospor...	55 7e-07
60	emb Z28091 SCYKL091C	S.cerevisiae	chromosome XI reading frame OR...	50 8e-07
	emb A86344 A86344	Sequence 1003	from Patent EP0866129.	54 1e-06

	emb AF024652 AF024652 Glycine max polyphosphoinositide binding p...	54	1e-06
	emb AL114465 CNS01BNT Botrytis cinerea strain T4 cDNA library un...	51	2e-06
	gb C96579 C96579 C96579 Marchantia polymorpha immature sex organ...	42	4e-06
	emb AQ855615 AQ855615 CpG1709A CpIOWAgDNA1 Cryptosporidium parvu...	52	5e-06
5	gb L20972 YSJSEC14A Yarrowia lipolytica phosphatidylinositol-pho...	51	9e-06
	emb X81937 CASEC14 C.albicans SEC14 gene.	49	3e-05
	gb U61975 CAU61975 Candida albicans phosphatidylinositol/phospha...	49	3e-05
	gb BE123583 BE123583 NXNV_145_C08_F Nsf Xylem Normal wood Vertic...	49	4e-05
	emb AW739337 AW739337 gb40f01.y1 Moss EST library PPN Physcomitr...	49	4e-05
10	emb AW738979 AW738979 gb23b03.y1 Moss EST library PPN Physcomitr...	49	6e-05
	emb AW702333 AW702333 TgESTzz74g03.y1 TgRH*-Tachyzoite cDNA Toxo...	47	2e-04
	emb AI894440 AI894440 EST263895 tomato callus, TAMU Lycopersicon...	46	3e-04
	emb AI727743 AI727743 BNLGHi8966 Six-day Cotton fiber Gossypium ...	45	8e-04
	emb AL114440 CNS01BN4 Botrytis cinerea strain T4 cDNA library un...	45	0.001
15	emb AI729716 AI729716 BNLGHi14012 Six-day Cotton fiber Gossypium...	45	0.001
	emb AW348860 AW348860 GM210010A10E4R Gm-r1021 Glycine max cDNA 3...	44	0.001
	emb AI727901 AI727901 BNLGHi9413 Six-day Cotton fiber Gossypium ...	44	0.001
	emb Z69086 SPAC3H8 S.pombe chromosome I cosmid c3H8.	44	0.001
	emb AI731713 AI731713 BNLGHi10565 Six-day Cotton fiber Gossypium...	44	0.001
20	emb AI725627 AI725627 BNLGHi12489 Six-day Cotton fiber Gossypium...	44	0.002
	emb AW398657 AW398657 EST309157 L. pennellii trichome, Cornell U...	43	0.003
	emb AW625133 AW625133 EST313950 tomato radicle, 5 d post-imbibit...	43	0.003
	emb AI487421 AI487421 EST245743 tomato ovary, TAMU Lycopersicon ...	43	0.003
	emb AI486549 AI486549 EST244870 tomato ovary, TAMU Lycopersicon ...	43	0.003
25	emb AW508716 AW508716 si35e11.y1 Gm-r1030 Glycine max cDNA clone...	43	0.003
	gb BE020974 BE020974 sm54b08.y1 Gm-c1028 Glycine max cDNA clone ...	43	0.003
	emb AI460982 AI460982 sa77d02.y1 Gm-c1004 Glycine max cDNA clone...	43	0.004
	emb AA787291 AA787291 nld01a1.r1 Aspergillus nidulans 24hr asexu...	43	0.004
	emb AW350019 AW350019 GM210006B20G9R Gm-r1021 Glycine max cDNA 3...	43	0.004
30	emb AW689904 AW689904 NF025E09ST1F1000 Developing stem Medicago ...	42	0.005
	emb AW254728 AW254728 ML1015 peppermint glandular trichome Menth...	42	0.007
	emb AW267807 AW267807 EST305935 DSIR Medicago truncatula cDNA cl...	41	0.010
	emb AW676817 AW676817 DG1_1_H07.b1_A002 Dark Grown 1 (DG1) Sorgh...	41	0.010
	emb X87371 SCX731 S.cerevisiae DNA from chromosome X (cosmids 7,...	41	0.010
35	emb Z49420 SCYJL145W S.cerevisiae chromosome X reading frame ORF...	41	0.010
	emb AZ213346 AZ213346 Sheared DNA-77B10.TR Sheared DNA Trypanoso...	41	0.014
	emb AW720085 AW720085 LjNEST13f5r Lotus japonicus nodule library...	41	0.014
	emb AL078627 SPBC365 S.pombe chromosome II cosmid c365.	34	0.016
	emb AV425459 AV425459 AV425459 Lotus japonicus young plants (two...	40	0.019
40	emb AI495137 AI495137 sb03h08.y1 Gm-c1004 Glycine max cDNA clone...	40	0.019
	emb AW731571 AW731571 GA_Ea0030L14 Gossypium arboreum 7-10 dpa ...	40	0.019
	emb AI812357 AI812357 1D3 Pine Lambda Zap Xylem library Pinus ta...	40	0.019
	emb AJ273448 AJ273448 AJ273448 Metarhizium anisopliae ARSEF 2575...	40	0.019
	dbj D89132 D89132 Schizosaccharomyces pombe mRNA, partial cds, c...	34	0.020
45	emb AW925728 AW925728 HVSMEg0005F19 Hordeum vulgare pre-anthesis...	40	0.026

Query= AC004450.116_at 12091_at /id_source genbank /description
gb|aac64313.1| (ac004450) unknown protein [arabidopsis thaliana]
/blast_score 0 /ec_number /family /chip nova /gb_link
50 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004450|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004450|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004450|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac004450>
(2633 letters)

55 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

60 Score E
Sequences producing significant alignments: (bits) Value

- emb|AW310456|AW310456 sB36d02.x1 Gm-c1028 Glycine max cDNA clone... 243 5e-72
 emb|AW623933|AW623933 EST321878 tomato flower buds 3-8 mm, Corne... 166 3e-69
 emb|AW693705|AW693705 NF068B10ST1F1080 Developing stem Medicago ... 214 2e-65
 5 emb|AW203623|AW203623 sB36d02.y1 Gm-c1028 Glycine max cDNA clone... 205 2e-60
 emb|AW928464|AW928464 EST337252 tomato flower buds 8 mm to pre-a... 212 1e-53
 emb|AW289771|AW289771 NXNV005G02F Nsf Xylem Normal wood Vertical... 189 4e-49
 emb|AW720506|AW720506 LjNEST18d11r Lotus japonicus nodule librar... 142 3e-41
 emb|AI166211|AI166211 a063p06u Hybrid aspen plasmid library Popu... 114 2e-37
 10 emb|AI165948|AI165948 B004p66u Hybrid aspen plasmid library Popu... 62 2e-29
 emb|AW508607|AW508607 si34b12.y1 Gm-r1030 Glycine max cDNA clone... 78 3e-27
 emb|AW309153|AW309153 sF94h02.y1 Gm-c1019 Glycine max cDNA clone... 91 9e-26
 emb|AW830563|AW830563 sm28e08.y1 Gm-c1028 Glycine max cDNA clone... 104 7e-23
 emb|AI166124|AI166124 B008P77U Hybrid aspen plasmid library Popu... 105 2e-21
 15 emb|AI487660|AI487660 EST245982 tomato ovary, TAMU Lycopersicon ... 103 6e-21
 emb|AI489289|AI489289 EST247628 tomato ovary, TAMU Lycopersicon ... 103 6e-21
 emb|AW185557|AW185557 se81d11.y1 Gm-c1023 Glycine max cDNA clone... 85 3e-20
 emb|AI898473|AI898473 EST267916 tomato ovary, TAMU Lycopersicon ... 100 4e-20
 emb|AW695390|AW695390 NF094D01ST1F1012 Developing stem Medicago ... 77 9e-17
 20 emb|AW277644|AW277644 sf84g03.y1 Gm-c1019 Glycine max cDNA clone... 71 3e-12
 emb|AW759290|AW759290 sl39d05.y1 Gm-c1027 Glycine max cDNA clone... 67 6e-10
 emb|AI759735|AI759735 sb63e04.y1 Gm-c1017 Glycine max cDNA clone... 66 2e-09
 emb|AW100893|AW100893 sd62g04.y1 Gm-c1008 Glycine max cDNA clone... 62 1e-08
 emb|AW694269|AW694269 NF074E05ST1F1038 Developing stem Medicago ... 58 2e-07
 25 emb|AI988575|AI988575 sd04d10.y1 Gm-c1020 Glycine max cDNA clone... 36 3e-07
 emb|AQ638650|AQ638650 927P1-3G7.TP 927P1 Trypanosoma brucei geno... 52 2e-05
 emb|AW561069|AW561069 EST316117 DSIR Medicago truncatula cDNA cl... 52 2e-05
 emb|AW677337|AW677337 DG1_5_F09.g1_A002 Dark Grown 1 (DG1) Sorgh... 51 3e-05
 emb|AW677330|AW677330 DG1_5_D09.g1_A002 Dark Grown 1 (DG1) Sorgh... 46 0.001
 30 emb|AI736413|AI736413 sb28d01.y1 Gm-c1009 Glycine max cDNA clone... 41 0.027
 emb|X96932|NTASCOXRP N.tabacum gene encoding ascorbate oxidase-r... 40 0.086
 emb|A46243|A46243 Sequence 6 from Patent WO9521929. 40 0.086
 emb|AW931746|AW931746 EST357589 tomato fruit mature green, TAMU ... 39 0.16
 emb|AW617831|AW617831 EST324230 L. hirsutum trichome, Cornell Un... 39 0.16
 35 emb|AW672358|AW672358 LG1_359_D11.b1_A002 Light Grown 1 (LG1) So... 38 0.31
 emb|AC004157|AC004157 Plasmodium falciparum chromosome 12 clone ... 38 0.42
 emb|AW065005|AW065005 ST38E01 Pine TriplEx shoot tip library Pin... 37 0.58
 emb|AQ254402|AQ254402 CpG0808B CpIOWAgDNA1 Cryptosporidium parvu... 36 1.1
 emb|AF177330|AF177330 Saccharomyces cerevisiae iron transporter ... 36 1.1
 40 emb|AZ219717|AZ219717 Sheared DNA-88B11.TF Sheared DNA Trypanoso... 36 1.1
 emb|AI729567|AI729567 BNLGHi13639 Six-day Cotton fiber Gossypium... 36 1.1
 emb|Z21487|SCCHRIIFG S.cerevisiae RIM, MSI1, PGI, and ribosomal ... 36 1.1
 emb|Z36076|SCYBR207W S.cerevisiae chromosome II reading frame OR... 36 1.1
 emb|AW094274|AW094274 EST287454 tomato mixed elicitor, BTI Lycop... 35 2.1
 45 emb|AF129037|AF129037 Magnolia hypoleuca chloroplast trnT-trnL i... 35 2.1
 emb|AI211514|AI211514 p0g02a1.r1 Aspergillus nidulans 24hr asexu... 35 2.8
 emb|AW038170|AW038170 EST279827 tomato mixed elicitor, BTI Lycop... 35 2.8
 emb|AE001274|AE001274 Leishmania major chromosome 1, complete se... 35 2.8
 emb|Z69944|SPAC1F12 S.pombe chromosome I cosmid c1F12. 35 2.8
 50 emb|AB028188|AB028188 Penicillium digitatum DNA fragment contain... 34 5.3
 emb|AA898910|AA898910 NCP3E1T3 Perithecial Neurospora crassa cDN... 34 7.3
 emb|AI822825|AI822825 L30-661T3 Ice plant Lambda Uni-Zap XR expr... 34 7.3
 emb|AL353821|NC68B2 Neurospora crassa DNA linkage group V Cosmid... 34 7.3
 emb|AI724262|AI724262 RHIZ1_33_A04.y2_A001 Rhizome1 Sorghum hale... 34 7.3
 55 emb|AW397716|AW397716 sg83e02.y1 Gm-c1026 Glycine max cDNA clone... 34 7.3

Query= AL033545.26_at 12115_at /id_source genbank /description

emb|caa22152.1| (al033545) extensin-like protein [arabidopsis

thaliana] /blast_score 1.00e-87 /ec_number /family /chip nova

60 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-

post/entrez/query?db=n&form=6&dopt=g&uid=gb|al033545|/ncgi

<http://www.ncgr.org/cgi-bin/ff?al033545>
(1140 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E		(bits)	Value
10	Sequences producing significant alignments:				
	emb AI507807 AI507807 sb12h09.y1 Gm-c1004 Glycine max cDNA clone...	52	7e-08		
	emb AW443491 AW443491 EST308421 tomato mixed elicitor, BTI Lycop...	48	2e-07		
	emb AW719418 AW719418 LjNEST4c12r Lotus japonicus nodule library...	50	2e-07		
15	gb BE020862 BE020862 sm53c05.y1 Gm-c1028 Glycine max cDNA clone ...	50	2e-07		
	emb AI777049 AI777049 EST252016 tomato callus, TAMU Lycopersicon...	51	2e-07		
	emb AW032807 AW032807 EST276366 tomato callus, TAMU Lycopersicon...	51	2e-07		
	emb AI776903 AI776903 EST258003 tomato resistant, Cornell Lycop...	47	3e-07		
	emb AW092951 AW092951 EST286131 tomato mixed elicitor, BTI Lycop...	47	3e-07		
20	emb AW203388 AW203388 sf29f06.y1 Gm-c1028 Glycine max cDNA clone...	50	3e-07		
	emb AW597294 AW597294 si71c07.y1 Gm-c1031 Glycine max cDNA clone...	50	3e-07		
	emb AW622484 AW622484 EST313272 tomato root during/after fruit s...	47	3e-07		
	emb AW707234 AW707234 sk22d10.y1 Gm-c1028 Glycine max cDNA clone...	50	3e-07		
	emb AW568382 AW568382 si70b03.y1 Gm-c1031 Glycine max cDNA clone...	50	3e-07		
25	emb AW568746 AW568746 si72e11.y1 Gm-c1031 Glycine max cDNA clone...	50	3e-07		
	emb AV422321 AV422321 AV422321 Lotus japonicus young plants (two...	50	3e-07		
	emb AW830420 AW830420 sm26e07.y1 Gm-c1028 Glycine max cDNA clone...	50	3e-07		
	emb AW650542 AW650542 EST328996 tomato germinating seedlings, TA...	47	3e-07		
	emb AI441446 AI441446 sa86a06.y1 Gm-c1004 Glycine max cDNA clone...	50	3e-07		
30	emb AW234379 AW234379 sf24e05.y1 Gm-c1028 Glycine max cDNA clone...	50	3e-07		
	emb AI437875 AI437875 sa40g10.y1 Gm-c1004 Glycine max cDNA clone...	50	3e-07		
	emb AV416097 AV416097 AV416097 Lotus japonicus young plants (two...	50	3e-07		
	emb AV413898 AV413898 AV413898 Lotus japonicus young plants (two...	50	3e-07		
	emb AI441173 AI441173 sa52c02.y1 Gm-c1004 Glycine max cDNA clone...	50	3e-07		
35	emb AV415427 AV415427 AV415427 Lotus japonicus young plants (two...	50	3e-07		
	emb AI772831 AI772831 EST253931 tomato resistant, Cornell Lycop...	47	3e-07		
	gb BE020429 BE020429 sm40f03.y1 Gm-c1028 Glycine max cDNA clone ...	50	3e-07		
	emb AI443594 AI443594 sa42b01.y1 Gm-c1004 Glycine max cDNA clone...	50	3e-07		
	emb AW569805 AW569805 si81g01.y1 Gm-c1031 Glycine max cDNA clone...	50	3e-07		
40	emb AW093202 AW093202 EST286382 tomato mixed elicitor, BTI Lycop...	46	4e-07		
	emb AW906384 AW906384 EST342506 potato-stolon, Cornell Universit...	46	6e-07		
	emb AW597346 AW597346 si91f06.y1 Gm-c1031 Glycine max cDNA clone...	50	6e-07		
	emb AV423170 AV423170 AV423170 Lotus japonicus young plants (two...	50	6e-07		
	emb AW351202 AW351202 GM210010B20H11R Gm-r1021 Glycine max cDNA ...	48	8e-07		
45	emb AW649092 AW649092 EST327546 tomato germinating seedlings, TA...	46	8e-07		
	emb AV424931 AV424931 AV424931 Lotus japonicus young plants (two...	48	8e-07		
	emb AW350777 AW350777 GM210009B10D3R Gm-r1021 Glycine max cDNA 3...	48	1e-06		
	emb AW597304 AW597304 si71d07.y1 Gm-c1031 Glycine max cDNA clone...	48	1e-06		
	emb AW706307 AW706307 sj54f10.y1 Gm-c1033 Glycine max cDNA clone...	48	1e-06		
50	emb AW133241 AW133241 se16b08.y1 Gm-c1013 Glycine max cDNA clone...	48	1e-06		
	emb AW568935 AW568935 si73c12.y1 Gm-c1031 Glycine max cDNA clone...	48	1e-06		
	gb BE020648 BE020648 sm51g03.y1 Gm-c1028 Glycine max cDNA clone ...	48	1e-06		
	emb AW567667 AW567667 si77d01.y1 Gm-c1031 Glycine max cDNA clone...	48	1e-06		
	emb AI495459 AI495459 sa98c07.y1 Gm-c1004 Glycine max cDNA clone...	48	1e-06		
55	emb AW234280 AW234280 sf23c12.y1 Gm-c1028 Glycine max cDNA clone...	48	1e-06		
	emb AW348755 AW348755 GM210003A22D8R Gm-r1021 Glycine max cDNA 3...	47	2e-06		
	emb AW309755 AW309755 sf24d05.x1 Gm-c1028 Glycine max cDNA clone...	47	2e-06		
	emb AW703937 AW703937 sk25h11.y1 Gm-c1028 Glycine max cDNA clone...	47	2e-06		
	emb AW596777 AW596777 sj16e12.y1 Gm-c1032 Glycine max cDNA clone...	47	2e-06		
60	emb AW620542 AW620542 sj06e05.y1 Gm-c1032 Glycine max cDNA clone...	47	2e-06		
	emb AW706297 AW706297 sj54e12.y1 Gm-c1033 Glycine max cDNA clone...	47	2e-06		

	emb AW666031 AW666031 sk31c05.y1 Gm-c1028 Glycine max cDNA clone...	47 2e-06
	emb AW760039 AW760039 sl57c07.y1 Gm-c1027 Glycine max cDNA clone...	47 2e-06
	gb BE057556 BE057556 sm03h08.y1 Gm-c1015 Glycine max cDNA clone ...	47 2e-06
	emb AW596055 AW596055 si97d01.y1 Gm-c1032 Glycine max cDNA clone...	47 2e-06
5	emb AI901127 AI901127 sc21a04.y1 Gm-c1013 Glycine max cDNA clone...	47 2e-06
	emb AW666132 AW666132 sk32f02.y1 Gm-c1028 Glycine max cDNA clone...	48 2e-06
	emb AW756628 AW756628 sl25b06.y1 Gm-c1027 Glycine max cDNA clone...	47 2e-06
	emb AW234369 AW234369 sf24d05.y1 Gm-c1028 Glycine max cDNA clone...	47 2e-06
	emb AI441736 AI441736 sa82b04.y1 Gm-c1004 Glycine max cDNA clone...	47 2e-06
10	emb AW756748 AW756748 sl26g04.y1 Gm-c1027 Glycine max cDNA clone...	47 2e-06
	emb AW317359 AW317359 sg48c11.y1 Gm-c1025 Glycine max cDNA clone...	45 2e-06
	emb AW306872 AW306872 sf49g05.y1 Gm-c1009 Glycine max cDNA clone...	50 2e-06
	emb AW597518 AW597518 sj48b01.y1 Gm-c1033 Glycine max cDNA clone...	50 2e-06
	emb AW307412 AW307412 sf56f11.y1 Gm-c1009 Glycine max cDNA clone...	50 2e-06
15	emb AW597680 AW597680 sj49e04.y1 Gm-c1033 Glycine max cDNA clone...	50 2e-06
	emb AW831618 AW831618 sm04g03.y1 Gm-c1027 Glycine max cDNA clone...	47 2e-06
	emb AI736342 AI736342 sb27c03.y1 Gm-c1009 Glycine max cDNA clone...	50 2e-06
	emb AI441411 AI441411 sa59e12.y1 Gm-c1004 Glycine max cDNA clone...	50 2e-06
	emb AW666398 AW666398 sk36a11.y1 Gm-c1028 Glycine max cDNA clone...	47 3e-06
20	emb AW759615 AW759615 sl45f02.y1 Gm-c1027 Glycine max cDNA clone...	47 3e-06
	emb AW309747 AW309747 sf24c01.x1 Gm-c1028 Glycine max cDNA clone...	47 4e-06
	emb AW309357 AW309357 sf16d03.x1 Gm-c1028 Glycine max cDNA clone...	47 4e-06
	gb BE022318 BE022318 sm73d03.y1 Gm-c1028 Glycine max cDNA clone ...	47 4e-06
	emb AW234182 AW234182 sf22b12.y1 Gm-c1028 Glycine max cDNA clone...	47 4e-06
25	emb AW704401 AW704401 sk30f03.y1 Gm-c1028 Glycine max cDNA clone...	47 4e-06
	emb AI443444 AI443444 sa33g05.y1 Gm-c1004 Glycine max cDNA clone...	50 4e-06
	gb BE022257 BE022257 sm72g11.y1 Gm-c1028 Glycine max cDNA clone ...	49 5e-06
	emb AW666281 AW666281 sk34f10.y1 Gm-c1028 Glycine max cDNA clone...	49 5e-06
	emb AW706178 AW706178 sj52g11.y1 Gm-c1033 Glycine max cDNA clone...	49 5e-06
30	emb AV422555 AV422555 AV422555 Lotus japonicus young plants (two...	50 5e-06
	emb AI438033 AI438033 sa35a09.y1 Gm-c1004 Glycine max cDNA clone...	49 5e-06
	emb AV406879 AV406879 AV406879 Lotus japonicus young plants (two...	50 5e-06
	emb AI522822 AI522822 sa74b08.y1 Gm-c1004 Glycine max cDNA clone...	49 5e-06
	emb AV417663 AV417663 AV417663 Lotus japonicus young plants (two...	50 5e-06
35	emb AV412992 AV412992 AV412992 Lotus japonicus young plants (two...	50 5e-06
	emb AV419296 AV419296 AV419296 Lotus japonicus young plants (two...	50 5e-06
	emb AI442014 AI442014 sa66e07.y1 Gm-c1004 Glycine max cDNA clone...	47 5e-06
	gb L22305 ALFCORC Medicago sativa bimodular protein (corC) mRNA,...	50 7e-06
	emb AW560195 AW560195 EST315243 DSIR Medicago truncatula cDNA cl...	45 7e-06
40	emb AW559226 AW559226 EST306062 DSIR Medicago truncatula cDNA cl...	45 7e-06
	emb AW570545 AW570545 sj63d10.y1 Gm-c1033 Glycine max cDNA clone...	48 7e-06
	emb AW309693 AW309693 sf23c12.x1 Gm-c1028 Glycine max cDNA clone...	45 7e-06
	emb AW152920 AW152920 se32g01.y1 Gm-c1015 Glycine max cDNA clone...	48 7e-06
	emb AW830131 AW830131 sm23c07.y1 Gm-c1028 Glycine max cDNA clone...	48 7e-06
45	emb AI736269 AI736269 sb26b02.y1 Gm-c1008 Glycine max cDNA clone...	48 7e-06
	emb AW595988 AW595988 si96d11.y1 Gm-c1032 Glycine max cDNA clone...	44 7e-06
	emb AW703893 AW703893 sk25d10.y1 Gm-c1028 Glycine max cDNA clone...	48 7e-06
	emb AW666325 AW666325 sk35b10.y1 Gm-c1028 Glycine max cDNA clone...	48 7e-06
	emb AI441694 AI441694 sa60a10.y1 Gm-c1004 Glycine max cDNA clone...	48 7e-06
50	emb AI442516 AI442516 sa32e08.y1 Gm-c1004 Glycine max cDNA clone...	48 7e-06

Query= AL078579.130_at 12240_at /id_source genbank /description

emb|cab43974.1| (al078579) putative protein [arabidopsis thaliana]

/blast_score 0 /ec_number /family /chip nova /gb_link

55 <http://www3.ncbi.nlm.nih.gov/htbin->

post/entrez/query?db=n&form=6&dopt=g&uid=gb|al078579| /ncgi

<http://www.ncgr.org/cgi-bin/ff?al078579>

(1899 letters)

60 Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	
5	Sequences producing significant alignments:	(bits)	Value
	emb AI896265 AI896265 EST265708 tomato callus, TAMU Lycopersicon...	69	5e-22
	emb AI896298 AI896298 EST265741 tomato callus, TAMU Lycopersicon...	69	5e-22
	emb AI352900 AI352900 MB73-10F PZ204.BNlib Brassica napus cDNA c...	83	3e-15
10	emb AI960998 AI960998 sc93g09.y1 Gm-c1019 Glycine max cDNA clone...	58	2e-14
	emb AW618619 AW618619 EST320605 L. pennellii trichome, Cornell U...	67	4e-10
	emb AW618077 AW618077 EST314127 L. pennellii trichome, Cornell U...	67	5e-10
	emb AW684309 AW684309 NF015D01NR1F1000 Nodulated root Medicago t...	60	4e-08
	emb AW477120 AW477120 ga42b04.y1 Moss EST library PPU Physcomitr...	57	2e-07
15	emb AW459393 AW459393 sh23f12.y1 Gm-c1016 Glycine max cDNA clone...	44	1e-06
	emb AW459655 AW459655 sh90b07.y1 Gm-c1016 Glycine max cDNA clone...	44	1e-06
	gb M82834 TRBAEMAJ Trypanosoma cruzi DNA, repeat region.	44	0.005
	emb AL031746 PFMAL1P3 Plasmodium falciparum MAL1P3, complete seq...	39	0.11
	gb J03998 PFAGAR Plasmodium falciparum glutamic acid-rich protei...	39	0.11
20	emb AQ361416 AQ361416 mgxb0004C14f CUGI Rice Blast BAC Library P...	39	0.15
	emb AQ160297 AQ160297 mgxb0005E12r CUGI Rice Blast BAC Library P...	39	0.15
	emb AQ399340 AQ399340 mgxb0016L08f CUGI Rice Blast BAC Library P...	39	0.15
	emb AQ397636 AQ397636 mgxb0003C21f CUGI Rice Blast BAC Library P...	39	0.15
	emb AQ254981 AQ254981 mgxb0007C19r CUGI Rice Blast BAC Library P...	39	0.15
25	emb AQ161580 AQ161580 mgxb0008O12r CUGI Rice Blast BAC Library P...	39	0.15
	emb AQ400016 AQ400016 mgxb0006B12f CUGI Rice Blast BAC Library P...	37	0.53
	emb AQ399347 AQ399347 mgxb0003K11f CUGI Rice Blast BAC Library P...	36	0.73
	emb AQ161764 AQ161764 mgxb0009C18r CUGI Rice Blast BAC Library P...	35	1.4
	emb AV412173 AV412173 AV412173 Lotus japonicus young plants (two...	35	1.4
30	gb L38454 PFAORFAE Plasmodium falciparum (clone pS31H) ORF mRNA,...	27	1.8
	emb AQ162745 AQ162745 mgxb0016M17r CUGI Rice Blast BAC Library P...	35	1.9
	emb AQ398363 AQ398363 mgxb0014B01f CUGI Rice Blast BAC Library P...	35	1.9
	emb AQ161887 AQ161887 mgxb0010E10r CUGI Rice Blast BAC Library P...	35	1.9
	emb AQ161814 AQ161814 mgxb0009M14r CUGI Rice Blast BAC Library P...	35	1.9
35	emb AQ255508 AQ255508 mgxb0014J05r CUGI Rice Blast BAC Library P...	35	1.9
	emb AQ254973 AQ254973 mgxb0007C03r CUGI Rice Blast BAC Library P...	35	1.9
	emb AQ654450 AQ654450 Sheared DNA-25M9.TR Sheared DNA Trypanosom...	35	1.9
	emb AQ906953 AQ906953 GSSTc02997 Trypanosome cruzi random genomi...	35	2.5
	emb AL116053 CNS01CVX Botrytis cinerea strain T4 cDNA library un...	34	2.6
40	gb BE052627 BE052627 GA_Ea0032J13f Gossypium arboreum 7-10 dpa ...	34	2.6
	emb AI668074 AI668074 TENG0996 T. Cruzi epimastigote normalised ...	34	3.5
	emb AF242312 AF242312 Euphorbia esula cyclophilin mRNA, partial ...	34	3.5
	emb AC004157 AC004157 Plasmodium falciparum chromosome 12 clone ...	34	3.6
	emb AA550286 AA550286 1415m3 gmbPfHB3.1, G. Roman Reddy Plasmodi...	34	3.6
45	emb Z49390 SCYJL115W S.cerevisiae chromosome X reading frame ORF...	34	3.6
	emb AQ845473 AQ845473 LMAJFV1_lm25h11.y1 Leishmania major FV1 ra...	34	3.6
	emb AQ902283 AQ902283 LMAJFV1_lm47f04.x1 Leishmania major FV1 ra...	34	3.6
	emb AQ845786 AQ845786 LMAJFV1_lm25h11.x1 Leishmania major FV1 ra...	34	3.6
	gb L07593 YSCASF Saccharomyces cerevisiae ASF1 gene, complete cds.	34	3.6
50	emb X53731 SCSPA2G S. cerevisiae SPA2 gene.	34	4.8
	emb AQ324737 AQ324737 mgxb0019L21r CUGI Rice Blast BAC Library P...	34	4.8
	emb AQ501529 AQ501529 V20F5 mTn-3xHA/lacZ Insertion Library Sacc...	34	4.8
	emb AQ161923 AQ161923 mgxb0010K22r CUGI Rice Blast BAC Library P...	34	4.8
	emb AW618616 AW618616 EST320602 L. pennellii trichome, Cornell U...	34	4.8
55	emb AI437671 AI437671 sa38b01.y1 Gm-c1004 Glycine max cDNA clone...	34	4.8
	emb AW703668 AW703668 sk11h05.y1 Gm-c1023 Glycine max cDNA clone...	34	4.8
	emb X97560 SC32KBF S.cerevisiae 32kb DNA fragment of chromosome ...	34	4.8
	emb Z73126 SCYLL021W S.cerevisiae chromosome XII reading frame O...	34	4.8
	emb AV414692 AV414692 AV414692 Lotus japonicus young plants (two...	33	5.0
60	emb Z37997 SC9877 S.cerevisiae chromosome IX cosmid 9877.	33	5.0
	emb X52898 TCGAP T. cruzi gap gene for glyceraldehyde-3-phosphat...	33	5.0

- emb|AF052832|AF052832 Trypanosoma cruzi CL Brener cosmid 1b21 ch... 33 5.0
 emb|AV423850|AV423850 AV423850 Lotus japonicus young plants (two... 33 5.0
 emb|AC006281|AC006281 Plasmodium falciparum chromosome 12 clone ... 26 5.3
 emb|AW459042|AW459042 sh18d12.y1 Gm-c1016 Glycine max cDNA clone... 33 6.5
 5 gb|L06323|THEGLUMEMP Theileria parva glutamine rich membrane pro... 33 6.5
 emb|W66263|W66263 TgESTzy71f09.r1 TgME49 Tachyzoite cDNA Toxopla... 33 6.5
 emb|AQ948528|AQ948528 Sheared DNA-37G19.TR Sheared DNA Trypanoso... 33 6.9
 emb|AL035476|PFMAL4P3 Plasmodium falciparum chromosome 4 strain ... 33 6.9
 emb|AI080842|AI080842 TENU3699 T. cruzi epimastigote normalized ... 33 6.9
 10 gb|U75347|ENU75347 Emericella nidulans fatty acid synthase, alph... 33 6.9
 emb|AQ659013|AQ659013 Sheared DNA-13G3.TR Sheared DNA Trypanosom... 33 6.9
 emb|AF100160|AF100160 Glycine max hydrophobic seed protein precu... 33 6.9
 emb|AF118381|AF118381 Brassica napus tonoplast intrinsic protein... 33 8.9
 emb|AW099672|AW099672 sd29e10.y2 Gm-c1012 Glycine max cDNA clone... 33 8.9
 15 emb|AA519692|AA519692 TgESTzz27f06.r1 TgME49 invivo Bradyzoite c... 33 8.9
 emb|AQ255413|AQ255413 mgxb0012P02r CUGI Rice Blast BAC Library P... 33 8.9
 emb|Z73626|SCYPL270W S.cerevisiae chromosome XVI reading frame O... 33 8.9
 emb|X96876|SCCHRIVFY S.cerevisiae DNA of cosmid from chromosome ... 32 9.4
 gb|U43564|SCU43564 Saccharomyces cerevisiae CDC53 gene, complete... 32 9.4
 20 emb|Z29537|NTPROTIH N.tabacum (Samsun NN) gene for proteinase i... 32 9.4
 emb|AF155848|AF155848 Lysinema ciliatum chloroplast atpB-rbcL in... 32 9.4
 gb|U38804|PPU38804 Porphyra purpurea chloroplast, complete genome. 32 9.4
 emb|AW333913|AW333913 S27H9 AGS-1 Pneumocystis carinii f. sp. ca... 32 9.4
 emb|AI510981|AI510981 T7187 MVAT4 bloodstream form of serodeme W... 32 9.4
 25 emb|AF102653|AF102653 Podranea ricasoliana ribulose 1,5-bisphosp... 32 9.4
 emb|Z74180|SCYDL132W S.cerevisiae chromosome IV reading frame OR... 32 9.4

Query= AJ011674.2_at 12278_at /id_source genbank /description
 "emb|caa09731.1| (aj011674) receptor-like protein kinase, rlk3
 30 [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase
 /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|aj011674|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|aj011674|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|aj011674|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?aj011674>
 35 (2196 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

40 Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

- 45 emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 375 e-120
 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 332 e-105
 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 339 e-105
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 330 e-105
 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 333 e-104
 50 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 332 e-104
 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 328 e-103
 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 329 e-100
 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 321 1e-99
 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 316 2e-98
 55 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 323 2e-98
 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 324 4e-98
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 195 4e-97
 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 312 4e-95
 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 314 4e-95
 60 emb|AW620957|AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone... 285 3e-94
 emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 306 6e-94

- gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 221 1e-93
 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 270 3e-93
 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 264 2e-90
 gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 289 2e-90
 5 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 275 7e-90
 dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 274 9e-89
 emb|Y12530|BOARLKGEN B.oleraceae gene encoding serine/threonine ... 127 6e-88
 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 272 6e-88
 gb|BE057261|BE057261 sm99f12.y1 Gm-c1015 Glycine max cDNA clone... 313 3e-84
 10 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 122 2e-82
 emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 302 9e-81
 emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 128 3e-78
 emb|AW760240|AW760240 sl59g07.y1 Gm-c1027 Glycine max cDNA clone... 283 4e-75
 emb|AW831390|AW831390 sm22a06.y1 Gm-c1028 Glycine max cDNA clone... 213 3e-73
 15 emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 127 6e-73
 gb|BE034949|BE034949 ML07F03 ML Mesembryanthemum crystallinum cD... 266 3e-71
 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 118 1e-70
 emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 114 4e-69
 emb|AI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 261 2e-68
 20 emb|AI486193|AI486193 EST244514 tomato ovary, TAMU Lycopersicon ... 182 4e-68
 emb|AW442344|AW442344 EST311740 tomato fruit red ripe, TAMU Lyco... 210 8e-68
 emb|AB024422|AB024422 S2 Brassica oleracea SRK13-b gene, exon 2, ... 110 9e-68
 emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 111 2e-67
 emb|AB024420|AB024419 S2 Brassica oleracea SRK13 gene, exon 2, 3,... 109 2e-67
 25 emb|AI896155|AI896155 EST265598 tomato callus, TAMU Lycopersicon... 186 3e-67
 emb|AB013718|AB013717 S2 Brassica rapa gene for SRK46Bra, exon 2,... 109 3e-66
 emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 120 2e-65
 dbj|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 120 3e-65
 emb|X79432|BOSRK3 B.oleracea SRK3 gene. 116 1e-64
 30 emb|AW203661|AW203661 sf36g06.y1 Gm-c1028 Glycine max cDNA clone... 208 2e-63
 emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 241 2e-62
 emb|AI967314|AI967314 Ljirnp00-017 Ljirnp Lambda HybriZap two... 134 1e-60
 emb|AI897876|AI897876 EST267319 tomato ovary, TAMU Lycopersicon ... 171 3e-60
 emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 231 2e-59
 35 emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 231 2e-59
 emb|AI486584|AI486584 EST244905 tomato ovary, TAMU Lycopersicon ... 171 3e-59
 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 136 1e-58
 emb|AW220677|AW220677 EST297146 tomato fruit mature green, TAMU ... 227 2e-58
 emb|AW309544|AW309544 sf20h08.x1 Gm-c1028 Glycine max cDNA clone... 167 4e-57
 40 emb|AW666141|AW666141 sk32f11.y1 Gm-c1028 Glycine max cDNA clone... 176 7e-56
 emb|AW033458|AW033458 EST277029 tomato callus, TAMU Lycopersicon... 219 8e-56
 emb|AI901283|AI901283 sc31d08.y1 Gm-c1014 Glycine max cDNA clone... 175 9e-56
 emb|Y16999|TCA16999 Theobroma cacao microsatellite DNA, clone mT... 131 1e-55
 emb|AI822907|AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr... 117 1e-53
 45 emb|AI822355|AI822355 L0-804T3 Ice plant Lambda Uni-Zap XR expre... 116 4e-53
 emb|AW667985|AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ... 111 7e-53
 emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 140 9e-53
 emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 78 4e-52
 emb|AI899009|AI899009 EST268452 tomato ovary, TAMU Lycopersicon ... 160 5e-52
 50 emb|AW034624|AW034624 EST278308 tomato callus, TAMU Lycopersicon... 205 1e-51
 emb|AI771857|AI771857 EST252957 tomato ovary, TAMU Lycopersicon ... 156 6e-51
 emb|AI488101|AI488101 EST246423 tomato ovary, TAMU Lycopersicon ... 156 6e-51
 emb|AI898581|AI898581 EST268024 tomato ovary, TAMU Lycopersicon ... 160 6e-51
 emb|AW039406|AW039406 EST281663 tomato mixed elicitor, BTI Lycop... 115 1e-50
 55 emb|AI896953|AI896953 EST266396 tomato callus, TAMU Lycopersicon... 183 1e-50
 emb|AI899156|AI899156 EST268599 tomato ovary, TAMU Lycopersicon ... 160 3e-50
 emb|Z18884|BOSRKRPC B.oleracea encoding S-receptor kinase relate... 125 2e-49
 emb|AI895623|AI895623 EST265066 tomato callus, TAMU Lycopersicon... 196 5e-49
 emb|AW054349|AW054349 L30-1774T3 Ice plant Lambda Uni-Zap XR exp... 116 6e-49
 60 emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 100 8e-49
 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 74 4e-48

emb|AI822347|AI822347 L0-796T3 Ice plant Lambda Uni-Zap XR expre... 116 5e-47
 emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 189 8e-47
 emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 160 9e-47
 5 emb|AW706972|AW706972 sk20a03.y1 Gm-c1028 Glycine max cDNA clone... 188 1e-46
 gb|U51330|TAU51330 Triticum aestivum leaf rust resistance kinase... 78 1e-46
 emb|AI967315|AI967315 Ljirnp00-018 Ljirnp Lambda HybriZap two... 142 2e-46
 emb|AW279355|AW279355 sf65g10.y1 Gm-c1013 Glycine max cDNA clone... 111 4e-46
 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 130 5e-46
 emb|AI775997|AI775997 EST257097 tomato resistant, Cornell Lycope... 186 5e-46
 10 emb|AI930642|AI930642 sb37f05.y1 Gm-c1013 Glycine max cDNA clone... 182 1e-44
 emb|AF085164|AF085164 Hordeum vulgare receptor-like kinase LRK10... 78 1e-44
 emb|AI731504|AI731504 BNLGHi9991 Six-day Cotton fiber Gossypium ... 67 3e-44
 emb|AW394449|AW394449 sh05d09.y1 Gm-c1016 Glycine max cDNA clone... 119 4e-44
 emb|AI938169|AI938169 sc40d07.y1 Gm-c1014 Glycine max cDNA clone... 179 6e-44
 15 emb|Z18861|BOSRKPA B.oleracea encoding S-receptor kinase relate... 114 7e-44
 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 76 1e-43
 emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 125 1e-43
 emb|Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 74 1e-43
 emb|AW687052|AW687052 NF005E02RT1F1017 Developing root Medicago ... 177 2e-43
 20 emb|AI055189|AI055189 coau0003E19 Cotton Boll Abscission Zone cD... 107 4e-43
 gb|BE058691|BE058691 sn19e05.y1 Gm-c1016 Glycine max cDNA clone ... 92 4e-43
 emb|Z18883|BOSRKRPB B.oleracea encoding S-receptor kinase relate... 176 4e-43

Query= AC002392.162_at 12307_at /id_source genbank /description
 25 gb|aad12037.1| (ac002392) putative receptor-like protein kinase
 [arabidopsis thaliana] /blast_score 0 /ec_number /family kinase /chip
 nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002392| /ncgi
 30 http://www.ncgr.org/cgi-bin/ff?ac002392
 (2631 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

35 Searching.....done

	Score	E	(bits)	Value
40	Sequences producing significant alignments:			
	emb AW774582 AW774582	EST333733	KV3 Medicago truncatula cDNA clo...	204 5e-74
	emb AI729170 AI729170	BNLGHi12834	Six-day Cotton fiber Gossypium...	245 1e-63
	emb Z73295 CRPK1	C.roseus	mRNA for receptor-like protein kinase.	146 5e-56
	emb AF220602 AF220602	Lycopersicon	pimpinellifolium Rio Grande 7...	112 7e-54
45	gb U59317 LPU59317	Lycopersicon	pimpinellifolium serine/threonin...	108 7e-54
	gb U13923 LEU13923	Lycopersicon	pimpinellifolium serine/threonin...	108 7e-54
	emb AW222552 AW222552	EST299363	tomato fruit red ripe, TAMU Lyco...	210 3e-53
	gb BE053916 BE053916	GA_Ea0031D03f	Gossypium arboreum 7-10 dpa ...	209 8e-53
	emb AF220603 AF220603	Lycopersicon	esculentum VFNT Cherry Pto lo...	112 4e-52
50	emb AW200786 AW200786	se93e06.y1	Gm-c1027 Glycine max cDNA clone...	206 5e-52
	emb AW729859 AW729859	GA_Ea0026H04	Gossypium arboreum 7-10 dpa ...	206 7e-52
	emb AW774672 AW774672	EST333823	KV3 Medicago truncatula cDNA clo...	82 7e-51
	emb AW667985 AW667985	GA_Ea0012C15	Gossypium arboreum 7-10 dpa ...	158 2e-50
	gb U59316 LEU59316	Lycopersicon	esculentum serine/threonine prot...	111 9e-50
55	gb U59318 LEU59318	Lycopersicon	esculentum serine/threonine prot...	102 3e-49
	emb AF121450 AF121450	Capsicum annuum	protein kinase homolog C11...	104 1e-48
	emb AF108892 AF108892	AF108892	Capsicum annuum root 1st-branched...	194 3e-48
	emb AI967314 AI967314	Ljirnp00-017	Ljirnp Lambda HybriZap two...	129 5e-48
	gb U59315 LPU59315	Lycopersicon	pimpinellifolium serine/threonin...	103 1e-47
60	gb U02271 LEU02271	Lycopersicon	pimpinellifolium Rio Grande-PtoR...	103 1e-47
	emb AF197947 AF197947	Glycine max	receptor protein kinase-like p...	185 3e-47

- emb|AB032474|AB032474 *Brassica oleracea* SRK60 mRNA for S60 S-loc... 113 5e-47
emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 182 2e-46
dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 112 2e-46
emb|AW773915|AW773915 EST332901 *Medicago truncatula* cDNA clo... 82 3e-46
5 emb|AF053127|AF053127 *Malus domestica* leucine-rich receptor-like... 130 4e-46
dbj|D38564|BOLRPKB *Brassica campestris* mRNA for receptor protein... 110 4e-46
emb|AB012106|AB012106 *Brassica rapa* mRNA for SRK45, complete cds. 111 5e-46
dbj|D38563|BOLRPKA *Brassica campestris* mRNA for receptor protein... 109 6e-46
emb|AW982539|AW982539 HVSMEg0003I16f *Hordeum vulgare* pre-anthesi... 146 6e-46
10 emb|AI736063|AI736063 sb22d04.y1 *Gm-c1007* Glycine max cDNA clone... 147 6e-46
emb|AW256717|AW256717 EST304854 KV2 *Medicago truncatula* cDNA clo... 82 7e-46
dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 94 2e-45
dbj|E05046|E05046 DNA encoding ZmPK1 homologue protein in tobacco. 94 2e-45
emb|AW979740|AW979740 EST341365 tomato root deficiency, Cornell ... 184 2e-45
15 emb|AI895365|AI895365 EST264808 tomato callus, TAMU Lycopersicon... 184 2e-45
emb|Y14600|SBRLK1 *Sorghum bicolor* mRNA for protein serine/threon... 82 3e-45
gb|U28007|LEU28007 *Lycopersicon esculentum* Pto kinase interactor... 127 1e-44
emb|A67797|A67797 Sequence 2 from Patent WO9743427. 79 2e-44
gb|U93048|DCU93048 *Daucus carota* somatic embryogenesis receptor-... 79 2e-44
20 emb|AF121451|AF121451 *Capsicum annuum* protein kinase homolog C11... 105 5e-44
emb|AB041503|AB041503 *Populus nigra* PnPK1 mRNA for protein kinas... 133 6e-44
emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 81 2e-43
emb|AA738545|AA738545 SbRLK3 *Sorghum bicolor* cv. TX430 leaf Sorg... 78 3e-43
gb|U20948|ITU20948 *Ipomoea trifida* receptor protein kinase (IRK1... 99 1e-42
25 emb|AF121449|AF121449 *Capsicum annuum* protein kinase homolog C15... 99 1e-42
emb|AW219672|AW219672 EST302154 tomato root during/after fruit s... 125 1e-42
emb|AW030530|AW030530 EST273785 tomato callus, TAMU Lycopersicon... 162 1e-42
emb|AI898917|AI898917 EST268360 tomato ovary, TAMU Lycopersicon ... 122 1e-42
emb|AI489287|AI489287 EST247626 tomato ovary, TAMU Lycopersicon ... 122 2e-42
30 emb|AI730776|AI730776 BNLGHi7867 Six-day Cotton fiber *Gossypium* ... 151 2e-42
emb|AA738544|AA738544 SbRLK2 *Sorghum bicolor* cv. TX430 leaf Sorg... 78 2e-42
emb|AB032473|AB032473 *Brassica oleracea* SRK18 mRNA for S18 S-loc... 115 6e-42
gb|L08607|BNASRECKIN *Brassica napus* S-receptor kinase mRNA, comp... 110 9e-42
emb|AB041504|AB041504 *Populus nigra* PnPK2 mRNA for protein kinas... 132 9e-42
35 gb|M97667|BNASTKR *Brassica napus* ssp. *oleifera* serine/threonine ... 115 2e-41
emb|AW036763|AW036763 EST252152 tomato ovary, TAMU Lycopersicon ... 164 2e-41
emb|AW036762|AW036762 EST252151 tomato ovary, TAMU Lycopersicon ... 164 2e-41
emb|AW668493|AW668493 GA__Ea0014C20 *Gossypium arboreum* 7-10 dpa ... 127 4e-41
gb|U00443|BNU00443 *Brassica napus* cultivar T2 S-receptor kinase ... 110 4e-41
40 emb|AW776704|AW776704 EST335769 DSIL *Medicago truncatula* cDNA cl... 113 2e-40
emb|AF131222|AF131222 *Lophopyrum elongatum* protein serine/threon... 97 2e-40
emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 133 2e-40
emb|AB013720|AB013720 *Brassica oleracea* mRNA for SRK23Bol, parti... 111 3e-40
emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 105 3e-40
45 emb|AW615998|AW615998 EST325448 tomato flower buds 0-3 mm, Come... 117 3e-40
emb|AW218745|AW218745 EST301225 tomato root during/after fruit s... 120 5e-40
emb|AI731501|AI731501 BNLGHi9983 Six-day Cotton fiber *Gossypium* ... 98 6e-40
gb|M76647|BNASKR6A *Brassica oleracea* receptor protein kinase (SK... 108 9e-40
emb|AF121448|AF121448 *Capsicum annuum* protein kinase homolog C11... 95 2e-39
50 emb|AI771280|AI771280 EST252296 tomato ovary, TAMU Lycopersicon ... 165 2e-39
emb|AI486547|AI486547 EST244868 tomato ovary, TAMU Lycopersicon ... 123 2e-39
emb|AW094468|AW094468 EST287648 tomato mixed elicitor, BTI Lycop... 156 2e-39
emb|AB008191|AB008191 *Brassica rapa* mRNA for SRK29, complete cds. 108 3e-39
emb|AI771841|AI771841 EST252941 tomato ovary, TAMU Lycopersicon ... 164 4e-39
55 emb|AI485090|AI485090 EST243394 tomato ovary, TAMU Lycopersicon ... 164 4e-39
emb|AI731504|AI731504 BNLGHi9991 Six-day Cotton fiber *Gossypium* ... 78 4e-39
emb|AF078082|AF078082 *Phaseolus vulgaris* receptor-like protein k... 111 4e-39
emb|Y18260|BOY18260 *Brassica oleracea* mRNA for SRK15 protein, pa... 107 6e-39
emb|AB024416|AB024416 *Brassica oleracea* SRK2-b mRNA, complete cds. 107 6e-39
60 emb|AW267961|AW267961 EST306183 DSIR *Medicago truncatula* cDNA cl... 94 7e-39
emb|Y18259|BOY18259 *Brassica oleracea* mRNA for SRK5 protein, par... 107 1e-38

	emb AI486766 AI486766 EST245088 tomato ovary, TAMU Lycopersicon ...	89	1e-38
	emb AI485862 AI485862 EST244183 tomato ovary, TAMU Lycopersicon ...	162	1e-38
	emb AI487456 AI487456 EST245778 tomato ovary, TAMU Lycopersicon ...	123	2e-38
	gb BE060160 BE060160 HVSMEg0011B12f Hordeum vulgare pre-anthesis...	75	2e-38
5	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2.	107	3e-38
	emb AF142596 AF142596 Nicotiana tabacum LRR receptor-like protei...	78	3e-38
	emb AW617255 AW617255 EST323666 L. hirsutum trichome, Cornell Un...	148	4e-38
	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR...	71	4e-38
	emb AW774790 AW774790 EST333941 KV3 Medicago truncatula cDNA clo...	95	5e-38
10	emb Y14286 BOY14286 Brassica oleracea SFR3 gene, partial.	105	5e-38
	emb AW726024 AW726024 GA_Ea0020G24 Gossypium arboreum 7-10 dpa ...	124	6e-38
	emb AI898390 AI898390 EST267833 tomato ovary, TAMU Lycopersicon ...	121	1e-37
	gb BE020963 BE020963 sm54a06.y1 Gm-c1028 Glycine max cDNA clone ...	125	3e-37
	emb AI730535 AI730535 BNLGHi7007 Six-day Cotton fiber Gossypium ...	73	5e-37
15	emb AF085167 AF085167 Hordeum vulgare receptor-like kinase ARK1A...	81	7e-37
	emb AW687267 AW687267 NF007G07RT1F1055 Developing root Medicago ...	140	8e-37
	emb AW648736 AW648736 EST327106 tomato germinating seedlings, TA...	98	1e-36
	emb AW650851 AW650851 EST329305 tomato germinating seedlings, TA...	126	2e-36
20	Query= AB023448.2_s_at12332_s_at /id_source genbank /description dbj baa82810.1 (ab023448) basic endochitinase [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi (1008 letters)		
25	Database: plantfungal 661,018 sequences; 426,114,510 total letters		
	Searching.....done		
30	Score E Sequences producing significant alignments: (bits) Value		
	emb AF135130 AF135130 Arabis holboellii from Denmark class I chi...	438	0.0
	emb X16939 NTECHITR Nicotiana tabacum mRNA for endochitinase (EC...	491	e-158
35	gb M15173 TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial...	494	e-158
	gb S44869 S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ...	490	e-158
	emb A16119 A16119 Intracellular chitinase mRNA (SEQ ID NO: 2).	493	e-158
	emb X15494 STCHITIN Potato endochitinase gene (EC 3.2.1.14).	541	e-153
	emb X07130 STCHIT Solanum tuberosum mRNA for endochitinase (EC 3...	541	e-153
40	emb Y10373 MTCHITIN1 M.truncatula mRNA for chitinase.	482	e-151
	gb U02606 STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par...	442	e-150
	gb U02605 STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par...	443	e-150
	emb Z15140 LECHI9 L.esculentum mRNA for chitinase.	442	e-149
	gb U02607 STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par...	440	e-148
45	emb Z78202 PACHI1 Persea americana mRNA for endochitinase.	467	e-148
	gb U83592 MSU83592 Medicago sativa class I chitinase mRNA, compl...	310	e-146
	gb U83591 MSU83591 Medicago sativa class I chitinase mRNA, compl...	310	e-146
	gb L37876 PEACHI2I Pisum sativum chitinase class I (chi2) gene, ...	309	e-146
	emb AF000966 AF000966 Poa pratensis chitinase (Chi2) gene, compl...	472	e-146
50	emb Z54234 VVCHIT1MR V.vinifera mRNA for chitinase.	463	e-146
	gb M13968 PHVCHM P.vulgaris chitinase mRNA, complete cds.	286	e-145
	emb AJ012821 CAR012821 Cicer arietinum mRNA for class I chitinase.	305	e-144
	emb X76041 TACHIG T.aestivum (Chinese spring) chi gene for endoc...	466	e-144
	gb U78888 GHU78888 Gossypium hirsutum class I endochitinase mRNA...	332	e-144
55	emb AF034566 AF034566 Gossypium hirsutum class I chitinase mRNA,...	333	e-144
	emb AF000965 AF000965 Poa pratensis chitinase (Chi3) pseudogene ...	469	e-144
	emb X14133 STENCHIT Potato mRNA fragment for endochitinase (EC 3...	435	e-143
	gb S43926 S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa...	284	e-143
	emb X88800 VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p...	296	e-143
60	gb U02287 HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen...	459	e-141
	gb M94106 ALCCHINTIA Allium sativum chitinase mRNA, 3' end.	455	e-140

- gb|M94105|ALCCHITIN *Allium sativum* chitinase mRNA, 3' end. 448 e-140
 emb|AB015655|AB015655 *Cucurbita* sp. mRNA for chitinase, complete... 286 e-139
 emb|AF000964|AF000964 *Poa pratensis* chitinase (Chi1) gene, compl... 408 e-139
 gb|L34211|BLYCHI33A *Hordeum vulgare* chitinase (CHI33) gene, comp... 448 e-138
 5 gb|U02608|STU02608 *Solanum tuberosum* chitinase (chtB4) mRNA, par... 408 e-137
 emb|X63899|PSCHITIN *P. sativum* mRNA for chitinase. 270 e-135
 emb|AF061805|AF061805 *Elaeagnus umbellata* acidic chitinase mRNA,... 430 e-134
 emb|AF202731|AF202731 *Glycine max* endochitinase homolog (Chn1) m... 273 e-134
 gb|L34210|BLYCHI26A *Hordeum vulgare* chitinase (CHI26) gene, comp... 475 e-133
 10 emb|A37990|A37990 Sequence 9 from Patent EP0616035. 475 e-133
 gb|M62904|BLYCHI H. *vulgare* L. 26kD chitinase mRNA, complete cds. 475 e-133
 emb|AF098302|AF098302 *Brassica juncea* chitinase mRNA, complete cds. 265 e-132
 gb|U30324|TCU30324 *Theobroma cacao* class I chitinase gene, compl... 238 e-131
 emb|X95610|CSHITIB *C. sativa* mRNA for chitinase Ib. 259 e-130
 15 gb|U48687|CSU48687 *Castanea sativa* endochitinase mRNA, complete ... 259 e-130
 emb|AF141372|AF141372 *Petroselinum crispum* chitinase precursor (... 463 e-130
 emb|AF135137|AF135137 *Arabis fecunda* country USA class I chitina... 459 e-128
 emb|AF061806|AF061806 *Elaeagnus umbellata* basic chitinase mRNA, ... 297 e-128
 emb|AB023464|AB023464 *Arabis gemmifera* ChiB gene for basic endoc... 455 e-127
 20 emb|AF135152|AF135152 *Arabis parishii* country USA class I chitin... 455 e-127
 emb|AF135141|AF135141 *Arabis gunnisoniana* class I chitinase gene... 455 e-127
 emb|AF135135|AF135135 *Arabis drummondii* class I chitinase gene, ... 455 e-127
 emb|AF135143|AF135143 *Arabis lemmonii* country USA class I chitin... 452 e-126
 emb|X67693|STMREN *S. tuberosum* mRNA for endochitinase. 452 e-126
 25 emb|AF135132|AF135132 *Arabis gunnisoniana* from USA class I chiti... 452 e-126
 emb|AF135144|AF135144 *Arabis lemmonii* country USA class I chitin... 451 e-126
 emb|AF135140|AF135140 *Arabis glabra* country USA class I chitinas... 449 e-125
 gb|U30465|LEU30465 *Lycopersicon esculentum* class II chitinase (C... 447 e-125
 emb|AF135153|AF135153 *Arabis parishii* country USA class I chitin... 445 e-124
 30 gb|L22032|ULMCHITIN *Ulmus americana* chitinase (pHS2) mRNA, compl... 295 e-124
 emb|AF135148|AF135148 *Arabis lyallii* class I chitinase gene, par... 444 e-124
 emb|AF135151|AF135151 *Arabis microphylla* country USA class I chi... 444 e-124
 emb|AF135150|AF135150 *Arabis microphylla* country USA class I chi... 443 e-124
 emb|AF135147|AF135147 *Arabis lignifera* country USA class I chiti... 443 e-124
 35 emb|AF135136|AF135136 *Arabis fecunda* country USA class I chitina... 443 e-124
 emb|AF135145|AF135145 *Arabis lignifera* country USA class I chiti... 443 e-123
 emb|AF135146|AF135146 *Arabis lignifera* country USA class I chiti... 441 e-123
 emb|AF135149|AF135149 *Arabis microphylla* class I chitinase gene,... 441 e-123
 emb|AF043247|AF043247 *Solanum tuberosum* class I chitinase (ChtC1... 431 e-122
 40 emb|AF043248|AF043248 *Solanum tuberosum* class I chitinase (ChtC2... 431 e-122
 emb|Z15138|LECHI14 *L. esculentum* mRNA for chitinase (partial). 439 e-122
 emb|AF135142|AF135142 *Halimolobos perplexa* var. *perplexa* class I... 435 e-121
 emb|AF135134|AF135134 *Arabis blepharophylla* class I chitinase ge... 434 e-121
 gb|U01660|U01660 *Populus trichocarpa* x *Populus deltoides* acidic ... 207 e-121
 45 emb|AF135138|AF135138 *Arabis glabra* country USA class I chitinas... 431 e-120
 emb|AF135133|AF135133 *Arabis blepharophylla* country USA class I ... 423 e-118
 gb|M95835|BNACH25A *Brassica napus* (clone BnCh25) endochitinase g... 422 e-117
 emb|AW034530|AW034530 EST278146 tomato callus, TAMU *Lycopersicon*... 418 e-116
 emb|AW560048|AW560048 EST315096 DSIR *Medicago truncatula* cDNA cl... 350 e-112
 50 emb|AW687771|AW687771 NF013C08RT1F1065 Developing root *Medicago* ... 311 e-111
 emb|AW033115|AW033115 EST276674 tomato callus, TAMU *Lycopersicon*... 391 e-108
 emb|AW034645|AW034645 EST278376 tomato callus, TAMU *Lycopersicon*... 366 e-106
 emb|AF082713|AF082713 AF082713 *Capsicum annuum* leaf mRNA *Capsicu*... 364 e-106
 emb|AW738053|AW738053 EST339480 tomato flower buds, anthesis, Co... 379 e-104
 55 emb|AF141373|AF141373 *Petroselinum crispum* chitinase precursor (... 237 e-104
 emb|Z70032|CSACHIT2 *C. sinensis* mRNA for class II acidic chitinase. 197 e-104
 emb|AW030745|AW030745 EST274000 tomato callus, TAMU *Lycopersicon*... 360 e-104
 emb|AF141374|AF141374 *Petroselinum crispum* chitinase precursor (... 237 e-104
 emb|AW033034|AW033034 EST276593 tomato callus, TAMU *Lycopersicon*... 367 e-103
 60 emb|AW216454|AW216454 EST295084 tomato callus, TAMU *Lycopersicon*... 373 e-102
 emb|AW267781|AW267781 EST305909 DSIR *Medicago truncatula* cDNA cl... 316 e-102

emb|AW033757|AW033757 EST277328 tomato callus, TAMU Lycopersicon... 285 e-101
 emb|AW037673|AW037673 EST279276 tomato mixed elicitor, BTI Lycop... 281 e-100
 emb|AW216787|AW216787 EST295501 tomato callus, TAMU Lycopersicon... 364 e-100
 emb|AI771248|AI771248 EST252264 tomato ovary, TAMU Lycopersicon ... 363 1e-99
 5 emb|AW031102|AW031102 EST274409 tomato callus, TAMU Lycopersicon... 275 1e-98
 emb|X15349|HVENDCHT Barley (H.vulgare) mRNA for endochitinase. 359 2e-98
 emb|AW622028|AW622028 EST312826 tomato root during/after fruit s... 269 9e-97
 emb|Z15139|LECHI17 L.esculentum mRNA for chitinase. 242 2e-96
 emb|AW032161|AW032161 EST275615 tomato callus, TAMU Lycopersicon... 334 2e-96
 10 emb|AW560177|AW560177 EST315225 DSIR Medicago truncatula cDNA cl... 295 1e-95

Query= AL021637.176_s_at 12341_s_at /id_source genbank /description
 emb|caal6619.1| (al021637) vacuolar sorting receptor-like protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 15 /gb_link /ncgi
 (1881 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

20

Searching.....done

	Score	E	(bits)	Value
25	Sequences producing significant alignments:			
	gb U79958 PSU79958	Pisum sativum BP-80 vacuolar sorting receptor...	810	0.0
	emb AB006809 AB006809	Cucurbita sp. mRNA for PV72, complete cds.	780	0.0
	emb AW267745 AW267745	EST305873 DSIR Medicago truncatula cDNA cl...	453	e-126
	emb AW931583 AW931583	EST357426 tomato fruit mature green, TAMU...	308	e-112
30	emb AW309187 AW309187	sg05d06.y1 Gm-cl019 Glycine max cDNA clone...	405	e-112
	gb BE054150 BE054150	GA_Ea0034H17f Gossypium arboreum 7-10 dpa ...	398	e-110
	emb AW622833 AW622833	EST306903 tomato flower buds 3-8 mm, Corne...	387	e-106
	emb AW689392 AW689392	NF018F12ST1F1000 Developing stem Medicago ...	371	e-102
	emb AW737948 AW737948	EST339375 tomato flower buds, anthesis, Co...	342	3e-94
35	emb AW774434 AW774434	EST333585 KV3 Medicago truncatula cDNA clo...	263	2e-90
	emb AW932529 AW932529	EST358372 tomato fruit mature green, TAMU ...	326	3e-88
	emb AW615949 AW615949	EST325315 tomato flower buds 0-3 mm, Corne...	216	1e-87
	emb AI728635 AI728635	BNLGH11276 Six-day Cotton fiber Gossypium...	281	8e-84
	emb AI782787 AI782787	EST263666 tomato susceptible, Cornell Lyco...	307	2e-82
40	emb AI443067 AI443067	sa47a01.y1 Gm-cl004 Glycine max cDNA clone...	305	6e-82
	emb AW747297 AW747297	WS1_67_G06.b1_A002 Water-stressed 1 (WS1) ...	292	8e-78
	emb AI727826 AI727826	BNLGH19195 Six-day Cotton fiber Gossypium ...	280	1e-77
	emb AI484571 AI484571	EST242801 tomato ovary, TAMU Lycopersicon ...	284	1e-75
	emb AW685785 AW685785	NF030C07NR1F1000 Nodulated root Medicago t...	166	1e-71
45	emb AV406766 AV406766	AV406766 Lotus japonicus young plants (two...	260	2e-68
	emb AW509740 AW509740	ga63h11.y1 Moss EST library PPU Physcomitr...	232	1e-65
	emb AV428420 AV428420	AV428420 Lotus japonicus young plants (two...	249	4e-65
	emb AW695542 AW695542	NF096C05ST1F1037 Developing stem Medicago ...	124	1e-58
	emb AW289687 AW289687	NXNV004E04F Nsf Xylem Normal wood Vertical...	226	4e-58
50	emb AW064744 AW064744	ST35C06 Pine TriplEx shoot tip library Pin...	198	2e-56
	emb AW309191 AW309191	sg05d10.y1 Gm-cl019 Glycine max cDNA clone...	171	3e-52
	emb AW096632 AW096632	EST289812 tomato mixed elicitor, BTI Lycop...	165	7e-52
	emb AW568619 AW568619	si60a11.y1 Gm-r1030 Glycine max cDNA clone...	205	1e-51
	emb AF209910 AF209910	Prunus dulcis vacuolar sorting receptor pr...	160	5e-51
55	emb AW623959 AW623959	EST321904 tomato flower buds 3-8 mm, Corne...	75	1e-50
	emb AW397829 AW397829	sg68h03.y1 Gm-cl007 Glycine max cDNA clone...	201	2e-50
	emb AW256542 AW256542	EST304679 KV2 Medicago truncatula cDNA clo...	151	2e-50
	emb AI967865 AI967865	Ljirmp14-100-f3 Ljirmp Lambda HybriZap ...	197	3e-49
	emb AW680054 AW680054	WS1_3_A01.g1_A002 Water-stressed 1 (WS1) S...	150	6e-47
60	emb AA660289 AA660289	00158 MtrHE Medicago truncatula cDNA 5', m...	107	9e-44
	emb AW056624 AW056624	ST53G07 Pine TriplEx shoot tip library Pin...	178	1e-43

	emb AW690002 AW690002 NF026G04ST1F1000 Developing stem Medicago ...	109	2e-43
	emb AW290400 AW290400 NXNV019G06F Nsf Xylem Normal wood Vertical...	177	3e-43
	emb AI162330 AI162330 A016P01U Hybrid aspen plasmid library Popu...	131	2e-39
	emb AI161766 AI161766 A006P54U Hybrid aspen plasmid library Popu...	93	3e-38
5	emb AW737369 AW737369 EST338892 tomato flower buds, anthesis, Co...	149	5e-35
	gb BE125908 BE125908 DG1_59_E01.b1_A002 Dark Grown 1 (DG1) Sorgh...	149	5e-35
	emb AW201441 AW201441 sf03b09.y1 Gm-c1027 Glycine max cDNA clone...	113	1e-34
	emb AW398931 AW398931 EST309431 L. pennellii trichome, Cornell U...	95	2e-34
	gb BE049814 BE049814 NXNV_144_F04_F Nsf Xylem Normal wood Vertic...	143	6e-33
10	emb AW126100 AW126100 N100297e rootphos(-) Medicago truncatula c...	100	5e-30
	emb AW508719 AW508719 si35f03.y1 Gm-r1030 Glycine max cDNA clone...	125	1e-27
	gb L38113 L38113 BNAF0628E Mustard flower buds Brassica rapa cDN...	117	4e-26
	emb AW317388 AW317388 sg48g10.y1 Gm-c1025 Glycine max cDNA clone...	80	1e-25
	emb AW706755 AW706755 sk02f10.y1 Gm-c1023 Glycine max cDNA clone...	118	2e-25
15	emb AA660955 AA660955 00852 MtRHE Medicago truncatula cDNA 5' si...	74	7e-25
	emb AW616461 AW616461 EST322872 L. hirsutum trichome, Cornell Un...	69	2e-24
	emb AW348825 AW348825 GM210003B11E6R Gm-r1021 Glycine max cDNA 3...	68	8e-24
	emb AW932524 AW932524 EST358367 tomato fruit mature green, TAMU ...	80	1e-23
	emb AW774190 AW774190 EST333273 KV3 Medicago truncatula cDNA clo...	101	2e-20
20	emb AW125944 AW125944 N100139e rootphos(-) Medicago truncatula c...	66	6e-20
	emb AW093844 AW093844 EST287024 tomato mixed elicitor, BTI Lycop...	96	7e-19
	emb AW906386 AW906386 EST342508 potato stolon, Cornell Universit...	67	2e-16
	gb BE060808 BE060808 HVSMEg0013H06f Hordeum vulgare pre-anthesis...	87	4e-16
	emb AW620693 AW620693 sj08d10.y1 Gm-c1032 Glycine max cDNA clone...	76	1e-15
25	emb AW256398 AW256398 EST304465 KV2 Medicago truncatula cDNA clo...	74	6e-14
	emb AW037563 AW037563 EST278890 tomato mixed elicitor, BTI Lycop...	79	8e-14
	emb AW691052 AW691052 NF037B05ST1F1000 Developing stem Medicago ...	72	4e-13
	emb AW686287 AW686287 NF040A08NR1F1000 Nodulated root Medicago t...	77	4e-13
	emb AW685952 AW685952 NF036G09NR1F1000 Nodulated root Medicago t...	46	2e-11
30	emb AW760128 AW760128 sl58d09.y1 Gm-c1027 Glycine max cDNA clone...	58	1e-10
	emb AW119909 AW119909 sd54d08.y1 Gm-c1016 Glycine max cDNA clone...	66	8e-10
	emb AI794754 AI794754 sb68f11.y1 Gm-c1019 Glycine max cDNA clone...	64	4e-09
	emb AW774852 AW774852 EST334003 KV3 Medicago truncatula cDNA clo...	64	4e-09
	emb AW127457 AW127457 M110648 DSIL Medicago truncatula cDNA clon...	58	3e-07
35	emb AW443352 AW443352 EST308282 tomato mixed elicitor, BTI Lycop...	56	1e-06
	emb AW747372 AW747372 WS1_67_G06.g1_A002 Water-stressed 1 (WS1) ...	55	2e-06
	emb AI939286 AI939286 sc69h02.y1 Gm-c1016 Glycine max cDNA clone...	46	0.001
	emb AF198615 AF198615 Neospora caninum microneme protein Nc-P38 ...	43	0.009
	emb AI822258 AI822258 L0-701T3 Ice plant Lambda Uni-Zap XR expre...	36	0.019
40	gb BE035779 BE035779 MO16H05 MO Mesembryanthemum crystallinum cD...	36	0.025
	emb AI822869 AI822869 L30-712T3 Ice plant Lambda Uni-Zap XR expr...	36	0.025
	emb AI822754 AI822754 L0-1287T3 Ice plant Lambda Uni-Zap XR expr...	36	0.025
	emb AI756736 AI756736 EtESTea24h07.y1 Eimeria S5-2 Sporozoite st...	34	0.035
	gb M36941 BLYHORDCA Hordeum vulgare C-hordein gene, complete cds.	33	0.079
45	emb AU036628 AU036628 Schizosaccharomyces pombe genomic clone ha...	40	0.083
	emb AA948752 AA948752 L0-271M13R Ice plant Lambda Uni-Zap XR exp...	35	0.086
	emb AW760788 AW760788 sl35a03.y1 Gm-c1027 Glycine max cDNA clone...	39	0.11
	emb AW830924 AW830924 sm19c06.y1 Gm-c1027 Glycine max cDNA clone...	39	0.11
	emb AQ008266 AQ008266 CpG0480B CpIOWAgDNA1 Cryptosporidium parvu...	39	0.16
50	emb AW696326 AW696326 NF106G11ST1F1087 Developing stem Medicago ...	38	0.21
	emb AI974517 AI974517 T110467e KV0 Medicago truncatula cDNA clon...	38	0.21
	emb AV408651 AV408651 AV408651 Lotus japonicus young plants (two...	38	0.21
	emb AQ651638 AQ651638 Sheared DNA-7G23.TF Sheared DNA Trypanosom...	37	0.40
	emb AQ942781 AQ942781 Sheared DNA-42B17.TF Sheared DNA Trypanoso...	37	0.56
55	gb BE036036 BE036036 MO18H02 MO Mesembryanthemum crystallinum cD...	36	0.76
	gb C95899 C95899 C95899 Marchantia polymorpha immature sex organ...	36	1.0
	emb AA966307 AA966307 v8c01a1.r1 Aspergillus nidulans 24hr asexu...	36	1.0
	emb AI759219 AI759219 EtESTea26c02.y1 Eimeria S5-2 Sporozoite st...	28	1.3
	gb UI1583 YSCH9196 Saccharomyces cerevisiae chromosome VIII cosm...	35	1.4
60	emb AQ639257 AQ639257 927P1-10E12.TV 927P1 Trypanosoma brucei ge...	35	1.4
	emb AQ943504 AQ943504 Sheared DNA-43F22.TF Sheared DNA Trypanoso...	35	1.4

emb|AW623282|AW623282 EST321227 tomato flower buds 3-8 mm, Corne... 35 1.4
 dbj|D85226|D85226 Brassica campestris DNA for S glycoprotein, pa... 28 1.6
 emb|AF001525|AF001525 Musa acuminata ripening-associated protein... 35 2.0

5 Query= X84728.6_s_at 12349_s_at /id_source genbank /description
 gb|aaa17993.1| (m91192) phenylalanine ammonia-lyase [trifolium
 subterraneum] /blast_score 0 /ec_number /family /chip nova /gb_link
 /ncgi
 (1962 letters)

10

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

15

Score E

Sequences producing significant alignments: (bits) Value

20 gb|L11747|POPPALGA Populus tricocarpa X Populus deltoides (hybri... 354 0.0
 emb|X99997|BFPAL B.finlaysoniana mRNA for phenylalanine ammonia-... 352 0.0
 emb|X58180|MSPAL M.sativa PAL mRNA for phenylalanine ammonia-lyase. 351 0.0
 gb|U43338|CLU43338 Citrus limon phenylalanine ammonia-lyase (pal... 350 0.0
 gb|L36822|SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas... 350 0.0
 emb|AF036948|AF036948 Prunus avium phenylalanine ammonia-lyase (... 349 0.0
 25 emb|AJ250836|CAR250836 Cicer arietinum mRNA for phenylalanine am... 349 0.0
 emb|X17462|PCPAL4 P.crispum RNA for PAL4, phenylalanine ammonia-... 349 0.0
 emb|X81158|PCPAL2 P.crispum mRNA for phenylalanine ammonia-lyase 2. 349 0.0
 emb|X81159|PCPAL3 P.crispum mRNA for phenylalanine ammonia-lyase 3. 348 0.0
 dbj|D83075|D83075 Lithospermum erythrorhizon mRNA for phenylalan... 348 0.0
 30 emb|AF237955|AF237955 Rubus idaeus phenylalanine ammonia-lyase 2... 348 0.0
 emb|AJ002221|DLJ002221 Digitalis lanata mRNA for phenylalanine a... 347 0.0
 gb|M29232|IPBPAL Sweet potato phenylalanine ammonia-lyase mRNA (... 345 0.0
 dbj|D26596|CMEPAL Camellia sinensis mRNA for phenylalanine ammon... 344 0.0
 dbj|D17467|TOBPAL1 Tobacco mRNA for phenylalanine ammonia-lyase,... 344 0.0
 35 emb|X78269|NTPHEAL N.tabacum (Samsun NN) mRNA for phenylalanine ... 343 0.0
 dbj|D83076|D83076 Lithospermum erythrorhizon mRNA for phenylalan... 343 0.0
 dbj|D78640|IPBPALA Ipomoea batatas mRNA for phenylalanine ammoni... 342 0.0
 emb|Y12461|HAPHAMLY Helianthus annuus mRNA for phenylalanine amm... 341 0.0
 emb|AB042520|AB042520 Catharanthus roseus mRNA for phenylalanine... 339 0.0
 40 emb|AF237954|AF237954 Rubus idaeus phenylalanine ammonia-lyase 1... 330 0.0
 dbj|D10001|PEAPAL P.sativum mRNA for phenylalanine ammonia-lyase... 349 0.0
 emb|X63103|STPAL1 S.tuberosum PAL-1 gene for phenylalanine ammon... 353 0.0
 emb|AJ238754|CCL238754 Citrus clementina X Citrus reticulata mRN... 350 0.0
 emb|AJ238753|CCL238753 Citrus clementina X Citrus reticulata mRN... 353 0.0
 45 dbj|D10003|PEAPAL2 P.sativum gene for phenylalanine ammonia-lyas... 349 0.0
 dbj|E04042|E04042 cDNA sequence coding for pea phenylalanine amm... 349 0.0
 emb|AF165998|AF165998 Vigna unguiculata phenylalanine ammonia-ly... 355 0.0
 gb|U16130|PAU16130 Persea americana phenylalanine ammonia lyase ... 331 0.0
 dbj|D30656|POPPALA Populus kitakamiensis gene for phenylalanine ... 356 0.0
 50 gb|M84466|TOBTPA1A Tobacco phenylalanine ammonialyase (tpal) gen... 352 0.0
 emb|AB008200|AB008200 Nicotiana tabacum palB gene for phenylalan... 352 0.0
 dbj|D85850|D85850 Daucus carota gDcPAL1 gene for phenylalanine a... 347 0.0
 emb|X52953|DMPAL1 Glycine max PAL1 gene for phenylalanine ammoni... 355 0.0
 emb|X99705|TAPALGEN1 T.aestivum PAL gene. 342 0.0
 55 gb|M91192|TFRPAL1X Trifolium subterraneum phenylalanine ammonia-... 345 0.0
 gb|M90692|TOMPAL5A Lycopersicon esculentum phenylalanine ammonia... 347 0.0
 emb|AB008199|AB008199 Nicotiana tabacum palA gene for phenylalan... 344 0.0
 emb|Y07654|PCPAL1 P.crispum pal1 gene. 350 0.0
 emb|X16772|PCPAL1EX2 P.crispum PAL-1 gene for phenylalanine ammo... 350 0.0
 60 dbj|D43803|POPPALG4B Populus kitakamiensis gene for phenylalanin... 336 0.0
 gb|M83314|TOMPHEAMLY Lycopersicon esculentum phenylalanine ammon... 353 0.0

- emb|X76130|CMPAL C.melo (cantaloupe) pal mRNA. 318 0.0
 dbj|D30657|POPPALB Populus kitakamiensis gene for phenylalanine ... 333 0.0
 dbj|D43802|POPPALG2BA Populus kitakamiensis gene for phenylalani... 336 0.0
 emb|AF081215|AF081215 Capsicum chinense phenylalanine ammonia-ly... 346 0.0
 5 dbj|D10002|PEAPAL1 P.sativum gene for phenylalanine ammonia-lyas... 349 0.0
 emb|Z49147|HVPAL7RM H.vulgare partial PAL mRNA for phenylalanine... 342 0.0
 emb|X63104|STPAL2 S.tuberosum PAL-2 gene for phenylalanine ammon... 353 0.0
 gb|U39792|PTU39792 Pinus taeda phenylalanine ammonia-lyase (lpPA... 311 0.0
 gb|M11939|PHVPAL Phaseolus vulgaris L. phenylalanine ammonia-lya... 354 0.0
 10 dbj|E04043|E04043 cDNA sequence coding for kidney bean phenylala... 354 0.0
 emb|AB015871|AB015871 Vitis vinifera gene for phenylalanine ammo... 350 0.0
 emb|Z49145|HVPAL2MR H.vulgare partial PAL mRNA for phenylalanine... 341 0.0
 emb|Z49146|HVPAL3MR H.vulgare partial PAL mRNA for phenylalanine... 311 0.0
 emb|X75967|VVPAL V.vinifera PAL mRNA for phenylalanine ammonia l... 350 0.0
 15 gb|S46988|S46988 phenylalanine ammonia-lyase [soybeans, mRNA, 14... 344 0.0
 emb|AF206634|AF206634 Prunus persica cultivar Loring phenylalani... 336 0.0
 emb|AF167487|AF167487 Eucalyptus globulus phenylalanine ammonia ... 334 e-178
 emb|X99725|TAPALGEN2 T.aestivum PAL gene, coding region. 300 e-137
 emb|AW218834|AW218834 EST301314 tomato root during/after fruit s... 347 e-134
 20 emb|AW031612|AW031612 EST275066 tomato callus, TAMU Lycopersicon... 327 e-132
 emb|AJ289609|BPE289609 Betula pendula partial pal gene for pheny... 205 e-128
 emb|AJ278116|BPE278116 Betula pendula partial pal gene for phen... 205 e-128
 emb|AW219303|AW219303 EST301785 tomato root during/after fruit s... 339 e-126
 emb|AW726548|AW726548 GA__Ea0022A01 Gossypium arboreum 7-10 dpa ... 323 e-124
 25 emb|AI166817|AI166817 xylem.est.611 Poplar xylem Lambda ZAPII li... 251 e-117
 gb|BE035366|BE035366 MM06H04 MM Mesembryanthemum crystallinum cD... 235 e-115
 emb|AW776946|AW776946 EST336011 DSIL Medicago truncatula cDNA cl... 280 e-114
 gb|BE020072|BE020072 sm38f08.y1 Gm-c1028 Glycine max cDNA clone ... 233 e-112
 emb|AF019965|AF019965 Pinus monticola phenylalanine ammonia lyas... 205 e-110
 30 emb|AF218453|AF218453 Coffea arabica clone 369.1.6r phenylalanin... 247 e-105
 emb|AW216505|AW216505 EST295219 tomato callus, TAMU Lycopersicon... 209 e-104
 emb|AI166477|AI166477 xylem.est.305 Poplar xylem Lambda ZAPII li... 291 e-100
 emb|AV428905|AV428905 AV428905 Lotus japonicus young plants (two... 243 1e-98
 emb|AW220322|AW220322 EST302805 tomato root during/after fruit s... 255 2e-98
 35 emb|AW734312|AW734312 sk81e07.y1 Gm-c1016 Glycine max cDNA clone... 324 6e-98
 emb|AW034774|AW034774 EST278810 tomato callus, TAMU Lycopersicon... 325 3e-93
 emb|AW329762|AW329762 N201031e rootphos(-) Medicago truncatula c... 337 1e-91
 emb|AI777483|AI777483 EST258362 tomato susceptible, Cornell Lyco... 294 3e-90
 emb|AW621418|AW621418 EST312216 tomato root during/after fruit s... 330 2e-89
 40 emb|AW443181|AW443181 EST308111 tomato mixed elicitor, BTI Lycop... 329 6e-89
 emb|AW781748|AW781748 sl90e11.y1 Gm-c1037 Glycine max cDNA clone... 326 3e-88
 emb|X68126|MSPALMR Malus sp. PAL mRNA for phenylalanine ammonia-... 324 1e-87
 emb|AW760268|AW760268 sl48b08.y1 Gm-c1027 Glycine max cDNA clone... 323 3e-87
 emb|AW278641|AW278641 sf63c08.y1 Gm-c1013 Glycine max cDNA clone... 316 4e-85
 45 emb|AF218454|AF218454 Coffea arabica clone 430.4 phenylalanine a... 243 6e-85
 emb|AI899698|AI899698 EST269141 tomato susceptible, Cornell Lyco... 314 2e-84
 emb|AW455294|AW455294 EST311832 tomato root during/after fruit s... 313 3e-84
 emb|AW685111|AW685111 NF026A05NR1F1000 Nodulated root Medicago t... 236 6e-84
 emb|AW667320|AW667320 GA__Ea0008P06 Gossypium arboreum 7-10 dpa ... 189 2e-83
 50 gb|BE021354|BE021354 sm57e05.y1 Gm-c1028 Glycine max cDNA clone ... 308 9e-83
 emb|AI772657|AI772657 EST253757 tomato resistant, Cornell Lycop... 299 2e-80
 emb|AI894514|AI894514 EST263957 tomato callus, TAMU Lycopersicon... 294 1e-78
 gb|L11883|WHTWALI4A Triticum aestivum phenylalanine ammonia-lyas... 87 4e-16
- 55 Query= AL022347.131_at 12360_at /id_source genbank /description
 emb|caa18468.1| (al022347) serine/threonine kinase-like protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022347| /ncgi -
 60 http://www.ncgr.org/cgi-bin/ff?al022347
 (1554 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5 Searching.....done

		Score	E	
	Sequences producing significant alignments:	(bits)	Value	
10	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k...	251	1e-65	
	gb BE034949 BE034949 ML07F03 ML Mesembryanthemum crystallinum cD...	231	8e-60	
	emb AW031255 AW031255 EST274630 tomato callus, TAMU Lycopersicon...	231	1e-59	
	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2.	230	2e-59	
	emb Y18260 BOY18260 Brassica oleracea mRNA for SRK15 protein, pa...	227	1e-58	
15	emb AB024416 AB024416 Brassica oleracea SRK2-b mRNA, complete cds.	226	4e-58	
	emb AB008191 AB008191 Brassica rapa mRNA for SRK29, complete cds.	225	7e-58	
	emb Y18259 BOY18259 Brassica oleracea mRNA for SRK5 protein, par...	225	7e-58	
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	224	1e-57	
	gb BE034855 BE034855 ML05C11 ML Mesembryanthemum crystallinum cD...	186	1e-57	
20	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	222	6e-57	
	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	221	8e-57	
	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	221	2e-56	
	gb BE057261 BE057261 sm99f12.y1 Gm-c1015 Glycine max cDNA clone ...	220	3e-56	
	emb Y14285 BOY14285 Brassica oleracea mRNA for SFR1 protein.	219	6e-56	
25	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR...	218	8e-56	
	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	216	3e-55	
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	215	5e-55	
	emb AF088885 AF088885 Nicotiana tabacum receptor-like kinase CHR...	213	3e-54	
	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti...	211	1e-53	
30	emb Y12531 BOBRLKGEN B.oleraceae gene encoding serine/threonine ...	116	6e-53	
	emb AB032474 AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc...	207	2e-52	
	emb Y14286 BOY14286 Brassica oleracea SFR3 gene, partial.	117	1e-51	
	dbj D38564 BOLRPKB Brassica campestris mRNA for receptor protein...	204	1e-51	
	emb AW736407 AW736407 EST332421 KV3 Medicago truncatula cDNA clo...	198	4e-51	
35	dbj D38563 BOLRPKA Brassica campestris mRNA for receptor protein...	202	7e-51	
	gb U20948 ITU20948 Ipomoea trifida receptor protein kinase (IRK1...	201	1e-50	
	emb AI896155 AI896155 EST265598 tomato callus, TAMU Lycopersicon...	166	1e-50	
	dbj D30049 BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti...	196	2e-49	
	emb AW760240 AW760240 sl59g07.y1 Gm-c1027 Glycine max cDNA clone...	196	4e-49	
40	emb AW033458 AW033458 EST277029 tomato callus, TAMU Lycopersicon...	196	4e-49	
	emb AB024420 AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,...	114	4e-48	
	emb AJ245480 BNA245480 Brassica napus slg gene for S-locus glyco...	113	7e-48	
	emb Y12530 BOARLKGEN B.oleraceae gene encoding serine/threonine ...	115	1e-47	
	emb Z18921 BOSRKL B.oleracea gene for S-receptor kinase-like pro...	111	2e-47	
45	emb AB024422 AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ...	112	3e-47	
	emb AB000970 AB000970 Brassica campestris gene for receptor kina...	111	3e-47	
	emb X79432 BOSRK3 B.oleracea SRK3 gene.	107	6e-47	
	emb Z30211 BOSRK29G B.oleracea (alboglabra) srk29 gene.	108	6e-47	
	emb AB013718 AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,...	111	2e-46	
50	emb AW684339 AW684339 NF015G04NR1F1000 Nodulated root Medicago t...	120	3e-46	
	emb AB000971 AB000971 Brassica campestris pseudogene for recepto...	105	8e-46	
	emb AI895838 AI895838 EST265281 tomato callus, TAMU Lycopersicon...	184	2e-45	
	emb AW039406 AW039406 EST281663 tomato mixed elicitor, BTI Lycop...	107	3e-45	
	emb AJ245479 BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,...	106	4e-45	
55	emb AW034624 AW034624 EST278308 tomato callus, TAMU Lycopersicon...	182	6e-45	
	dbj D88193 D88193 Brassica rapa DNA for S-receptor kinase, compl...	109	9e-45	
	emb Z18884 BOSRKRPC B.oleracea encoding S-receptor kinase relate...	116	1e-43	
	emb AI775997 AI775997 EST257097 tomato resistant, Cornell Lycop...	177	2e-43	
	emb AI895623 AI895623 EST265066 tomato callus, TAMU Lycopersicon...	177	3e-43	
60	emb AI901283 AI901283 sc31d08.y1 Gm-c1014 Glycine max cDNA clone...	171	9e-42	
	emb AW706972 AW706972 sk20a03.y1 Gm-c1028 Glycine max cDNA clone...	171	9e-42	

emb|Z18861|BOSRK RPA B.oleracea encoding S-receptor kinase relate... 111 4e-41
emb|AW216673|AW216673 EST295387 tomato callus, TAMU Lycopersicon... 169 6e-41
emb|AW154835|AW154835 EST290228 tomato root deficiency, Cornell ... 169 6e-41
emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 97 3e-40
5 emb|AI898854|AI898854 EST268297 tomato ovary, TAMU Lycopersicon ... 163 4e-39
emb|AW620957|AW620957 sj98a07.y1 Gm-cl023 Glycine max cDNA clone... 162 7e-39
emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 160 4e-38
emb|AW667985|AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ... 96 2e-37
emb|Z18883|BOSRK RPB B.oleracea encoding S-receptor kinase relate... 156 3e-37
10 emb|Y16999|TCA16999 Theobroma cacao microsatellite DNA, clone mT... 116 5e-37
emb|AW455306|AW455306 EST311844 tomato root during/after fruit s... 124 9e-37
emb|AI730535|AI730535 BNLGHi7007 Six-day Cotton fiber Gossypium ... 80 1e-36
emb|AI967314|AI967314 Ljirmp00-017 Ljirmp Lambda HybriZap two... 94 3e-36
emb|AW223870|AW223870 EST300681 tomato fruit red ripe, TAMU Lyco... 96 6e-36
15 emb|AW224241|AW224241 EST300968 tomato fruit red ripe, TAMU Lyco... 96 6e-36
emb|AI486766|AI486766 EST245088 tomato ovary, TAMU Lycopersicon ... 110 8e-36
emb|AW934655|AW934655 EST353547 tomato flower buds 0-3 mm, Corne... 87 1e-34
emb|AW617954|AW617954 EST314028 L. pennellii trichome, Cornell U... 87 1e-34
dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 100 2e-34
20 dbj|E05046|E05046 DNA encoding ZmPK1 homologue protein in tobacco. 100 2e-34
emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 88 3e-34
emb|Z18862|BOSRK RPD B.oleracea encoding S-receptor kinase protein. 80 5e-34
emb|AI896183|AI896183 EST265626 tomato callus, TAMU Lycopersicon... 96 5e-34
emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 120 1e-33
25 emb|AI055189|AI055189 coau0003E19 Cotton Boll Abscission Zone cD... 91 1e-33
emb|AW694732|AW694732 NF079D07ST1F1061 Developing stem Medicago ... 144 2e-33
emb|AV422094|AV422094 AV422094 Lotus japonicus young plants (two... 102 2e-33
emb|AI937984|AI937984 sc06e07.y1 Gm-cl012 Glycine max cDNA clone... 144 2e-33
emb|AW756743|AW756743 sl26f10.y1 Gm-cl027 Glycine max cDNA clone... 143 3e-33
30 emb|AW290044|AW290044 NXNV009D10F Nsf Xylem Normal wood Vertical... 91 4e-33
emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 93 6e-33
emb|AI772117|AI772117 EST253217 tomato resistant, Cornell Lycope... 142 6e-33
emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 117 8e-33
emb|A67797|A67797 Sequence 2 from Patent WO9743427. 76 2e-32
35 gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor... 76 2e-32
emb|AW221202|AW221202 EST297671 tomato fruit mature green, TAMU ... 85 4e-32
emb|AI938653|AI938653 sb56g02.y1 Gm-cl018 Glycine max cDNA clone... 82 4e-32
emb|AW201125|AW201125 se98b06.y1 Gm-cl027 Glycine max cDNA clone... 86 5e-32
emb|AW697111|AW697111 NF112D03ST1F1028 Developing stem Medicago ... 83 7e-32
40 emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 138 8e-32
emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 138 8e-32
emb|AI938169|AI938169 sc40d07.y1 Gm-cl014 Glycine max cDNA clone... 138 1e-31
emb|AF085164|AF085164 Hordeum vulgare receptor-like kinase LRK10... 73 2e-31
emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 88 2e-31
45 emb|AW220677|AW220677 EST297146 tomato fruit mature green, TAMU ... 136 5e-31
emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 88 7e-31
emb|Z18863|BOSRK PGA B.oleracea S-receptor kinase pseudogene. 74 9e-31
emb|AI895816|AI895816 EST265259 tomato callus, TAMU Lycopersicon... 78 2e-30
Query= AF081067.3_s_at 12500_s_at /id_source genbank /description
50 gb|aac32192.1|(af081067) iaa-ala hydrolase; iaa-amino acid hydrolase
[arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
/gb_link /ncgi
(1323 letters)

55 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

60 Score E
Sequences producing significant alignments: (bits) Value

- emb|AW031251|AW031251 EST274626 tomato callus, TAMU Lycopersicon... 372 e-102
emb|AW032461|AW032461 EST276020 tomato callus, TAMU Lycopersicon... 363 2e-99
emb|AI938425|AI938425 sc45a04.y1 Gm-c1015 Glycine max cDNA clone... 347 1e-94
5 emb|AW930806|AW930806 EST356649 tomato fruit mature green, TAMU ... 346 2e-94
emb|AW930422|AW930422 EST340795 tomato fruit mature green, TAMU ... 346 3e-94
gb|BE123972|BE123972 EST394097 DSIL Medicago truncatula cDNA clo... 278 8e-92
emb|AW776450|AW776450 EST335515 DSIL Medicago truncatula cDNA cl... 324 1e-87
emb|AW034511|AW034511 EST278127 tomato callus, TAMU Lycopersicon... 323 2e-87
10 emb|AI965412|AI965412 sc71d05.y1 Gm-c1016 Glycine max cDNA clone... 322 3e-87
emb|AW185064|AW185064 se86c08.y1 Gm-c1023 Glycine max cDNA clone... 321 6e-87
emb|AI813025|AI813025 2H4 Pine Lambda Zap Xylem library Pinus ta... 321 6e-87
emb|AI895246|AI895246 EST264689 tomato callus, TAMU Lycopersicon... 317 1e-85
emb|AI896622|AI896622 EST266065 tomato callus, TAMU Lycopersicon... 312 3e-84
15 gb|BE021087|BE021087 sm55c04.y1 Gm-c1028 Glycine max cDNA clone ... 277 2e-78
emb|AW746042|AW746042 WS1_39_B06.b1_A002 Water-stressed 1 (WS1) ... 277 1e-73
gb|BE021086|BE021086 sm55c03.y1 Gm-c1028 Glycine max cDNA clone ... 276 2e-73
emb|AW934118|AW934118 EST359961 tomato fruit mature green, TAMU ... 274 1e-72
emb|AW649568|AW649568 EST328022 tomato germinating seedlings, TA... 264 1e-69
20 emb|AW694276|AW694276 NF074C12ST1F1097 Developing stem Medicago ... 261 1e-68
emb|AW719214|AW719214 LjNEST1c1r Lotus japonicus nodule library,... 257 1e-67
emb|AW279413|AW279413 sf79c03.y1 Gm-c1019 Glycine max cDNA clone... 253 1e-66
emb|AW032091|AW032091 EST275545 tomato callus, TAMU Lycopersicon... 252 6e-66
emb|AW233984|AW233984 sf32g07.y1 Gm-c1028 Glycine max cDNA clone... 242 6e-63
25 emb|AI729732|AI729732 BNLGHi14072 Six-day Cotton fiber Gossypium... 241 8e-63
emb|AW233987|AW233987 sf32g10.y1 Gm-c1028 Glycine max cDNA clone... 239 4e-62
emb|AW648744|AW648744 EST327198 tomato germinating seedlings, TA... 237 1e-61
emb|AW931177|AW931177 EST357020 tomato fruit mature green, TAMU ... 237 1e-61
emb|AW616709|AW616709 EST323120 L. hirsutum trichome, Cornell Un... 237 1e-61
30 emb|AW686159|AW686159 NF034F08NR1F1000 Nodulated root Medicago t... 231 7e-60
emb|AW234471|AW234471 sf25e09.y1 Gm-c1028 Glycine max cDNA clone... 227 2e-58
emb|AW266116|AW266116 L30-2803T3 Ice plant Lambda Uni-Zap XR exp... 178 3e-58
emb|AI727696|AI727696 BNLGHi8625 Six-day Cotton fiber Gossypium ... 216 5e-58
emb|AW201351|AW201351 sf02a12.y1 Gm-c1027 Glycine max cDNA clone... 183 3e-57
35 emb|AI728658|AI728658 BNLGHi11350 Six-day Cotton fiber Gossypium... 222 5e-57
emb|AW348121|AW348121 GM210001A11H6R Gm-r1021 Glycine max cDNA 3... 161 6e-56
emb|AW596930|AW596930 sj84f04.y1 Gm-c1034 Glycine max cDNA clone... 210 1e-53
emb|AW559656|AW559656 EST314768 DSIR Medicago truncatula cDNA cl... 208 1e-52
40 emb|AW220836|AW220836 EST297305 tomato fruit mature green, TAMU ... 204 1e-51
emb|AW782248|AW782248 sm03d05.y1 Gm-c1027 Glycine max cDNA clone... 204 1e-51
emb|AW775988|AW775988 EST335053 DSIL Medicago truncatula cDNA cl... 201 1e-50
emb|AI444000|AI444000 sa29b03.y1 Gm-c1004 Glycine max cDNA clone... 199 6e-50
emb|AW202407|AW202407 sf14f07.y1 Gm-c1027 Glycine max cDNA clone... 198 1e-49
45 emb|AI779032|AI779032 EST259911 tomato susceptible, Cornell Lyco... 198 1e-49
emb|AW035625|AW035625 EST281363 tomato callus, TAMU Lycopersicon... 197 1e-49
emb|AI782331|AI782331 EST263210 tomato susceptible, Cornell Lyco... 191 1e-47
emb|AI440607|AI440607 sa68d03.y1 Gm-c1004 Glycine max cDNA clone... 190 2e-47
emb|AW685271|AW685271 NF025F04NR1F1000 Nodulated root Medicago t... 189 4e-47
50 emb|AW290830|AW290830 NXNV047E02F Nsf Xylem Normal wood Vertical... 188 6e-47
emb|AW039575|AW039575 EST282023 tomato mixed elicitor, BTI Lycop... 186 4e-46
emb|AW906099|AW906099 EST342220 potato stolon, Cornell Universit... 185 8e-46
emb|AW931325|AW931325 EST357168 tomato fruit mature green, TAMU ... 185 8e-46
emb|AW202273|AW202273 sf13b01.y1 Gm-c1027 Glycine max cDNA clone... 182 5e-45
55 emb|AW096584|AW096584 EST289764 tomato mixed elicitor, BTI Lycop... 181 1e-44
emb|AW559298|AW559298 EST306341 DSIR Medicago truncatula cDNA cl... 181 1e-44
emb|AW220837|AW220837 EST297306 tomato fruit mature green, TAMU ... 180 2e-44
emb|AW746169|AW746169 WS1_39_B06.g1_A002 Water-stressed 1 (WS1) ... 127 4e-44
emb|AW677446|AW677446 DG1_7_D07.b1_A002 Dark Grown 1 (DG1) Sorgh... 178 7e-44
60 emb|AW559359|AW559359 EST314407 DSIR Medicago truncatula cDNA cl... 178 9e-44
emb|AW616711|AW616711 EST323122 L. hirsutum trichome, Cornell Un... 177 1e-43

emb|AW310207|AW310207 sf32g10.x1 Gm-c1028 Glycine max cDNA clone... 176 4e-43
 emb|AW617757|AW617757 EST324264 L. hirsutum trichome, Cornell Un... 173 2e-42
 emb|AI054863|AI054863 coau0002F22 Cotton Boll Abscission Zone cD... 103 8e-42
 5 emb|AW736524|AW736524 EST332538 KV3 Medicago truncatula cDNA clo... 169 5e-41
 emb|AI775651|AI775651 EST256751 tomato resistant, Cornell Lycopen... 168 1e-40
 emb|AW310204|AW310204 sf32g07.x1 Gm-c1028 Glycine max cDNA clone... 166 5e-40
 emb|AI489091|AI489091 EST247430 tomato ovary, TAMU Lycopersicon ... 162 4e-39
 emb|AW567617|AW567617 si65e08.y1 Gm-r1030 Glycine max cDNA clone... 157 1e-37
 emb|AJ005340|LUAJ5340 Linum usitatissimum mRNA for IAA amidohydr... 156 3e-37
 10 emb|AW277663|AW277663 sf85a06.y1 Gm-c1019 Glycine max cDNA clone... 155 1e-36
 emb|AI736325|AI736325 sb27a06.y1 Gm-c1009 Glycine max cDNA clone... 149 6e-35
 emb|AW685732|AW685732 NF034F02NR1F1000 Nodulated root Medicago t... 122 1e-33
 emb|AI781477|AI781477 EST262356 tomato susceptible, Cornell Lyco... 113 3e-32
 emb|AW980900|AW980900 EST392053 GVN Medicago truncatula cDNA clo... 139 5e-32
 15 emb|AI778980|AI778980 EST259859 tomato susceptible, Cornell Lyco... 138 1e-31
 emb|AI773172|AI773172 EST254272 tomato resistant, Cornell Lycopen... 133 2e-30
 gb|BE054249|BE054249 GA_Ea0033L21f Gossypium arboreum 7-10 dpa ... 120 3e-30
 emb|AW220773|AW220773 EST297242 tomato fruit mature green, TAMU ... 128 1e-28
 emb|AW398085|AW398085 EST297968 L. pennellii trichome, Cornell U... 100 1e-28
 20 emb|AI725556|AI725556 BNLGHi12118 Six-day Cotton fiber Gossypium... 125 7e-28
 emb|AV407386|AV407386 AV407386 Lotus japonicus young plants (two... 105 2e-25
 emb|AV425676|AV425676 AV425676 Lotus japonicus young plants (two... 115 1e-24
 emb|AW649713|AW649713 EST328167 tomato germinating seedlings, TA... 114 2e-24
 emb|AW102170|AW102170 sd84c02.y1 Gm-c1009 Glycine max cDNA clone... 114 2e-24
 25 emb|AW091914|AW091914 EST285094 tomato mixed elicitor, BTI Lycop... 112 5e-24
 emb|AW039945|AW039945 EST282436 tomato mixed elicitor, BTI Lycop... 112 5e-24
 emb|AW928798|AW928798 EST337586 tomato flower buds 8 mm to pre-a... 111 1e-23
 emb|AQ911427|AQ911427 LMAJFV1_ln04f02.x1 Leishmania major FV1 ra... 69 1e-21
 emb|AW042912|AW042912 ST27A02 Pine TriPEX shoot tip library Pin... 92 7e-21
 30 emb|AT000037|AT000037 AT000037 Apple young fruit cDNA library Ma... 101 1e-20
 gb|BE049708|BE049708 NXNV_142_E09_FF Nsf Xylem Normal wood Vertic... 100 3e-20
 emb|AW684765|AW684765 NF021G11NR1F1000 Nodulated root Medicago t... 98 1e-19
 emb|AW423725|AW423725 sh50h06.y1 Gm-c1017 Glycine max cDNA clone... 98 1e-19
 emb|AW278733|AW278733 sf96f12.y1 Gm-c1019 Glycine max cDNA clone... 95 8e-19
 35 emb|AW495793|AW495793 NXNV_065_E02_FF Nsf Xylem Normal wood Vert... 94 2e-18
 emb|AW568805|AW568805 si61d03.y1 Gm-r1030 Glycine max cDNA clone... 89 7e-17
 emb|AQ948883|AQ948883 Sheared DNA-46E23.TF Sheared DNA Trypanoso... 69 1e-16
 emb|AI974654|AI974654 T113109e KV2 Medicago truncatula cDNA clon... 79 4e-16
 emb|AW255631|AW255631 ML690 peppermint glandular trichome Menta... 86 7e-16
 40 emb|AW102109|AW102109 sd83c02.y1 Gm-c1009 Glycine max cDNA clone... 83 6e-15
 emb|X68950|TRUROCAN T.repens gene for urocanase. 58 5e-14

Query= AF049236.28_at 12521_at /id_source genbank /description
 gb|aac14413.1| (af049236) unknown [arabidopsis thaliana] /blast_score
 45 0 /ec_number /family /chip nova /gb_link /ncgi
 (1347 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

50

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

55

emb|AB012932|AB012932 Vigna radiata mRNA for Ca²⁺/H⁺ exchanger, ... 324 e-141
 emb|AW119450|AW119450 sd47b12.y1 Gm-c1016 Glycine max cDNA clone... 328 7e-89
 emb|AW395054|AW395054 sh38h04.y1 Gm-c1017 Glycine max cDNA clone... 323 2e-87
 emb|AI748459|AI748459 sb53b12.y1 Gm-c1016 Glycine max cDNA clone... 321 6e-87
 60 emb|AB018526|AB018526 Ipomoea nil mRNA for H⁺/Ca²⁺ exchanger 2, ... 262 4e-86
 emb|AW132719|AW132719 se09c07.y1 Gm-c1013 Glycine max cDNA clone... 293 2e-78

- gb|BE059799|BE059799 sn37c09.y1 Gm-c1016 Glycine max cDNA clone ... 270 1e-71
emb|AW424368|AW424368 sh64g04.y1 Gm-c1015 Glycine max cDNA clone... 221 6e-70
emb|AW283631|AW283631 LG1_242_D12.g1_A002 Light Grown 1 (LG1) So... 243 2e-63
emb|AW668567|AW668567 GA_Ea0014K15 Gossypium arboreum 7-10 dpa ... 141 1e-61
5 emb|AW648038|AW648038 EST326492 tomato germinating seedlings, TA... 230 2e-59
emb|AW132572|AW132572 se05h06.y1 Gm-c1013 Glycine max cDNA clone... 151 3e-52
emb|AW399625|AW399625 EST310125 L. pennellii trichome, Cornell U... 154 4e-49
gb|U18944|SCU18944 Saccharomyces cerevisiae putative transmembra... 195 5e-49
gb|U36603|SCU36603 Saccharomyces cerevisiae vacuolar H⁺/Ca²⁺ exc... 195 5e-49
10 emb|Z74176|SCYDL128W S.cerevisiae chromosome IV reading frame OR... 195 5e-49
emb|AJ001273|SCMNR1W30 Saccharomyces cerevisiae MNR1 gene, strai... 194 1e-48
emb|AW737408|AW737408 EST338751 tomato flower buds, anthesis, Co... 149 5e-48
emb|AJ001272|SCMNR1MNR Saccharomyces cerevisiae mnr1 gene, strai... 191 1e-47
emb|AI896399|AI896399 EST265830 tomato callus, TAMU Lycopersicon... 190 2e-47
15 emb|AF053229|AF053229 Neurospora crassa calcium/proton exchanger... 167 3e-46
emb|AW329785|AW329785 N201056e rootphos(-) Medicago truncatula c... 168 4e-46
emb|AW471762|AW471762 si15e11.y1 Gm-c1029 Glycine max cDNA clone... 99 8e-43
emb|AW133119|AW133119 se14e12.y1 Gm-c1013 Glycine max cDNA clone... 173 3e-42
emb|AW459585|AW459585 sh89a07.y1 Gm-c1016 Glycine max cDNA clone... 164 1e-39
20 emb|AL022598|SPCC1795 S.pombe chromosome III cosmid c1795. 150 1e-39
emb|AL035247|SPCC895 S.pombe chromosome III cosmid c895. 150 1e-39
emb|AW934664|AW934664 EST353556 tomato flower buds 0-3 mm, Corne... 120 1e-39
emb|AW508855|AW508855 si41b10.y1 Gm-r1030 Glycine max cDNA clone... 136 3e-39
emb|AW034341|AW034341 EST277912 tomato callus, TAMU Lycopersicon... 159 4e-38
25 emb|AI484823|AI484823 EST243084 tomato ovary, TAMU Lycopersicon ... 106 2e-35
emb|AW931722|AW931722 EST357565 tomato fruit mature green, TAMU ... 145 6e-34
emb|AW289857|AW289857 NXNV007A07F Nsf Xylem Normal wood Vertical... 145 8e-34
emb|AW423904|AW423904 sh57f03.y1 Gm-c1015 Glycine max cDNA clone... 144 1e-33
emb|AW691013|AW691013 NF036F12ST1F1000 Developing stem Medicago ... 105 9e-33
30 emb|AW737653|AW737653 EST339080 tomato flower buds, anthesis, Co... 140 3e-32
emb|AI900767|AI900767 sb93a03.y1 Gm-c1017 Glycine max cDNA clone... 83 3e-31
emb|AW329767|AW329767 N201036e rootphos(-) Medicago truncatula c... 136 3e-31
emb|AW695100|AW695100 NF091E10ST1F1082 Developing stem Medicago ... 98 1e-30
emb|AW596212|AW596212 si99e01.y1 Gm-c1032 Glycine max cDNA clone... 86 2e-30
35 emb|AI899610|AI899610 EST269053 tomato susceptible, Cornell Lyco... 121 7e-30
emb|AW688561|AW688561 NF009A06ST1F1000 Developing stem Medicago ... 80 2e-29
emb|AW929865|AW929865 EST354135 tomato flower buds 8 mm to pre-a... 88 9e-29
emb|AI780101|AI780101 EST260980 tomato susceptible, Cornell Lyco... 88 8e-28
emb|AW689061|AW689061 NF014H11ST1F1000 Developing stem Medicago ... 87 3e-27
40 emb|AW691346|AW691346 NF043G04ST1F1000 Developing stem Medicago ... 85 4e-27
emb|AW697283|AW697283 NF115A12ST1F1088 Developing stem Medicago ... 85 5e-27
emb|AW690182|AW690182 NF029D06ST1F1000 Developing stem Medicago ... 85 9e-27
emb|AW694830|AW694830 NF080D09ST1F1077 Developing stem Medicago ... 85 1e-26
emb|AI211369|AI211369 o6g04a1.r1 Aspergillus nidulans 24hr asexu... 121 1e-26
45 emb|AW394839|AW394839 sh36a06.y1 Gm-c1017 Glycine max cDNA clone... 118 1e-25
emb|AW119664|AW119664 sd50f07.y1 Gm-c1016 Glycine max cDNA clone... 117 1e-25
emb|AW181027|AW181027 MgA0398r MgA Library Mycosphaerella gramin... 116 3e-25
emb|AI771453|AI771453 EST252553 tomato ovary, TAMU Lycopersicon ... 84 3e-24
emb|AW695020|AW695020 NF082E03ST1F1021 Developing stem Medicago ... 76 7e-24
50 emb|AI211368|AI211368 o6g04a1.fl Aspergillus nidulans 24hr asexu... 111 9e-24
emb|AW692971|AW692971 NF057G06ST1F1000 Developing stem Medicago ... 85 1e-23
emb|AI966081|AI966081 sc27a12.y1 Gm-c1013 Glycine max cDNA clone... 110 3e-23
emb|AW696697|AW696697 NF109H04ST1F1043 Developing stem Medicago ... 58 8e-22
emb|AW690067|AW690067 NF027E05ST1F1000 Developing stem Medicago ... 58 8e-22
55 emb|AW218225|AW218225 EST303406 tomato radicle, 5 d post-imbibit... 105 1e-21
emb|AW696232|AW696232 NF104B05ST1F1044 Developing stem Medicago ... 61 1e-19
emb|AW041446|AW041446 EST284310 tomato mixed elicitor, BTI Lycop... 95 9e-19
emb|AW041435|AW041435 EST284299 tomato mixed elicitor, BTI Lycop... 95 9e-19
emb|AW693419|AW693419 NF064H07ST1F1000 Developing stem Medicago ... 58 5e-18
60 emb|AW432234|AW432234 sh70h05.y1 Gm-c1015 Glycine max cDNA clone... 93 6e-18
emb|AT002674|AT002674 AT002674 POSLM01 Pleurotus ostreatus cDNA ... 82 1e-14

- emb|AW310634|AW310634 sg22e01.x1 Gm-c1024 Glycine max cDNA clone... 82 1e-14
 emb|AA965697|AA965697 o3g02a1.fl Aspergillus nidulans 24hr asexu... 81 2e-14
 emb|AI759554|AI759554 EtESTea22b04.x1 Eimeria S5-2 Sporozoite st... 52 2e-13
 emb|AW923051|AW923051 DG1_48_G08.g1_A002 Dark Grown 1 (DG1) Sorg... 74 2e-12
 5 emb|AW695860|AW695860 NF099D07ST1F1061 Developing stem Medicago ... 74 3e-12
 emb|AW704472|AW704472 sk53e05.y1 Gm-c1019 Glycine max cDNA clone... 74 3e-12
 emb|AA901983|AA901983 NCM5F6T7 Mycelial Neurospora crassa cDNA c... 72 9e-12
 gb|BE022406|BE022406 sm85d09.y1 Gm-c1015 Glycine max cDNA clone ... 72 9e-12
 emb|AW694605|AW694605 NF078B03ST1F1027 Developing stem Medicago ... 58 4e-11
 10 emb|AI756356|AI756356 EtESTea42h07.y1 Eimeria S5-2 Sporozoite st... 67 3e-10
 emb|AW875004|AW875004 00125 leafy spurge Lambda HybriZAP 2.1 two... 47 6e-10
 emb|AL116004|CNS01CUK Botrytis cinerea strain T4 cDNA library un... 63 5e-09
 emb|AI488088|AI488088 EST246410 tomato ovary, TAMU Lycopersicon ... 59 7e-08
 emb|AQ325110|AQ325110 mgxb0020F10r CUGI Rice Blast BAC Library P... 58 1e-07
 15 emb|AW694277|AW694277 NF074D01ST1F1012 Developing stem Medicago ... 58 1e-07
 emb|AI812387|AI812387 1G6 Pine Lambda Zap Xylem library Pinus ta... 54 3e-06
 emb|AW985137|AW985137 NXNV_133_D09_F Nsf Xylem Normal wood Verti... 52 8e-06
 emb|AW934474|AW934474 EST353378 tomato flower buds 0-3 mm, Corne... 51 1e-05
 gb|BE059619|BE059619 sn34f03.y1 Gm-c1016 Glycine max cDNA clone ... 50 4e-05
 20 emb|AI043540|AI043540 L30-547T3 Ice plant Lambda Uni-Zap XR expr... 48 2e-04
 emb|AW221661|AW221661 EST298472 tomato fruit red ripe, TAMU Lyco... 48 2e-04
 emb|AW285659|AW285659 LG1_319_G05.g1_A002 Light Grown 1 (LG1) So... 46 5e-04
 emb|AI489262|AI489262 EST247601 tomato ovary, TAMU Lycopersicon ... 46 5e-04
 emb|AV422679|AV422679 AV422679 Lotus japonicus young plants (two... 46 7e-04
 25 emb|AV424693|AV424693 AV424693 Lotus japonicus young plants (two... 46 7e-04
 emb|AW287551|AW287551 LG1_242_D12.b1_A002 Light Grown 1 (LG1) So... 46 7e-04
 emb|AV425896|AV425896 AV425896 Lotus japonicus young plants (two... 46 7e-04
 gb|BE123551|BE123551 NXNV_149_F02_F Nsf Xylem Normal wood Vertic... 44 0.003
 emb|AV412612|AV412612 AV412612 Lotus japonicus young plants (two... 42 0.012
 30 emb|AQ855371|AQ855371 CpG1905B CplOWAgDNA1 Cryptosporidium parvu... 40 0.030
 emb|AW038228|AW038228 EST279885 tomato mixed elicitor, BTI Lycop... 40 0.030
 emb|AL114296|CNS01BJ4 Botrytis cinerea strain T4 cDNA library un... 40 0.057
 emb|AW285641|AW285641 LG1_319_E05.g1_A002 Light Grown 1 (LG1) So... 39 0.079
- 35 Query= AF033205.2_at 12538_at /id_source genbank /description
 gb|aac02973.1| (af033205) putative pectin methylesterase [arabidopsis
 thaliana] /blast_score 6.00e-38 /ec_number /family methylesterase
 /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 40 post/entrez/query?db=n&form=6&dopt=g&uid=gb|af033205|/ncgi
 http://www.ncgr.org/cgi-bin/ff?af033205
 (236 letters)
- Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters
- Searching.....done
- Score E
 50 Sequences producing significant alignments: (bits) Value
- emb|Z71753|NPPME3MR N.plumbaginifolia mRNA for pectin methyleste... 142 3e-34
 emb|Z71754|NPPME4MR N.plumbaginifolia mRNA for pectin methyleste... 142 3e-34
 emb|Z71752|NPPME2MR N.plumbaginifolia mRNA for pectin methyleste... 142 3e-34
 55 emb|AW429110|AW429110 EST306566 tomato flower buds 0-3 mm, Corne... 135 5e-32
 emb|AW429158|AW429158 EST306614 tomato flower buds 0-3 mm, Corne... 135 5e-32
 emb|AI781139|AI781139 EST262018 tomato susceptible, Cornell Lyco... 135 5e-32
 emb|AI780635|AI780635 EST261610 tomato susceptible, Cornell Lyco... 135 5e-32
 gb|U49330|SLU49330 Solanum lycopersicum pectin methylesterase (P... 135 5e-32
 60 emb|AW220185|AW220185 EST302668 tomato root during/after fruit s... 134 1e-31
 emb|AW154926|AW154926 EST290291 tomato root deficiency, Cornell ... 134 1e-31

- emb|X94443|VRPECMEST V.radiata mRNA for pectinmethylesterase. 133 2e-31
emb|AW458218|AW458218 sh79h10.y1 Gm-cl016 Glycine max cDNA clone... 133 2e-31
emb|AF152172|AF152172 Solanum tuberosum cultivar Desiree pectin ... 132 3e-31
5 emb|AJ249786|NTA249786 Nicotiana tabacum partial mRNA for pectin... 132 3e-31
emb|AI494978|AI494978 sa93d09.y1 Gm-cl004 Glycine max cDNA clone... 132 3e-31
gb|U82973|CSU82973 Citrus sinensis pectinesterase (PECS-1.1) gen... 131 6e-31
emb|AW774676|AW774676 EST333827 KV3 Medicago truncatula cDNA clo... 131 6e-31
emb|AW623150|AW623150 EST321095 tomato flower buds 3-8 mm, Corne... 131 6e-31
gb|U82976|CSU82976 Citrus sinensis pectinesterase mRNA, complete... 131 6e-31
10 emb|X97762|STBPE1 S.tuberosum mRNA BPE1 for pectin methylesterase. 131 7e-31
emb|X67425|PSPMEAG Pisum sativum pmeA gene for pectinesterase. 131 1e-30
emb|AF056493|AF056493 Pisum sativum pectin methylesterase mRNA, ... 131 1e-30
emb|AF081457|AF081457 Pisum sativum pectin methylesterase (rcpme... 131 1e-30
emb|AW329215|AW329215 N200427e rootphos(-) Medicago truncatula c... 130 2e-30
15 emb|AW257345|AW257345 EST305482 KV2 Medicago truncatula cDNA clo... 130 2e-30
emb|AI781140|AI781140 EST262019 tomato susceptible, Cornell Lyco... 129 3e-30
emb|AI441604|AI441604 sa68e03.y1 Gm-cl004 Glycine max cDNA clone... 129 3e-30
emb|AI166540|AI166540 xylem.est.362 Poplar xylem Lambda ZAPII li... 129 4e-30
emb|X68029|PVVPE2 P.vulgaris PvVPE2 mRNA for pectin esterase. 128 8e-30
20 emb|AW784073|AW784073 NXNV_117_D06_F Nsf Xylem Normal wood Verti... 126 2e-29
emb|AW429112|AW429112 EST306568 tomato flower buds 0-3 mm, Corne... 126 3e-29
emb|AW888107|AW888107 NXNV_129_C06_F Nsf Xylem Normal wood Verti... 125 5e-29
emb|AW774488|AW774488 EST333639 KV3 Medicago truncatula cDNA clo... 124 9e-29
emb|AF152171|AF152171 Solanum tuberosum cultivar Desiree pectin ... 121 8e-28
25 emb|A17010|A17010 tomato fruit pectin esterase seq ID no1. 121 1e-27
emb|AW930691|AW930691 EST356534 tomato fruit mature green, TAMU ... 121 1e-27
emb|AW934244|AW934244 EST360087 tomato fruit mature green, TAMU ... 121 1e-27
emb|AW930330|AW930330 EST340883 tomato fruit mature green, TAMU ... 121 1e-27
gb|S66607|S66607 Lycopersicon esculentum pectinmethylesterase-li... 121 1e-27
30 emb|AW221911|AW221911 EST298722 tomato fruit red ripe, TAMU Lyco... 121 1e-27
emb|AW221863|AW221863 EST298674 tomato fruit red ripe, TAMU Lyco... 121 1e-27
emb|X74638|LEPEC1 L.esculentum mRNA for pectin esterase. 121 1e-27
emb|AW696177|AW696177 NF103C11ST1F1085 Developing stem Medicago ... 121 1e-27
emb|AW760550|AW760550 sl51g07.y1 Gm-cl027 Glycine max cDNA clone... 120 2e-27
35 emb|AW289642|AW289642 NXNV003F09F Nsf Xylem Normal wood Vertical... 119 3e-27
gb|U50986|SLU50986 Solanum lycopersicum pectin methylesterase PM... 119 4e-27
gb|U70675|LEU70675 Lycopersicon esculentum fruit-specific pectin... 118 6e-27
gb|U70676|LEU70676 Lycopersicon esculentum pectin methylesteras... 118 6e-27
emb|Z71751|NPPME1MR N.plumbaginifolia mRNA for pectin methyleste... 118 8e-27
40 emb|AW932254|AW932254 EST358097 tomato fruit mature green, TAMU ... 118 8e-27
emb|AF229849|AF229849 Vigna radiata pectin methylesterase isoform... 118 8e-27
gb|U70677|LEU70677 Lycopersicon esculentum (LePME1) gene, partia... 118 8e-27
gb|U82974|CSU82974 Citrus sinensis pectinesterase (PECS-1.2) gen... 117 1e-26
emb|AI897776|AI897776 EST267219 tomato ovary, TAMU Lycopersicon ... 117 2e-26
45 gb|U50985|SLU50985 Solanum lycopersicum pectin methylesterase PM... 116 3e-26
emb|AW758821|AW758821 NXNV_091_A04_F Nsf Xylem Normal wood Verti... 116 3e-26
emb|A17011|A17011 tomato fruit pectin esterase with pPel DNA seq... 116 3e-26
emb|X74639|LEPEC2 L.esculentum mRNA for pectin esterase clone. 116 3e-26
emb|X07910|LEPECES Tomato mRNA for pectin esterase. 116 3e-26
50 emb|A15983|A15983 L.esculentum mRNA for pectin esterase. 116 3e-26
emb|AW623570|AW623570 EST321515 tomato flower buds 3-8 mm, Corne... 116 3e-26
emb|AW221834|AW221834 EST298645 tomato fruit red ripe, TAMU Lyco... 115 5e-26
emb|X97763|STBPE2 S.tuberosum mRNA BPE2 for pectin methylesterase. 115 5e-26
emb|A24196|A24196 L.esculentum pectin esterase clone pPE1. 113 2e-25
55 emb|AW687047|AW687047 NF005D06RT1F1057 Developing root Medicago ... 113 2e-25
emb|AW424141|AW424141 sh61d11.y1 Gm-cl015 Glycine max cDNA clone... 112 6e-25
emb|AW398532|AW398532 EST309032 L. pennellii trichome, Cornell U... 111 8e-25
emb|AW666622|AW666622 GA__Ea0005C20 Gossypium arboreum 7-10 dpa ... 110 2e-24
emb|AW163926|AW163926 Ljirnp17-358-e10 Ljirnp Lambda HybriZap... 110 2e-24
60 emb|AW620942|AW620942 sj95g05.y1 Gm-cl023 Glycine max cDNA clone... 108 5e-24
emb|AI440753|AI440753 sa53f07.y1 Gm-cl004 Glycine max cDNA clone... 108 7e-24

gb|U82977|CSU82977 Citrus sinensis pectinesterase mRNA, complete... 84 2e-23
 emb|AI731654|AI731654 BNLGHI10367 Six-day Cotton fiber Gossypium... 106 4e-23
 emb|AI731653|AI731653 BNLGHI10366 Six-day Cotton fiber Gossypium... 106 4e-23
 gb|U82975|CSU82975 Citrus sinensis pectinesterase (PECS-2.1) gen... 81 7e-23
 5 gb|BE123534|BE123534 NXNV_149_D04_F Nsf Xylem Normal wood Vertic... 103 2e-22
 emb|AI967495|AI967495 Ljirnp03-197-b4 Ljirnp Lambda HybriZap ... 102 3e-22
 emb|AB029461|AB029461 Salix gilgiana SgPME1 mRNA for pectin meth... 102 4e-22
 emb|AW647968|AW647968 EST326422 tomato germinating seedlings, TA... 100 3e-21
 emb|AW617630|AW617630 EST324041 L. hirsutum trichome, Cornell Un... 97 2e-20
 10 emb|Y07899|CPSPE1 C.papaya mRNA for pectinesterase. 97 3e-20
 emb|AW666437|AW666437 sk36e11.y1 Gm-cl028 Glycine max cDNA clone... 95 7e-20
 gb|L27101|PETPPE1A Petunia inflata pectinesterase (PPE1) gene, c... 92 6e-19
 emb|X95991|PPPECESTR P.persica mRNA for pectin esterase. 85 1e-18
 emb|AW598693|AW598693 sj94f11.y1 Gm-cl023 Glycine max cDNA clone... 91 1e-18
 15 emb|AW256326|AW256326 EST304533 KV2 Medicago truncatula cDNA clo... 87 3e-17
 emb|AW349192|AW349192 GM210004A21F6R Gm-r1021 Glycine max cDNA 3... 86 4e-17
 emb|AW287387|AW287387 LG1_303_C07.b1_A002 Light Grown 1 (LG1) So... 82 6e-16
 emb|AW278130|AW278130 sf40b03.y1 Gm-cl009 Glycine max cDNA clone... 69 7e-16
 emb|AW349615|AW349615 GM210006A11A5R Gm-r1021 Glycine max cDNA 3... 79 7e-15
 20 emb|AA556385|AA556385 240 Loblolly pine C Pinus taeda cDNA clone... 71 1e-12
 emb|AW218132|AW218132 EST303313 tomato radicle, 5 d post-imbibit... 55 2e-11
 emb|AW648115|AW648115 EST326569 tomato germinating seedlings, TA... 64 2e-10
 emb|AW220222|AW220222 EST302705 tomato root during/after fruit s... 62 4e-10

 25 Query= AL079344.155_at 12556_at /id_source genbank /description
 emb|cab45330.1| (al079344) nucleotide pyrophosphatase-like protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al079344|/ncgi
 30 http://www.ncgr.org/cgi-bin/ff?al079344
 (1386 letters)

 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
 35 Searching.....done

 Score E
 Sequences producing significant alignments: (bits) Value
 40
 emb|AW686852|AW686852 NF003B08RT1F1000 Developing root Medicago ... 226 3e-79
 emb|AW563733|AW563733 LG1_248_C01.g1_A002 Light Grown 1 (LG1) So... 205 5e-52
 gb|BE053112|BE053112 GA_Ea0031A01f Gossypium arboreum 7-10 dpa ... 166 2e-50
 emb|AV409759|AV409759 AV409759 Lotus japonicus young plants (two... 165 4e-44
 45 emb|AW704801|AW704801 sk55f12.y1 Gm-cl019 Glycine max cDNA clone... 148 3e-43
 emb|AL034352|SPBC725 S.pombe chromosome II cosmid c725. 87 6e-42
 gb|C96280|C96280 C96280 Marchantia polymorpha immature sex organ... 89 9e-37
 emb|AW599232|AW599232 gb12b03.y1 Moss EST library PPN Physcomitr... 154 1e-36
 emb|AW306350|AW306350 se49e12.y1 Gm-cl017 Glycine max cDNA clone... 116 2e-33
 50 emb|AV409781|AV409781 AV409781 Lotus japonicus young plants (two... 140 2e-32
 emb|AI812708|AI812708 18B6 Pine Lambda Zap Xylem library Pinus t... 138 9e-32
 emb|AW626639|AW626639 NXNV067G03 Nsf Xylem Normal wood Vertical ... 119 4e-26
 emb|X59720|SCCHRII S.cerevisiae chromosome III complete DNA seq... 68 2e-13
 gb|U18530|SCE9871 Saccharomyces cerevisiae chromosome V cosmids ... 61 3e-10
 55 emb|AQ397058|AQ397058 mgxb0003P19f CUGI Rice Blast BAC Library P... 40 7e-06
 emb|AV427570|AV427570 AV427570 Lotus japonicus young plants (two... 52 8e-06
 gb|H74550|H74550 501 Random-primed Brassica napus cDNA clone RRM... 49 1e-04
 emb|AW186036|AW186036 se62g09.y1 Gm-cl019 Glycine max cDNA clone... 46 5e-04
 emb|AW832253|AW832253 sm21f10.y1 Gm-cl027 Glycine max cDNA clone... 46 5e-04
 60 emb|AW596708|AW596708 sj15g06.y1 Gm-cl032 Glycine max cDNA clone... 46 5e-04
 emb|AW156479|AW156479 se26f12.y1 Gm-cl015 Glycine max cDNA clone... 44 0.002

	emb AQ845931 AQ845931 LMAJFV1_lm11d03.y1 Leishmania major FV1 ra...	44	0.002
	emb AW330350 AW330350 TENU5096 T.cruzi epimastigote normalized c...	41	0.016
	emb AI901162 AI901162 sc21e02.y1 Gm-c1013 Glycine max cDNA clone...	41	0.016
	emb AB004539 AB004539 Schizosaccharomyces pombe 38 kb genomic DN...	38	0.020
5	emb AL021766 SPBC27B12 S.pombe chromosome II cosmid c27B12.	38	0.020
	emb AQ502678 AQ502678 V50A6 mTn-3xHA/lacZ Insertion Library Sacc...	40	0.059
	emb AI919929 AI919929 1459 Pine Lambda Zap Xylem library Pinus t...	38	0.15
	emb AQ872628 AQ872628 V26H10 mTn-3xHA/lacZ Insertion Library, st...	38	0.21
	emb Z49337 SCYJL062W S.cerevisiae chromosome X reading frame ORF...	38	0.21
10	emb Z34288 SCXCDNA S.cerevisiae (S288C) X chromosome DNA (17137bp).	38	0.21
	emb AW349789 AW349789 GM210006B10E8R Gm-r1021 Glycine max cDNA 3...	37	0.29
	emb AW703931 AW703931 sk25h05.y1 Gm-c1028 Glycine max cDNA clone...	37	0.29
	emb AW733463 AW733463 sk73h10.y1 Gm-c1016 Glycine max cDNA clone...	28	0.38
	emb AW100199 AW100199 sd26h06.y1 Gm-c1012 Glycine max cDNA clone...	36	0.54
15	emb AW599349 AW599349 gb13g12.y1 Moss EST library PPN Physcomitr...	36	0.54
	emb Z73136 SCYLL031C S.cerevisiae chromosome XII reading frame O...	29	0.61
	emb AA898221 AA898221 NCC2C5T7 Conidial Neurospora crassa cDNA c...	35	1.0
	emb AF130334 AF130334 Bruguiera cylindrica internal transcribed ...	35	1.9
	gb B13384 B13384.jd152 Trypanosome Shotgun M13 genomic Trypanoso...	34	2.7
20	emb AQ500377 AQ500377 V40F1 mTn-3xHA/lacZ Insertion Library Sacc...	34	2.7
	emb AW102097 AW102097 sd83a09.y1 Gm-c1009 Glycine max cDNA clone...	34	2.7
	emb AW334235 AW334235 S32B4 AGS-1 Pneumocystis carinii f. sp. ca...	34	3.6
	emb AW648115 AW648115 EST326569 tomato germinating seedlings, TA...	34	3.6
	emb AQ500705 AQ500705 V33B7 mTn-3xHA/lacZ Insertion Library Sacc...	34	3.6
25	emb AW220222 AW220222 EST302705 tomato root during/after fruit s...	34	3.6
	emb AC016528 AC016528 Leishmania major chromosome 35 clone L4123...	34	3.6
	gb M55447 BLYRCAA2 Hordeum vulgare rubisco activase (RcaA2) mRNA...	34	3.6
	gb BE054837 BE054837 GA__Ea0002C16f Gossypium arboreum 7-10 dpa ...	33	5.0
	gb BE055267 BE055267 GA__Ea0004K24f Gossypium arboreum 7-10 dpa ...	33	5.0
30	emb AW109433 AW109433 gate0004K24f Gossypium arboreum 7-10 dpa f...	33	5.0
	emb AW666951 AW666951 GA__Ea0006H12 Gossypium arboreum 7-10 dpa ...	33	5.0
	emb AW661478 AW661478 833006F08.y1 C. reinhardtii CC-125 -S, Lam...	33	5.0
	emb AW731558 AW731558 GA__Ea0030J12 Gossypium arboreum 7-10 dpa ...	33	5.0
	emb AL031909 LMFL302 Leishmania major Friedlin chromosome 4 cosm...	33	5.0
35	emb AW108953 AW108953 gate0002C16f Gossypium arboreum 7-10 dpa f...	33	5.0
	emb AW667941 AW667941 GA__Ea0011O22 Gossypium arboreum 7-10 dpa ...	33	5.0
	dbj D83464 D83464 Candida intermedia 26S ribosomal RNA, partial ...	33	5.0
	emb AW730349 AW730349 GA__Ea0023E10 Gossypium arboreum 7-10 dpa ...	33	5.0
40	emb AW831354 AW831354 sm32e12.y1 Gm-c1028 Glycine max cDNA clone...	33	6.9
	emb AI211253 AI211253 o0g06a1.r1 Aspergillus nidulans 24hr asexu...	33	6.9
	emb AF197953 AF197953 Toxoplasma gondii histone acetyltransferas...	33	6.9
	emb AL353822 NC15E6 Neurospora crassa DNA linkage group V Cosmid...	33	6.9
	gb U68555 SPU68555 Saccharomyces paradoxus 26S ribosomal RNA gen...	33	6.9
	emb AB040996 AB040996 Saccharomyces sp. IFO 1815 gene for 26S rR...	33	6.9
45	emb AB040995 AB040995 Saccharomyces sp. IFO 1802 gene for 26S rR...	33	6.9
	emb AW667927 AW667927 GA__Ea0011M14 Gossypium arboreum 7-10 dpa ...	33	6.9
	emb AE001274 AE001274 Leishmania major chromosome I, complete se...	33	6.9
	emb AF130335 AF130335 Bruguiera exaristata internal transcribed ...	33	6.9
	emb AZ211966 AZ211966 Sheared DNA-106D6.TR Sheared DNA Trypanoso...	33	6.9
50	emb AV393427 AV393427 AV393427 Chlamydomonas reinhardtii C9 Chla...	33	6.9
	emb AI664729 AI664729 TENG0690 T. Cruzi epimastigote normalised ...	33	6.9
	emb AW720110 AW720110 LjNEST14a8r Lotus japonicus nodule library...	27	7.6
	gb U30821 CPU30821 Cyanophora paradoxa cyanelle, complete genome.	32	9.4
	emb AQ449508 AQ449508 500001C11.x1 CpIOWAM13mp18gDNA1 Cryptospor...	32	9.4
55	emb AU089911 AU089911 AU089911 Hordeum vulgare subsp. vulgare Up...	32	9.4
	emb AW219224 AW219224 EST301706 tomato root during/after fruit s...	32	9.4
	emb AA739819 AA739819 584 PtIFG2 Pinus taeda cDNA clone 8935M 3'...	32	9.4
	emb AW335019 AW335019 S42B7 AGS-1 Pneumocystis carinii f. sp. ca...	32	9.4
	emb AU089924 AU089924 AU089924 Hordeum vulgare subsp. vulgare Up...	32	9.4
60	emb AQ641373 AQ641373 RPCI93-DpnII-28A9.TV RPCI93-DpnII Trypanos...	32	9.4
	emb AW695807 AW695807 NF098G11ST1F1087 Developing stem Medicago ...	32	9.4

emb|AQ501198|AQ501198 V25G12 mTn-3xHA/lacZ Insertion Library Sac... 32 9.4

Query= X82624.2_at 12574_at /id_source genbank /description
emb|caa57944.1| (x82624) srg2at [arabidopsis thaliana] /blast_score
1.00e-25 /ec_number /family /chip nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|x82624| /ncgi
http://www.ncgr.org/cgi-bin/ff?x82624
(147 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
Sequences producing significant alignments: (bits) Value

20	emb AW756217 AW756217 sl17e08.y1 Gm-c1036 Glycine max cDNA clone...	96	1e-20
	emb AW561018 AW561018 EST316066 DSIR Medicago truncatula cDNA cl...	95	2e-20
	gb L47866 L47866 BNAF1507 Mustard flower buds Brassica rapa cDNA...	94	6e-20
	emb X94986 MEBGLA M.esculenta bglA gene.	94	6e-20
	emb AW257154 AW257154 EST305291 KV2 Medicago truncatula cDNA clo...	93	8e-20
	gb U39228 PAU39228 Prunus avium beta-glucosidase mRNA, partial cds.	93	8e-20
25	emb AI729894 AI729894 BNLGHi5504 Six-day Cotton fiber Gossypium ...	93	8e-20
	gb U95298 MEU95298 Manihot esculenta linamarase (pLIN-GEN) gene,...	93	8e-20
	gb S35175 S35175 linamarase=beta-glucosidase [Manihot esculenta=...	92	2e-19
	emb AF072736 AF072736 Pinus contorta beta-glucosidase mRNA, comp...	92	2e-19
30	emb AW568866 AW568866 si73c03.y1 Gm-c1031 Glycine max cDNA clone...	91	4e-19
	gb U50201 PSU50201 Prunus serotina prunasin hydrolase precursor ...	90	5e-19
	emb AW560545 AW560545 EST315593 DSIR Medicago truncatula cDNA cl...	90	7e-19
	emb AI900802 AI900802 sb93e10.y1 Gm-c1017 Glycine max cDNA clone...	89	2e-18
	gb BE058816 BE058816 sn21c08.y1 Gm-c1016 Glycine max cDNA clone ...	89	2e-18
	emb AW597982 AW597982 sj40c05.y1 Gm-c1008 Glycine max cDNA clone...	89	2e-18
35	emb AW395210 AW395210 sh45c06.y1 Gm-c1017 Glycine max cDNA clone...	89	2e-18
	emb AW570004 AW570004 si85e02.y1 Gm-c1031 Glycine max cDNA clone...	89	2e-18
	emb AW733524 AW733524 sk74g01.y1 Gm-c1016 Glycine max cDNA clone...	89	2e-18
	emb AW423986 AW423986 sh59a09.y1 Gm-c1015 Glycine max cDNA clone...	89	2e-18
	emb AW423387 AW423387 sh65b01.y1 Gm-c1015 Glycine max cDNA clone...	89	2e-18
40	emb AW597368 AW597368 si91h08.y1 Gm-c1031 Glycine max cDNA clone...	88	3e-18
	emb AW569966 AW569966 si83h05.y1 Gm-c1031 Glycine max cDNA clone...	88	3e-18
	emb AW569751 AW569751 si79h11.y1 Gm-c1031 Glycine max cDNA clone...	88	3e-18
	emb AW569883 AW569883 si82g07.y1 Gm-c1031 Glycine max cDNA clone...	88	3e-18
	emb AW317654 AW317654 sg55e02.y1 Gm-c1025 Glycine max cDNA clone...	87	5e-18
45	emb AW350857 AW350857 GM210009B10F4R Gm-r1021 Glycine max cDNA 3...	87	5e-18
	emb AW309715 AW309715 sf23f08.x1 Gm-c1028 Glycine max cDNA clone...	87	7e-18
	emb AF221526 AF221526 Prunus serotina prunasin hydrolase isoform...	86	9e-18
	emb AB003089 AB003089 Polygonum tinctorium mRNA for beta-glucosi...	86	9e-18
	emb AW279169 AW279169 sf67c06.y1 Gm-c1013 Glycine max cDNA clone...	85	2e-17
50	gb U72154 BNU72154 Brassica nigra beta-glucosidase (psr3.1) mRNA...	85	2e-17
	emb AW394514 AW394514 sh32a04.y1 Gm-c1017 Glycine max cDNA clone...	84	3e-17
	emb AW202129 AW202129 sf12c05.y1 Gm-c1027 Glycine max cDNA clone...	84	3e-17
	gb U26025 PSU26025 Prunus serotina amygdalin hydrolase isoform A...	84	5e-17
	dbj D83177 CSAF26G Costus speciosus mRNA for furostanol glycosid...	83	9e-17
55	emb AI774009 AI774009 EST255109 tomato resistant, Cornell Lycopen...	63	2e-16
	emb AF143377 AF143377 AF143377 Pisum sativum library (Fristensky...	82	2e-16
	emb AI772446 AI772446 EST253546 tomato resistant, Cornell Lycopen...	63	3e-16
	emb AW651266 AW651266 EST329720 tomato germinating seedlings, TA...	63	3e-16
	emb AW317658 AW317658 sg55f02.y1 Gm-c1025 Glycine max cDNA clone...	81	3e-16
60	emb AW042637 AW042637 ST24C01 Pine TriplEx shoot tip library Pin...	60	4e-16
	emb AW101162 AW101162 sd74h08.y1 Gm-c1008 Glycine max cDNA clone...	81	4e-16

- emb|AW132549|AW132549 se05f01.y1 Gm-c1013 Glycine max cDNA clone... 80 6e-16
gb|L41869|BLYBGQ6 Hordeum vulgare L. beta-glucosidase (BGQ60) ge... 65 6e-16
emb|AB003110|AB003110 Trichoderma reesei bgl2 gene for bete-gluc... 80 8e-16
emb|AW760442|AW760442 sl50d01.y1 Gm-c1027 Glycine max cDNA clone... 79 1e-15
5 emb|AJ005950|AJ005950 AJ005950 chickpea mRNA CAP-4 Cicer arietin... 79 1e-15
emb|X56734|TRBG361 Trifolium repens mRNA for non-cyanogenic beta... 78 2e-15
emb|AW201515|AW201515 sf04b02.y1 Gm-c1027 Glycine max cDNA clone... 78 4e-15
emb|AA415086|AA415086 Mg0020 RCW Lambda Zap Express Library Pyri... 78 4e-15
emb|AI941073|AI941073 sb84a09.y1 Gm-c1010 Glycine max cDNA clone... 63 5e-15
10 emb|AW311377|AW311377 sg38b12.y1 Gm-c1025 Glycine max cDNA clone... 63 5e-15
emb|AW677220|AW677220 DG1_6_D11.g1_A002 Dark Grown 1 (DG1) Sorgh... 77 7e-15
gb|U33817|SBU33817 Sorghum bicolor dhurrinase mRNA, nuclear gene... 77 7e-15
emb|AW744827|AW744827 LG1_384_D09.g1_A002 Light Grown 1 (LG1) So... 77 7e-15
emb|AW923243|AW923243 DG1_50_B11.g1_A002 Dark Grown 1 (DG1) Sorg... 77 7e-15
15 emb|AW923628|AW923628 DG1_56_E12.g1_A002 Dark Grown 1 (DG1) Sorg... 77 7e-15
emb|AW922651|AW922651 DG1_20_B09.g1_A002 Dark Grown 1 (DG1) Sorg... 77 7e-15
emb|AW286529|AW286529 LG1_334_A07.g1_A002 Light Grown 1 (LG1) So... 77 7e-15
emb|AI974587|AI974587 T113037e KV2 Medicago truncatula cDNA clon... 65 9e-15
emb|AW676749|AW676749 DG1_14_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 76 1e-14
20 emb|AB003109|AB003109 Humicola grisea var. thermoidea bgl4 gene ... 76 1e-14
emb|AI723853|AI723853 RHIZ1_28_C08.y1_A001 Rhizome1 Sorghum hale... 76 1e-14
emb|AI724790|AI724790 RHIZ1_9_C08.y2_A001 Rhizome1 Sorghum halep... 76 1e-14
emb|AW685200|AW685200 NF027E09NR1F1000 Nodulated root Medicago t... 65 1e-14
gb|BE124555|BE124555 EST393590 GVN Medicago truncatula cDNA clon... 65 1e-14
25 emb|AW774242|AW774242 EST333393 KV3 Medicago truncatula cDNA clo... 65 1e-14
emb|AW286277|AW286277 LG1_329_G04.g1_A002 Light Grown 1 (LG1) So... 76 1e-14
emb|AW286262|AW286262 LG1_329_E04.g1_A002 Light Grown 1 (LG1) So... 76 1e-14
emb|AW284398|AW284398 LG1_289_B04.g1_A002 Light Grown 1 (LG1) So... 76 1e-14
emb|AW283021|AW283021 LG1_301_G01.g1_A002 Light Grown 1 (LG1) So... 76 1e-14
30 emb|AW284016|AW284016 LG1_264_G03.g1_A002 Light Grown 1 (LG1) So... 76 1e-14
emb|AW282563|AW282563 LG1_312_A09.g1_A002 Light Grown 1 (LG1) So... 76 1e-14
emb|AW282564|AW282564 LG1_312_A08.g1_A002 Light Grown 1 (LG1) So... 76 1e-14
emb|AW565734|AW565734 LG1_348_H08.g1_A002 Light Grown 1 (LG1) So... 76 1e-14
emb|X82577|BNBGL B.napus mRNA for beta-glucosidase. 75 3e-14
35 emb|AF149311|AF149311 Rauvolfia serpentina raucaffricine-O-beta-... 75 3e-14
gb|BE021518|BE021518 sm59e05.y1 Gm-c1028 Glycine max cDNA clone ... 74 4e-14
emb|AF082991|AF082991 Avena sativa beta-D-glucosidase beta subun... 73 9e-14
emb|AW423704|AW423704 sh50f06.y1 Gm-c1017 Glycine max cDNA clone... 73 1e-13
emb|X78433|ASLBDG A.sativa L. mRNA for beta-D-glucosidase. 72 2e-13
40 emb|AF163097|AF163097 Dalbergia cochinchinensis dalcocinin 8'-O... 62 2e-13
emb|AW733253|AW733253 sk70d08.y1 Gm-c1016 Glycine max cDNA clone... 71 3e-13
emb|AW922447|AW922447 DG1_19_F09.g1_A002 Dark Grown 1 (DG1) Sorg... 60 5e-13
emb|AW671821|AW671821 LG1_351_F12.g1_A002 Light Grown 1 (LG1) So... 59 9e-13
gb|BE059820|BE059820 sn37e08.y1 Gm-c1016 Glycine max cDNA clone ... 68 3e-12
45 emb|AJ133406|DLA133406 Digitalis lanata mRNA for cardenolide 16-... 68 4e-12
emb|AW773684|AW773684 EST332670 KV3 Medicago truncatula cDNA clo... 61 6e-12
emb|AW099840|AW099840 sd17b01.y2 Gm-c1012 Glycine max cDNA clone... 60 6e-12
emb|X67838|BNDNAM B.napus DNA for myrosinase. 66 1e-11
emb|AW923660|AW923660 DG1_57_B08.g1_A002 Dark Grown 1 (DG1) Sorg... 66 1e-11
50 emb|AW284341|AW284341 LG1_275_C12.g1_A002 Light Grown 1 (LG1) So... 66 1e-11
emb|X79080|BNMYRMC B.napus mRNA for myrosinase MC. 66 2e-11
emb|Z21977|BNMYR1A B.napus Myr1.Bn1 gene encoding myrosinase, th... 66 2e-11
emb|X56733|TRBG104 T.repens mRNA for cyanogenic beta-glucosidase... 52 2e-11
emb|AF016864|AF016864 Orpinomyces sp. PC-2 beta-glucosidase (bgl... 64 5e-11
55 emb|X59881|SAMYRMB1 S.alba thioglucoside glucohydrolase (myrosin... 63 7e-11
emb|AW927073|AW927073 HVSMEg0009H02 Hordeum vulgare pre-anthesis... 57 1e-10
gb|L11258|BNAMYROS Brassica campestris myrosinase gene, complete... 62 2e-10

60 Query= AF024504.13_at 12630_at /id_source genbank /description
gb|aaf18681.1|af024504_11 (af024504) unknown protein [arabidopsis
thaliana] /blast_score 1.00e-129 /ec_number /family /chip nova

/gb_link <http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|af024504> /ncgi
<http://www.ncgr.org/cgi-bin/ff?af024504>
 (1374 letters)

5

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

10

Score E

Sequences producing significant alignments:

(bits) Value

emb|AW216758|AW216758 EST295472 tomato callus, TAMU Lycopersicon... 119 3e-34
 15 emb|AW219044|AW219044 EST301526 tomato root during/after fruit s... 108 7e-33
 emb|AW031258|AW031258 EST274633 tomato callus, TAMU Lycopersicon... 108 7e-33
 emb|AI772760|AI772760 EST253860 tomato resistant, Cornell Lycope... 108 7e-33
 emb|AI486533|AI486533 EST244854 tomato ovary, TAMU Lycopersicon ... 71 5e-29
 emb|AI898645|AI898645 EST268088 tomato ovary, TAMU Lycopersicon ... 71 6e-28
 20 emb|AW686482|AW686482 NF041H08NR1F1000 Nodulated root Medicago t... 112 8e-28
 emb|AW704059|AW704059 sk27d01.y1 Gm-cl028 Glycine max cDNA clone... 119 2e-27
 emb|AW350257|AW350257 GM210007B20B11R Gm-r1021 Glycine max cDNA ... 122 5e-27
 emb|AW759958|AW759958 sl56c04.y1 Gm-cl027 Glycine max cDNA clone... 115 7e-25
 emb|AW126130|AW126130 N100327e rootphos(-) Medicago truncatula c... 115 1e-24
 25 emb|AI776363|AI776363 EST257463 tomato resistant, Cornell Lycope... 114 1e-24
 emb|AI731720|AI731720 BNLGHi10579 Six-day Cotton fiber Gossypium... 112 5e-24
 emb|AW034441|AW034441 EST278012 tomato callus, TAMU Lycopersicon... 103 5e-24
 emb|AI896076|AI896076 EST265519 tomato callus, TAMU Lycopersicon... 102 1e-23
 emb|AI898707|AI898707 EST268150 tomato ovary, TAMU Lycopersicon ... 71 2e-22
 30 emb|AW310471|AW310471 sf36e11.x1 Gm-cl028 Glycine max cDNA clone... 105 6e-22
 emb|AW219445|AW219445 EST302023 tomato root during/after fruit s... 105 8e-22
 emb|AW648110|AW648110 EST326564 tomato germinating seedlings, TA... 105 1e-21
 emb|AW831572|AW831572 sm34h08.y1 Gm-cl028 Glycine max cDNA clone... 100 2e-20
 gb|BE124541|BE124541 EST393576 GVN Medicago truncatula cDNA clon... 89 8e-20
 35 emb|AW671843|AW671843 LG1_352_B09.b1_A002 Light Grown 1 (LG1) So... 64 2e-18
 emb|AW564955|AW564955 LG1_313_H09.b1_A002 Light Grown 1 (LG1) So... 64 2e-18
 emb|AW329431|AW329431 N200666e rootphos(-) Medicago truncatula c... 93 4e-18
 emb|AW929644|AW929644 EST338432 tomato flower buds 8 mm to pre-a... 73 7e-18
 emb|AW907159|AW907159 EST343282 potato stolon, Cornell Universit... 60 2e-14
 40 emb|AW565825|AW565825 LG1_352_B09.g1_A002 Light Grown 1 (LG1) So... 57 8e-14
 emb|AW625736|AW625736 EST319643 tomato radicle, 5 d post-imbibit... 56 8e-14
 emb|AI812987|AI812987 2D4 Pine Lambda Zap Xylem library Pinus ta... 52 4e-13
 gb|BE060164|BE060164 HVSMEg0011B20f Hordeum vulgare pre-anthesis... 76 5e-13
 emb|AW217067|AW217067 EST295781 tomato callus, TAMU Lycopersicon... 74 2e-12
 45 emb|AW398760|AW398760 EST309260 L. pennellii trichome, Cornell U... 54 2e-12
 emb|AW694156|AW694156 NF072H06ST1F1059 Developing stem Medicago ... 58 3e-12
 emb|AW773860|AW773860 EST332846 KV3 Medicago truncatula cDNA clo... 58 3e-12
 emb|AW394635|AW394635 sh33h09.y1 Gm-cl017 Glycine max cDNA clone... 55 3e-12
 emb|AW203644|AW203644 sf36e11.y1 Gm-cl028 Glycine max cDNA clone... 69 4e-12
 50 emb|AI728748|AI728748 BNLGHi11497 Six-day Cotton fiber Gossypium... 57 4e-12
 emb|AW697758|AW697758 Str1-D8 Sugar Beet germination cDNA librar... 46 5e-11
 emb|AW030302|AW030302 EST273557 tomato callus, TAMU Lycopersicon... 53 7e-11
 emb|AW982668|AW982668 HVSMEg0003O06f Hordeum vulgare pre-anthesi... 48 2e-10
 emb|AW287116|AW287116 LG1_265_G01.b2_A002 Light Grown 1 (LG1) So... 64 2e-09
 55 emb|AW734790|AW734790 sk88g11.y1 Gm-cl035 Glycine max cDNA clone... 42 5e-09
 emb|AT000776|AT000776 AT000776 Brassica rapa guard cell Brassica... 62 7e-09
 emb|AI775378|AI775378 EST256478 tomato resistant, Cornell Lycope... 42 1e-08
 emb|AW775488|AW775488 EST334553 DSIL Medicago truncatula cDNA cl... 58 2e-07
 emb|AW928719|AW928719 EST337507 tomato flower buds 8 mm to pre-a... 39 2e-07
 60 emb|AW282482|AW282482 LG1_313_B10.g1_A002 Light Grown 1 (LG1) So... 57 3e-07
 emb|AW225609|AW225609 T210061e KV0 Medicago truncatula cDNA clon... 40 4e-07

- emb|AT000645|AT000645 AT000645 Brassica rapa guard cell Brassica... 56 6e-07
 emb|AW731593|AW731593 GA_Ea0030P10 Gossypium arboreum 7-10 dpa ... 37 1e-06
 emb|AW282432|AW282432 LG1_313_H09.g1_A002 Light Grown 1 (LG1) So... 55 2e-06
 emb|AI736841|AI736841 sb34c09.y1 Gm-c1012 Glycine max cDNA clone... 50 5e-05
 5 emb|AW154916|AW154916 EST290281 tomato root deficiency, Cornell ... 40 6e-05
 emb|AI054948|AI054948 coau0002J14 Cotton Boll Abcission Zone cD... 49 7e-05
 emb|AI487433|AI487433 EST245755 tomato ovary, TAMU Lycopersicon ... 44 1e-04
 emb|AI490477|AI490477 EST248846 tomato ovary, TAMU Lycopersicon ... 44 1e-04
 emb|AI895257|AI895257 EST264700 tomato callus, TAMU Lycopersicon... 47 4e-04
 10 emb|AW564044|AW564044 LG1_281_A09.b1_A002 Light Grown 1 (LG1) So... 47 4e-04
 emb|AW565728|AW565728 LG1_348_E11.g1_A002 Light Grown 1 (LG1) So... 47 4e-04
 emb|AW922753|AW922753 DG1_45_C05.g1_A002 Dark Grown 1 (DG1) Sorg... 47 4e-04
 emb|AW746301|AW746301 WS1_40_G05.g1_A002 Water-stressed 1 (WS1) ... 47 4e-04
 emb|AW033344|AW033344 EST276915 tomato callus, TAMU Lycopersicon... 40 5e-04
 15 emb|AI486814|AI486814 EST245136 tomato ovary, TAMU Lycopersicon ... 46 5e-04
 emb|AI486642|AI486642 EST244963 tomato ovary, TAMU Lycopersicon ... 44 6e-04
 emb|AW774292|AW774292 EST333443 KV3 Medicago truncatula cDNA clo... 46 7e-04
 emb|AW472252|AW472252 si21g12.y1 Gm-c1029 Glycine max cDNA clone... 46 7e-04
 emb|AW705448|AW705448 sk49c01.y1 Gm-c1019 Glycine max cDNA clone... 35 0.001
 20 emb|AI728904|AI728904 BNLGHi11968 Six-day Cotton fiber Gossypium... 41 0.002
 emb|AI726718|AI726718 BNLGHi6425 Six-day Cotton fiber Gossypium ... 41 0.002
 emb|AW011001|AW011001 ST15E02 Pine TriPEX shoot tip library Pin... 45 0.002
 emb|AI563253|AI563253 EST00377 watermelon lambda zap library Cit... 44 0.002
 emb|AW568784|AW568784 si61a06.y1 Gm-r1030 Glycine max cDNA clone... 44 0.002
 25 emb|AI485669|AI485669 EST243990 tomato ovary, TAMU Lycopersicon ... 44 0.003
 emb|AW154917|AW154917 EST290282 tomato root deficiency, Cornell ... 44 0.003
 emb|AI895825|AI895825 EST265268 tomato callus, TAMU Lycopersicon... 44 0.003
 emb|AF109661|AF109661 AF109661 Capsicum annuum root susceptible ... 42 0.004
 emb|AI487481|AI487481 EST245803 tomato ovary, TAMU Lycopersicon ... 41 0.023
 30 emb|AV411141|AV411141 AV411141 Lotus japonicus young plants (two... 41 0.023
 emb|AW036093|AW036093 EST278179 tomato seed, TAMU Lycopersicon e... 30 0.025
 emb|AW036201|AW036201 EST278199 tomato seed, TAMU Lycopersicon e... 40 0.031
 emb|AW099579|AW099579 sd43g11.y1 Gm-c1016 Glycine max cDNA clone... 40 0.031
 emb|AW569827|AW569827 si82b01.y1 Gm-c1031 Glycine max cDNA clone... 40 0.031
 35 emb|AW099588|AW099588 sd43h11.y1 Gm-c1016 Glycine max cDNA clone... 40 0.031
 emb|AW306204|AW306204 se47d06.y1 Gm-c1017 Glycine max cDNA clone... 40 0.031
 emb|AW569325|AW569325 si76f02.y1 Gm-c1031 Glycine max cDNA clone... 40 0.031
 gb|BE058656|BE058656 sn19a10.y1 Gm-c1016 Glycine max cDNA clone ... 40 0.031
 emb|AW559559|AW559559 EST314607 DSIR Medicago truncatula cDNA cl... 40 0.043
 40 emb|AV427590|AV427590 AV427590 Lotus japonicus young plants (two... 40 0.043
 emb|AI777674|AI777674 EST258469 tomato susceptible, Cornell Lyco... 40 0.043
 emb|AI725930|AI725930 BNLGHi13647 Six-day Cotton fiber Gossypium... 40 0.059
 gb|BE021933|BE021933 sm64c08.y1 Gm-c1028 Glycine max cDNA clone ... 40 0.059
 gb|BE021787|BE021787 sm62e01.y1 Gm-c1028 Glycine max cDNA clone ... 39 0.081
 45 emb|AI965348|AI965348 sc70c09.y1 Gm-c1016 Glycine max cDNA clone... 39 0.11
 emb|AW729281|AW729281 GA_Ea0024J11 Gossypium arboreum 7-10 dpa ... 38 0.15
 emb|AI485216|AI485216 EST243520 tomato ovary, TAMU Lycopersicon ... 36 0.20
 emb|AI484866|AI484866 EST243127 tomato ovary, TAMU Lycopersicon ... 36 0.20
 emb|AI729570|AI729570 BNLGHi13679 Six-day Cotton fiber Gossypium... 38 0.21
 50 emb|AW688707|AW688707 NF010F12ST1F1000 Developing stem Medicago ... 37 0.29
 emb|AI483679|AI483679 EST249550 tomato ovary, TAMU Lycopersicon ... 37 0.39
 emb|AB029365|AB029365 Cephalotaxus harringtonia mitochondrial ge... 29 0.83

- Query= AC006920.138_at 12642_at /id_source genbank /description
 55 gb|aad22285.1|ac006920_9 (ac006920) unknown protein [arabidopsis
 thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006920|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006920|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006920|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac006920>
 60 (1512 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments:

(bits) Value

emb|AF223643|AF223643 Pisum sativum xyloglucan fucosyltransferas... 311 e-147

10 emb|AW719438|AW719438 LjNEST4f10r Lotus japonicus nodule library... 164 1e-64

emb|AA660464|AA660464 00349 MtRHE Medicago truncatula cDNA 5', m... 128 6e-38

emb|AW693268|AW693268 NF064A03ST1F1000 Developing stem Medicago ... 109 5e-32

emb|AW508697|AW508697 si35c12.y1 Gm-r1030 Glycine max cDNA clone... 77 6e-31

emb|AW689377|AW689377 NF018E07ST1F1000 Developing stem Medicago ... 78 2e-30

15 gb|BE058474|BE058474 sn16f08.y1 Gm-c1016 Glycine max cDNA clone ... 102 6e-21

emb|AW704030|AW704030 sk27a04.y1 Gm-c1028 Glycine max cDNA clone... 64 5e-20

emb|AU089974|AU089974 AU089974 Hordeum vulgare subsp. vulgare Up... 45 1e-19

emb|AW720399|AW720399 LjNEST22c8r Lotus japonicus nodule library... 83 1e-18

emb|AU089968|AU089968 AU089968 Hordeum vulgare subsp. vulgare Up... 45 5e-17

20 emb|AV417193|AV417193 AV417193 Lotus japonicus young plants (two... 88 2e-16

emb|AQ855554|AQ855554 CpG1646A CpIOWAgDNA1 Cryptosporidium parvu... 35 1.1

emb|Z37536|LTND9 L.tarentolae ND9 mRNA encoding putative NADH de... 35 2.1

emb|AW934637|AW934637 EST353529 tomato flower buds 0-3 mm, Corne... 35 2.1

emb|AF050740|AF050740 Plasmodium falciparum variant-specific sur... 35 2.1

25 emb|AI329848|AI329848 b8h09ne.r1 Neurospora crassa evening cDNA ... 35 2.1

emb|AW035275|AW035275 EST280638 tomato callus, TAMU Lycopersicon... 35 2.1

emb|AW933190|AW933190 EST359033 tomato fruit mature green, TAMU ... 35 2.1

emb|AL109832|SPAC630 S.pombe chromosome I cosmid c630. 34 2.9

emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, *** S... 34 4.0

30 emb|A85491|A85491 Sequence 150 from Patent EP0866129. 34 4.0

emb|AC004688|AC004688 Plasmodium falciparum chromosome 12 clone ... 34 4.0

emb|AA786891|AA786891 m7a05a1.r1 Aspergillus nidulans 24hr asexu... 34 4.0

gb|BE124954|BE124954 EST393989 GVN Medicago truncatula cDNA clon... 27 4.7

emb|AL356172|NCB23L21 Neurospora crassa DNA linkage group II BAC... 33 5.5

35 emb|AW617216|AW617216 EST323627 L. hirsutum trichome, Cornell Un... 33 5.5

emb|AL160493|LMFLCHR26 Leishmania major Friedlin assembled chrom... 33 7.6

emb|AF056622|AF056622 Vitis vinifera putative Cu/Zn superoxide d... 33 7.6

gb|BE053037|BE053037 GA__Ea0031O23f Gossypium arboreum 7-10 dpa ... 33 7.6

40

Query= AC004077.149_s_at 12989_s_at /id_source genbank /description
gb|aac26690.1| (ac004077) putative cytochrome p450 [arabidopsis
thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
/ncgi

(1488 letters)

45

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

50

Score E

Sequences producing significant alignments:

(bits) Value

emb|AW203670|AW203670 sf36h04.y1 Gm-c1028 Glycine max cDNA clone... 334 1e-90

55 emb|AW268012|AW268012 EST306234 DSIR Medicago truncatula cDNA cl... 246 2e-83

emb|AW041000|AW041000 EST283864 tomato mixed elicitor, BTI Lycop... 307 1e-82

emb|AW472433|AW472433 si25b07.y1 Gm-c1029 Glycine max cDNA clone... 306 3e-82

emb|AW560118|AW560118 EST315166 DSIR Medicago truncatula cDNA cl... 166 3e-64

emb|AW394771|AW394771 sh35b02.y1 Gm-c1017 Glycine max cDNA clone... 213 3e-54

60 emb|AW622568|AW622568 EST313368 tomato root during/after fruit s... 181 5e-51

emb|AW737712|AW737712 EST339139 tomato flower buds, anthesis, Co... 162 1e-45

	emb AW694002 AW694002 NF071F03ST1F1029 Developing stem Medicago ...	135	2e-45
	gb BE124930 BE124930 EST393965 GVN Medicago truncatula cDNA clon...	183	2e-45
	emb Z98974 SPAC19A8 S.pombe chromosome I cosmid c19A8.	114	1e-38
	emb AL111746 CNS019KA Botrytis cinerea strain T4 cDNA library un...	123	2e-38
5	emb AL111744 CNS019K8 Botrytis cinerea strain T4 cDNA library un...	123	3e-37
	emb AW922483 AW922483 DG1_19_A10.g1_A002 Dark Grown 1 (DG1) Sorg...	155	8e-37
	emb Z49211 SC9711X S.cerevisiae chromosome XIII cosmid 9711.	113	3e-36
	gb U34636 SCU34636 Saccharomyces cerevisiae cytochrome P450 gene...	113	3e-36
	emb AW928489 AW928489 EST337277 tomato flower buds 8 mm to pre-a...	149	5e-35
10	emb AL033396 CAC35A5 C.albicans cosmid Ca35A5.	117	2e-34
	emb AW310494 AW310494 sE36h04.x1 Gm-c1028 Glycine max cDNA clone...	124	2e-30
	emb AA676046 AA676046 TENF0565 T.cruzi epimastigote normalized c...	125	1e-27
	gb BE125362 BE125362 DG1_19_A10.b1_A002 Dark Grown 1 (DG1) Sorgh...	77	5e-21
	emb AW496913 AW496913 ga50a07.y1 Moss EST library PPU Physcomitr...	98	2e-19
15	emb AU012887 AU012887 AU012887 Schizosaccharomyces pombe late lo...	71	1e-12
	emb AJ238612 CRO238612 Catharanthus roseus mRNA for cytochrome P...	45	2e-12
	emb AW307234 AW307234 sf54d12.y1 Gm-c1009 Glycine max cDNA clone...	50	3e-12
	emb AF124815 AF124815 Mentha spicata cytochrome p450 mRNA, compl...	38	4e-10
	emb AV425399 AV425399 AV425399 Lotus japonicus young plants (two...	66	9e-10
20	emb AW234443 AW234443 sf25c03.y1 Gm-c1028 Glycine max cDNA clone...	51	4e-09
	emb AI495626 AI495626 sb11c08.y1 Gm-c1004 Glycine max cDNA clone...	51	4e-09
	emb AF000403 AF000403 Lotus japonicus putative cytochrome P450 ...	38	1e-08
	emb AF124816 AF124816 Mentha x piperita cytochrome p450 isoform ...	37	2e-08
	emb AW699711 AW699711 gb30h12.y1 Moss EST library PPN Physcomitr...	61	2e-08
25	emb AA556134 AA556134 TENF0475 T.cruzi epimastigote normalized c...	61	2e-08
	emb AA675972 AA675972 TENF0465 T.cruzi epimastigote normalized c...	61	2e-08
	emb AF124817 AF124817 Mentha x piperita cytochrome p450 isoform ...	37	2e-08
	emb AW255151 AW255151 ML1459 peppermint glandular trichome Menth...	37	1e-07
	emb AW720567 AW720567 LjNEST9g11rc Lotus japonicus nodule librar...	34	1e-07
30	emb AW719774 AW719774 LjNEST9G11r Lotus japonicus nodule library...	34	1e-07
	gb BE125544 BE125544 DG1_27_A10.b1_A002 Dark Grown 1 (DG1) Sorgh...	58	2e-07
	emb AW255409 AW255409 ML430 peppermint glandular trichome Mentha...	37	3e-07
	emb AW053855 AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp...	32	3e-07
	emb Y09291 TACYP51C6 T.aestivum mRNA for obtusifolius 14-alpha-d...	35	6e-07
35	emb Y09292 TACYP51C1 T.aestivum mRNA for obtusifolius 14-alpha-d...	35	7e-07
	emb AW145717 AW145717 ga33h06.y1 Moss EST library PPN Physcomitr...	55	1e-06
	gb U74319 SBU74319 Sorghum bicolor obtusifolius 14-alpha demethy...	32	1e-05
	emb AW255953 AW255953 MW299 peppermint glandular trichome Mentha...	37	1e-05
	emb AW163966 AW163966 Ljirnp17-385-h1 Ljirnp Lambda HybriZap ...	34	1e-05
40	emb AW728587 AW728587 GA_Ea0017C12 Gossypium arboreum 7-10 dpa ...	37	2e-05
	emb Z54096 SPAC13A11 S.pombe chromosome I cosmid c13A11.	44	3e-05
	emb AW666409 AW666409 sk36b12.y1 Gm-c1028 Glycine max cDNA clone...	51	3e-05
	emb AW255274 AW255274 ML276 peppermint glandular trichome Mentha...	37	3e-05
	emb Y10490 GMC450CP3 G.max mRNA for putative cytochrome P450, cl...	42	4e-05
45	emb AF022157 AF022157 Glycine max cytochrome P450 monooxygenase ...	50	4e-05
	emb AI731081 AI731081 BNLGH18648 Six-day Cotton fiber Gossypium ...	50	6e-05
	emb AW733598 AW733598 sk75f08.y1 Gm-c1016 Glycine max cDNA clone...	50	6e-05
	emb AW254782 AW254782 ML1065 peppermint glandular trichome Menth...	37	6e-05
	emb AW254794 AW254794 ML1076 peppermint glandular trichome Menth...	38	6e-05
50	emb AW256016 AW256016 MW370 peppermint glandular trichome Mentha...	37	6e-05
	emb AW254868 AW254868 ML1290 peppermint glandular trichome Menth...	37	7e-05
	emb AW310243 AW310243 sf33c07.x1 Gm-c1028 Glycine max cDNA clone...	49	1e-04
	emb AW570532 AW570532 sj63c04.y1 Gm-c1033 Glycine max cDNA clone...	49	1e-04
	emb AI495064 AI495064 sa90d10.y1 Gm-c1004 Glycine max cDNA clone...	49	1e-04
55	emb AI855736 AI855736 sc23f01.y1 Gm-c1013 Glycine max cDNA clone...	49	1e-04
	emb AI900822 AI900822 sb93h05.y1 Gm-c1017 Glycine max cDNA clone...	49	1e-04
	emb AW234028 AW234028 sf33c07.y1 Gm-c1028 Glycine max cDNA clone...	49	1e-04
	emb AW706535 AW706535 sj57g05.y1 Gm-c1033 Glycine max cDNA clone...	49	1e-04
	emb AW254954 AW254954 ML1124 peppermint glandular trichome Menth...	37	1e-04
60	emb AW255346 AW255346 ML357 peppermint glandular trichome Mentha...	37	1e-04
	emb AA824943 AA824943 CT226.complete Tomato Leaf cDNA from cv. V...	48	2e-04

	emb AW255059 AW255059 ML1354 peppermint glandular trichome Menth...	37	3e-04
	emb AW255126 AW255126 ML1418 peppermint glandular trichome Menth...	37	3e-04
	emb AW981162 AW981162 EST392356 DSIL Medicago truncatula cDNA cl...	47	3e-04
	emb AW299159 AW299159 EST305969 KV2 Medicago truncatula cDNA clo...	47	3e-04
5	emb AW706489 AW706489 sj57b08.y1 Gm-c1033 Glycine max cDNA clone...	46	5e-04
	emb AW620257 AW620257 si93g06.y1 Gm-c1031 Glycine max cDNA clone...	46	7e-04
	emb AW704313 AW704313 sk17f11.y1 Gm-c1028 Glycine max cDNA clone...	46	7e-04
	emb AW922821 AW922821 DG1_46_E11.g1_A002 Dark Grown 1 (DG1) Sorg...	46	0.001
	emb AI895869 AI895869 EST265312 tomato callus, TAMU Lycopersicon...	46	0.001
10	emb AJ238439 CAR238439 Cicer arietinum mRNA for a cytochrome P45...	46	0.001
	emb AW348613 AW348613 GM210002B22F6R Gm-r1021 Glycine max cDNA 3...	39	0.001
	emb AW255736 AW255736 ML798 peppermint glandular trichome Menta...	37	0.001
	emb AW101323 AW101323 sd77e08.y1 Gm-c1009 Glycine max cDNA clone...	39	0.001
	emb AW278093 AW278093 sf39f05.y1 Gm-c1009 Glycine max cDNA clone...	45	0.001
15	emb X70981 SMCYPEG2 S.melongena CYP71A1 mRNA for P450 hydroxylase.	32	0.002
	emb AI725768 AI725768 BNLGHI12931 Six-day Cotton fiber Gossypium...	45	0.002
	emb AB001379 AB001379 Glycyrrhiza echinata CYP81E1 mRNA for cyto...	45	0.002
	emb AB022732 AB022732 Glycyrrhiza echinata CYP Ge-31 mRNA for cy...	45	0.002
	emb AW218488 AW218488 EST303671 tomato radicle, 5 d post-imbibit...	32	0.002
20	emb AJ249800 CAR249800 Cicer arietinum partial mRNA for cytochro...	44	0.003
	emb AW432266 AW432266 sh71d11.y1 Gm-c1015 Glycine max cDNA clone...	44	0.003
	emb AF140614 AF140614 Manihot esculenta N-hydroxylating cytochro...	32	0.003
	emb AF022457 AF022457 Glycine max cytochrome P450 monooxygenase ...	41	0.003
	emb AJ271708 ABI271708 Agaricus bisporus partial mRNA for cytoch...	39	0.003
25	emb AW255619 AW255619 ML666 peppermint glandular trichome Menta...	33	0.003
	emb AI898152 AI898152 EST267595 tomato ovary, TAMU Lycopersicon ...	43	0.003
	emb AW152943 AW152943 se33a03.y1 Gm-c1015 Glycine max cDNA clone...	44	0.004
	emb AJ012581 CAR012581 Cicer arietinum mRNA for cytochrome P450.	44	0.004
	emb AI485298 AI485298 EST243602 tomato ovary, TAMU Lycopersicon ...	43	0.004
30	emb AI728374 AI728374 BNLGHI10609 Six-day Cotton fiber Gossypium...	43	0.005
	emb AI485472 AI485472 EST243793 tomato ovary, TAMU Lycopersicon ...	43	0.005

Query= AF003102.3_at 13435_at /id_source genbank /description

gb|aac49775.1| (af003102) ap2 domain containing protein rap2.9

35 [arabidopsis thaliana] /blast_score 1.00e-33 /ec_number /family
/chip nova /gb_link

<http://www3.ncbi.nlm.nih.gov/htbin->

post/entrez/query?db=n&form=6&dopt=g&uid=gb|af003102| /ncgi

<http://www.ncgr.org/cgi-bin/ff?af003102>

40 (417 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

45 Searching.....done

Score E

Sequences producing significant alignments:

(bits) Value

50	emb AW760536 AW760536 sl51e12.y1 Gm-c1027 Glycine max cDNA clone...	82	2e-15
	emb AW981184 AW981184 EST392378 DSIL Medicago truncatula cDNA cl...	57	5e-13
	emb AI728590 AI728590 BNLGHI11133 Six-day Cotton fiber Gossypium...	60	7e-13
	emb AI731959 AI731959 BNLGHI11511 Six-day Cotton fiber Gossypium...	60	7e-13
	emb AI775217 AI775217 EST256317 tomato resistant, Cornell Lycop...	59	7e-13
55	emb AW458973 AW458973 sh17e01.y1 Gm-c1016 Glycine max cDNA clone...	61	3e-12
	emb AW132527 AW132527 se05c02.y1 Gm-c1013 Glycine max cDNA clone...	61	3e-12
	emb AW102493 AW102493 sd88h04.y1 Gm-c1009 Glycine max cDNA clone...	61	4e-12
	emb AV421249 AV421249 AV421249 Lotus japonicus young plants (two...	62	2e-09
	emb AW691065 AW691065 NF040H08ST1F1000 Developing stem Medicago ...	61	3e-09
60	emb AW349295 AW349295 GM210004B12D12R Gm-r1021 Glycine max cDNA ...	46	8e-08
	emb AW101242 AW101242 sd97a09.y1 Gm-c1013 Glycine max cDNA clone...	56	2e-07

	emb AI898360 AI898360 EST267803 tomato ovary, TAMU Lycopersicon ...	39	6e-07
	emb AI496321 AI496321 sb05c05.y1 Gm-c1004 Glycine max cDNA clone...	50	9e-06
	emb AW208239 AW208239 M110892e GVSN Medicago truncatula cDNA clo...	48	3e-05
	emb AI489067 AI489067 EST247406 tomato ovary, TAMU Lycopersicon ...	45	3e-04
5	emb AI771636 AI771636 EST252736 tomato ovary, TAMU Lycopersicon ...	45	3e-04
	emb AW219417 AW219417 EST301995 tomato root during/after fruit s...	45	3e-04
	emb AI898830 AI898830 EST268273 tomato ovary, TAMU Lycopersicon ...	45	3e-04
	emb AI489478 AI489478 EST247817 tomato ovary, TAMU Lycopersicon ...	45	3e-04
	emb AI489770 AI489770 EST248109 tomato ovary, TAMU Lycopersicon ...	45	3e-04
10	emb AW672287 AW672287 LG1_358_A02.b1_A002 Light Grown 1 (LG1) So...	44	5e-04
	emb AI771296 AI771296 EST252312 tomato ovary, TAMU Lycopersicon ...	44	7e-04
	emb AI488844 AI488844 EST247183 tomato ovary, TAMU Lycopersicon ...	44	7e-04
	emb AJ238740 CRO238740 Catharanthus roseus mRNA for AP2-domain D...	43	0.001
	emb AV424732 AV424732 AV424732 Lotus japonicus young plants (two...	42	0.002
15	emb AW040122 AW040122 EST282621 tomato mixed elicitor, BTI Lycop...	33	0.002
	emb AW040111 AW040111 EST282610 tomato mixed elicitor, BTI Lycop...	33	0.002
	emb AI416505 AI416505 sal0g11.x1 Gm-c1003 Glycine max cDNA clone...	42	0.003
	emb AW597629 AW597629 sj96g05.y1 Gm-c1023 Glycine max cDNA clone...	42	0.003
	emb AI731684 AI731684 BNLGHi10485 Six-day Cotton fiber Gossypium...	42	0.003
20	emb AW727628 AW727628 GA_Ea0015E08 Gossypium arboreum 7-10 dpa ...	42	0.003
	emb AW109338 AW109338 gate0004G15f Gossypium arboreum 7-10 dpa f...	42	0.003
	emb AI416564 AI416564 sal0g11.y1 Gm-c1003 Glycine max cDNA clone...	42	0.003
	gb BE054117 BE054117 GA_Ea0004G15f Gossypium arboreum 7-10 dpa ...	42	0.003
	emb AW666769 AW666769 GA_Ea0005O23 Gossypium arboreum 7-10 dpa ...	42	0.003
25	emb AI731460 AI731460 BNLGHi9812 Six-day Cotton fiber Gossypium ...	42	0.003
	emb AW472387 AW472387 si24e07.y1 Gm-c1029 Glycine max cDNA clone...	42	0.003
	emb AI731267 AI731267 BNLGHi9029 Six-day Cotton fiber Gossypium ...	42	0.003
	emb AW832641 AW832641 sm15c04.y1 Gm-c1027 Glycine max cDNA clone...	41	0.003
	emb AW926228 AW926228 HVSMEg0006K15 Hordeum vulgare pre-anthesis...	41	0.004
30	emb AI795106 AI795106 sb76f04.y1 Gm-c1010 Glycine max cDNA clone...	41	0.004
	emb AW694919 AW694919 NF081D08ST1F1073 Developing stem Medicago ...	41	0.004
	emb AW706696 AW706696 sk01g02.y1 Gm-c1023 Glycine max cDNA clone...	41	0.004
	emb AI900613 AI900613 sc13f09.y1 Gm-c1013 Glycine max cDNA clone...	41	0.004
	emb AI937979 AI937979 sc06d12.y1 Gm-c1012 Glycine max cDNA clone...	41	0.004
35	emb AW220454 AW220454 EST302937 tomato root during/after fruit s...	41	0.005
	emb AW127214 AW127214 M110154 GVN Medicago truncatula cDNA clone...	41	0.005
	emb AW152963 AW152963 se33c03.y1 Gm-c1015 Glycine max cDNA clone...	41	0.005
	emb AW693001 AW693001 NF058C04ST1F1000 Developing stem Medicago ...	40	0.007
	emb AW278066 AW278066 sf39c09.y1 Gm-c1009 Glycine max cDNA clone...	40	0.007
40	emb AW318239 AW318239 sg62g03.y1 Gm-c1007 Glycine max cDNA clone...	40	0.007
	emb AW706818 AW706818 sk03g11.y1 Gm-c1023 Glycine max cDNA clone...	40	0.009
	emb AI166481 AI166481 xylem.est.309 Poplar xylem Lambda ZAPII li...	40	0.013
	emb AW759250 AW759250 sl38g10.y1 Gm-c1027 Glycine max cDNA clone...	39	0.018
	emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl...	39	0.018
45	emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl...	39	0.018
	emb AI896723 AI896723 EST266166 tomato callus, TAMU Lycopersicon...	39	0.018
	emb AW216598 AW216598 EST295312 tomato callus, TAMU Lycopersicon...	39	0.018
	emb AW034686 AW034686 EST278417 tomato callus, TAMU Lycopersicon...	39	0.018
	emb AI894724 AI894724 EST264167 tomato callus, TAMU Lycopersicon...	39	0.018
50	emb AW031292 AW031292 EST274667 tomato callus, TAMU Lycopersicon...	39	0.018
	emb AI487841 AI487841 EST246163 tomato ovary, TAMU Lycopersicon ...	39	0.018
	emb AW032262 AW032262 EST275716 tomato callus, TAMU Lycopersicon...	39	0.018
	emb AI486694 AI486694 EST245016 tomato ovary, TAMU Lycopersicon ...	39	0.018
	gb U89256 LEU89256 Lycopersicon esculentum DNA-binding protein P...	39	0.024
55	emb AI988644 AI988644 sd05h06.y1 Gm-c1020 Glycine max cDNA clone...	39	0.024
	emb AW278190 AW278190 sf40g11.y1 Gm-c1009 Glycine max cDNA clone...	39	0.024
	emb AW030009 AW030009 EST273264 tomato callus, TAMU Lycopersicon...	39	0.024
	emb AI894873 AI894873 EST264316 tomato callus, TAMU Lycopersicon...	39	0.024
	emb AW257352 AW257352 EST305489 KV2 Medicago truncatula cDNA clo...	39	0.024
60	emb AW030386 AW030386 EST273641 tomato callus, TAMU Lycopersicon...	39	0.024
	emb AV422393 AV422393 AV422393 Lotus japonicus young plants (two...	39	0.024

emb|AI973653|AI973653 sd07h05.y1 Gm-c1020 Glycine max cDNA clone... 39 0.024
 emb|AW349638|AW349638 GM210005B21A4R Gm-r1021 Glycine max cDNA 3... 39 0.024
 emb|AW396250|AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone... 39 0.024
 emb|AI896308|AI896308 EST265751 tomato callus, TAMU Lycopersicon... 38 0.033
 5 emb|AW774176|AW774176 EST333259 KV3 Medicago truncatula cDNA clo... 38 0.033
 emb|AW776668|AW776668 EST335733 DSIL Medicago truncatula cDNA cl... 38 0.033
 emb|AW507898|AW507898 si46f03.y1 Gm-r1030 Glycine max cDNA clone... 38 0.033
 emb|AW220395|AW220395 EST302878 tomato root during/after fruit s... 38 0.033
 emb|AW184868|AW184868 se69f03.y1 Gm-c1019 Glycine max cDNA clone... 38 0.033
 10 emb|AW308784|AW308784 sf71h01.y1 Gm-c1013 Glycine max cDNA clone... 38 0.033
 emb|AW574222|AW574222 EST316813 GVN Medicago truncatula cDNA clo... 38 0.033
 emb|AW035882|AW035882 EST282389 tomato callus, TAMU Lycopersicon... 38 0.033
 emb|AW394770|AW394770 sh35b01.y1 Gm-c1017 Glycine max cDNA clone... 38 0.046
 emb|AW164648|AW164648 se75g05.y1 Gm-c1023 Glycine max cDNA clone... 38 0.046
 15 emb|AI966402|AI966402 sc38e09.y1 Gm-c1014 Glycine max cDNA clone... 38 0.046
 gb|L22964|SOYCPGAD3A Glycine soja chloroplast 3-omega fatty acid ... 38 0.046
 emb|AI442716|AI442716 sa85d10.y1 Gm-c1004 Glycine max cDNA clone... 38 0.046
 emb|AW776927|AW776927 EST335992 DSIL Medicago truncatula cDNA cl... 38 0.046
 emb|AI900861|AI900861 sb95d04.y1 Gm-c1012 Glycine max cDNA clone... 38 0.046
 20 emb|AW930485|AW930485 EST340858 tomato fruit mature green, TAMU... 38 0.046
 emb|AI899237|AI899237 EST268680 tomato ovary, TAMU Lycopersicon ... 38 0.046
 emb|AW034216|AW034216 EST277787 tomato callus, TAMU Lycopersicon... 38 0.046
 emb|AI856708|AI856708 sb42g10.y1 Gm-c1014 Glycine max cDNA clone... 38 0.046
 emb|AW185124|AW185124 se87b06.y1 Gm-c1023 Glycine max cDNA clone... 38 0.046
 25 emb|AI895984|AI895984 EST265427 tomato callus, TAMU Lycopersicon... 38 0.046
 emb|AI778378|AI778378 EST259257 tomato susceptible, Cornell Lyco... 38 0.046
 emb|AI563167|AI563167 EST00291 watermelon lambda zap library Cit... 38 0.046

Query= AL022023.172_at 13966_at /id_source genbank /description
 30 emb|caal7775.1| (al022023) putative protein [arabidopsis thaliana]
 /blast_score 1.00e-173 /ec_number /family /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022023|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022023|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022023|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?al022023>
 35 (1161 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

		Score	E
	Sequences producing significant alignments:	(bits)	Value
45	emb AW185155 AW185155 se87e11.y1 Gm-c1023 Glycine max cDNA clone...	134	2e-30
	emb AW278569 AW278569 sf46b12.y1 Gm-c1009 Glycine max cDNA clone...	131	1e-29
	emb AW683973 AW683973 NF004E08NR1F1000 Nodulated root Medicago t...	97	2e-19
	emb AI055338 AI055338 coau0003L11 Cotton Boll Abscission Zone cD...	56	2e-07
	emb AW693058 AW693058 NF059E03ST1F1021 Developing stem Medicago ...	49	9e-05
50	emb AW686062 AW686062 NF033A11NR1F1000 Nodulated root Medicago t...	49	9e-05
	gb BE060490 BE060490 HVSMEg0012H04f Hordeum vulgare pre-anthesis...	37	0.22
	emb AW979446 AW979446 EST310344 tomato root deficiency, Cornell ...	35	1.0
	emb AI726520 AI726520 BNLGHi6046 Six-day Cotton fiber Gossypium ...	34	1.0
	gb M86518 PFAHMGLP Plasmodium falciparum high mobility group-lik...	35	1.1
55	emb AQ952389 AQ952389 Sheared DNA-32H3.TF Sheared DNA Trypanosom...	35	1.1
	emb AW775865 AW775865 EST334930 DSIL Medicago truncatula cDNA cl...	35	1.1
	emb AQ988902 AQ988902 04D1B01NE.R1 C. parvum Lambda Zap Express ...	35	1.1
	emb AV425088 AV425088 AV425088 Lotus japonicus young plants (two...	34	1.5
	emb AA676132 AA676132 TENF0683 T.cruzi epimastigote normalized c...	34	2.1
60	emb AL049183 PFMAL13P6 Plasmodium falciparum chromosome 13 strai...	33	2.8
	emb AF108883 AF108883 Capsicum annuum small GTP-binding protein ...	28	3.6

	emb X75082 STCITS S.tuberosum mRNA for mitochondrial citrate-syn...	33	3.9
	emb A46545 A46545 Sequence 1 from Patent WO9524487.	33	3.9
	emb X07693 SPNUC2 Fission yeast nuc2 gene encoding nuclear scaff...	33	3.9
	emb X83997 CPEAPC C.parasitica eapC gene.	33	3.9
5	emb AF143971 AF143971 Pinus taeda microsatellite PtTX3026 sequence.	33	3.9
	emb AW667663 AW667663 GA__Ea0010C16 Gossypium arboreum 7-10 dpa ...	33	5.0
	emb AI053174 AI053174 TENU1594 T. cruzi epimastigote normalized ...	32	5.3
	emb AW690972 AW690972 NF040A07ST1F1000 Developing stem Medicago ...	32	5.3
	emb AB012123 AB012123 Candida albicans CHS5 gene, complete cds.	32	5.3
10	emb AW761626 AW761626 gb27h09.y1 Moss EST library PPN Physcomitr...	32	6.9
	emb AI055163 AI055163 coau0003D12 Cotton Boll Abscission Zone cD...	32	6.9
	emb AW761333 AW761333 sl66b07.y1 Gm-c1027 Glycine max cDNA clone...	32	6.9
	emb AI822729 AI822729 L0-1261T3 Ice plant Lambda Uni-Zap XR expr...	32	6.9
	emb AW931465 AW931465 EST357308 tomato fruit mature green, TAMU ...	32	7.3
15	emb AA555413 AA555413 CpEST.644 uniZAPCpIOWAsporoLib3 Cryptospor...	32	7.3
	gb M80656 EIMPEM Eimeria maxima 230 kDa protein (pEM230) mRNA, 3...	32	7.3
	emb AI026260 AI026260 L0-455T3 Ice plant Lambda Uni-Zap XR expre...	32	7.3
	emb AQ640247 AQ640247 927P1-18B12.TV 927P1 Trypanosoma brucei ge...	32	7.3
	emb AQ491970 AQ491970 GN616G2 mTn-3xHA/lacZ Insertion Library Sa...	32	7.3
20	emb AF143965 AF143965 Pinus taeda microsatellite PtTX3011 sequence.	32	7.3
	gb U51031 YSCD9819 Saccharomyces cerevisiae chromosome IV cosmid...	32	7.3
	gb L06487 YSCZIP1A Saccharomyces cerevisiae ZIP1 protein gene, c...	32	7.3
	emb AQ850277 AQ850277 LMAJFV1_lm28b03.x1 Leishmania major FV1 ra...	32	9.4
	emb AJ225402 AJ225402 AJ225402 Absciscic acid-treated protonemata...	32	9.4
25	emb AW735860 AW735860 EST336628 tomato flower buds 0-3 mm, Corne...	32	9.4
	emb AW756470 AW756470 sl21g05.y1 Gm-c1036 Glycine max cDNA clone...	32	9.4
	Query= AC002521.68_at 14381_at /id_source genbank /description		
	gb aac05341.1 (ac002521) unknown protein [arabidopsis thaliana]		
30	/blast_score 0 /ec_number /family /chip nova /gb_link		
	http://www3.ncbi.nlm.nih.gov/htbin-		
	post/entrez/query?db=n&form=6&dopt=g&uid=gb ac002521 /ncgi		
	http://www.ncgr.org/cgi-bin/ff?ac002521		
	(999 letters)		
35	Database: plantfungal		
	661,018 sequences; 426,114,510 total letters		
	Searching.....done		
40			
	Score	E	
	Sequences producing significant alignments:		(bits) Value
	emb AI727718 AI727718 BNLGHi8830 Six-day Cotton fiber Gossypium ...	405	e-112
45	emb AI894939 AI894939 EST264382 tomato callus, TAMU Lycopersicon...	405	e-112
	emb AI727173 AI727173 BNLGHi7479 Six-day Cotton fiber Gossypium ...	404	e-112
	emb AW091566 AW091566 EST284842 tomato mixed elicitor, BTI Lycop...	364	e-100
	emb AW201381 AW201381 sf02d09.y1 Gm-c1027 Glycine max cDNA clone...	301	1e-98
	emb AW397167 AW397167 sg67f10.y1 Gm-c1007 Glycine max cDNA clone...	287	1e-94
50	emb AW038822 AW038822 EST280778 tomato mixed elicitor, BTI Lycop...	282	3e-75
	emb AI488594 AI488594 EST246933 tomato ovary, TAMU Lycopersicon ...	280	2e-74
	emb AW926055 AW926055 HVSMeg0006C20 Hordeum vulgare pre-anthesis...	160	2e-71
	gb T14872 T14872 crs323 lambdaZAPST Ricinus communis cDNA clone ...	187	4e-68
	emb AW329252 AW329252 N200470e rootphos(-) Medicago truncatula c...	246	2e-64
55	emb AW932653 AW932653 EST358496 tomato fruit mature green, TAMU...	246	2e-64
	emb AW508528 AW508528 si33a06.y1 Gm-r1030 Glycine max cDNA clone...	177	8e-60
	emb AW201152 AW201152 se98d11.y1 Gm-c1027 Glycine max cDNA clone...	137	1e-49
	emb AW011518 AW011518 ST21G07 Pine TriplEx shoot tip library Pin...	178	5e-44
	emb AW568929 AW568929 si74c04.y1 Gm-c1031 Glycine max cDNA clone...	169	3e-41
60	emb AW459302 AW459302 sh23c04.y1 Gm-c1016 Glycine max cDNA clone...	166	3e-40
	emb AV392100 AV392100 AV392100 Chlamydomonas reinhardtii C9 Chla...	114	1e-36

	emb Z67751 SC38KCXVI <i>S.cerevisiae</i> DNA (chromosome XVI; 38 kb).	87	8e-28
	emb Z73600 SCYPL244C <i>S.cerevisiae</i> chromosome XVI reading frame O...	87	9e-28
	emb AL096796 SPBC839 <i>S.pombe</i> chromosome II cosmid c839.	65	2e-25
	emb AL021816 SPBC24E9 <i>S.pombe</i> chromosome II cosmid c24E9.	65	2e-25
5	emb AW395997 AW395997 sh08a03.y1 Gm-c1016 Glycine max cDNA clone...	114	1e-24
	emb AT000300 AT000300 AT000300 Apple young fruit cDNA library Ma...	113	3e-24
	emb AI166335 AI166335 xylem.est.178 Poplar xylem Lambda ZAPII li...	90	2e-17
	emb AQ649102 AQ649102 Sheared DNA-16A11.TR Sheared DNA Trypanoso...	84	1e-15
	emb AQ449927 AQ449927 500006A04.x1 CplOWAM13mp18gDNA1 Cryptospor...	65	1e-09
10	emb AL354298 L5768AY <i>Leishmania major</i> Friedlin cosmid L5768.1 t7...	57	2e-07
	emb AW776002 AW776002 EST335067 DSIL <i>Medicago truncatula</i> cDNA cl...	50	3e-05
	gb BE033570 BE033570 MF03F06 MF <i>Mesembryanthemum crystallinum</i> cD...	47	2e-04
	emb AI727063 AI727063 BNLGHI7246 Six-day Cotton fiber <i>Gossypium</i> ...	44	0.002
	emb AW981371 AW981371 EST392524 DSIL <i>Medicago truncatula</i> cDNA cl...	41	0.016
15	emb AL132839 SPAC1093 <i>S.pombe</i> chromosome I cosmid c1093.	40	0.040
	emb AW981366 AW981366 EST392519 DSIL <i>Medicago truncatula</i> cDNA cl...	37	0.20
	emb AZ044909 AZ044909 A975/R Soybean genomic clone Glycine max g...	37	0.27
	emb AW220332 AW220332 EST302815 tomato root during/after fruit s...	36	0.37
	emb AI897952 AI897952 EST267395 tomato ovary, TAMU <i>Lycopersicon</i> ...	36	0.37
20	emb AW220428 AW220428 EST302911 tomato root during/after fruit s...	36	0.37
	emb AW932638 AW932638 EST358481 tomato fruit mature green, TAMU ...	36	0.37
	emb AQ845544 AQ845544 LMAJFV1_lm26h01.y1 <i>Leishmania major</i> FV1 ra...	35	0.70
	emb AC007862 AC007862 <i>Trypanosoma brucei</i> chromosome II clone RPC...	35	0.97
	emb AQ872760 AQ872760 V21H1 mTn-3xHA/lacZ Insertion Library, str...	35	1.3
25	emb Z38062 SC9687 <i>S.cerevisiae</i> chromosome IX cosmid 9687.	35	1.3
	emb AW428965 AW428965 EST306505 tomato flower buds 0-3 mm, Corne...	35	1.3
	emb X79743 SCBPPS <i>S.cerevisiae</i> BET1, PAN1 PRI1 and STS1 genes.	35	1.3
	emb AZ221045 AZ221045 Sheared DNA-64E9.TF Sheared DNA <i>Trypanosom</i> ...	35	1.3
	emb AF014809 AF014809 <i>Lycopersicon esculentum</i> proline transporte...	35	1.3
30	emb AF106079 AF106079 <i>Chlamydomonas reinhardtii</i> dynein heavy cha...	34	1.8
	gb M80437 YSCSEQ <i>Saccharomyces cerevisiae</i> gene, complete cds.	34	2.5
	gb J05603 YSCCTR <i>Saccharocyces cerevisiae</i> choline transport prot...	34	2.5
	emb Z72599 SCYGL077C <i>S.cerevisiae</i> chromosome VII reading frame O...	34	2.5
	gb T36987 T36987 EST102029 <i>S. cerevisiae</i> strain X2180-1A Sacchar...	34	2.5
35	emb Z71519 SCYNL243W <i>S.cerevisiae</i> chromosome XIV reading frame O...	33	3.4
	emb AW649403 AW649403 EST327857 tomato germinating seedlings, TA...	33	3.4
	emb Z22811 SCSLA2PA <i>S.cerevisiae</i> of Sla2p gene.	33	3.4
	emb Z69381 SCCXIV39K <i>S.cerevisiae</i> 38,855 bp segment of chromosom...	33	3.4
	emb AI898010 AI898010 EST267453 tomato ovary, TAMU <i>Lycopersicon</i> ...	33	3.4
40	gb L12352 YSCMOP2G <i>Saccharomyces cerevisiae</i> transmembrane protei...	33	3.4
	emb Z71518 SCYNL242W <i>S.cerevisiae</i> chromosome XIV reading frame O...	33	3.4
	emb AQ649183 AQ649183 Sheared DNA-6F2.TR Sheared DNA <i>Trypanosoma</i> ...	33	4.7
	emb AW181050 AW181050 MgA0550r MgA Library <i>Mycosphaerella gramin</i> ...	33	4.7
	emb AQ841780 AQ841780 T134030 Soybean RFLP probe Glycine max gen...	33	4.7
45	dbj D90206 CRECAH1G <i>C. reinhardtii</i> CAH1 gene for carbonic anhydr...	33	4.7
	emb X54487 CRCAH1 <i>Chlamydomonas reinhardtii</i> CAH1 gene for carbo...	33	4.7
	emb AW596179 AW596179 si99a03.y1 Gm-c1032 Glycine max cDNA clone...	33	4.7
	emb AI055366 AI055366 coau0003M17 Cotton Boll Abscission Zone cD...	33	4.7
	emb AW696344 AW696344 NF106H09ST1F1079 Developing stem <i>Medicago</i> ...	31	5.0
50	gb L36093 BLYPRX Barley peroxidase mRNA, complete cds.	32	6.5
	emb X58396 HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7).	32	6.5
	emb AL121851 LMFL2581 <i>Leishmania major</i> Friedlin chromosome 23 co...	32	6.5
	emb AW731480 AW731480 GA_Ea0030L23 <i>Gossypium arboreum</i> 7-10 dpa ...	32	6.5
	gb BE058697 BE058697 sn19e12.y1 Gm-c1016 Glycine max cDNA clone ...	32	6.5
55	emb AL031324 SPCC1672 <i>S.pombe</i> chromosome III cosmid c1672.	32	6.5
	emb AC007865 AC007865 <i>Trypanosoma brucei</i> chromosome II clone RPC...	28	6.8
	emb AW255798 AW255798 ML867 peppermint glandular trichome <i>Mentha</i> ...	26	7.0
	emb AW255452 AW255452 ML474 peppermint glandular trichome <i>Mentha</i> ...	26	7.0
	emb AI490316 AI490316 EST248642 tomato ovary, TAMU <i>Lycopersicon</i> ...	28	7.2
60	emb AF124817 AF124817 <i>Mentha x piperita</i> cytochrome p450 isoform ...	26	8.9
	emb AJ133001 CPL133001 <i>Craterostigma plantagineum</i> mRNA for phosp...	32	8.9

- emb|AW348239|AW348239 GM210001B12D9R Gm-r1021 Glycine max cDNA 3... 32 8.9
 emb|AQ903735|AQ903735 GSSTc04776 Trypanosome cruzi random genomi... 32 8.9
 emb|AB014483|AB014483 Nicotiana tabacum NtHSF1 mRNA for heat sho... 32 8.9
 emb|AF016328|AF016328 Hordeum vulgare Barperm2 (perm2) mRNA, par... 32 8.9
 5 emb|AW696053|AW696053 NF102A09ST1F1068 Developing stem Medicago ... 32 8.9
 emb|AW691566|AW691566 NF046E03ST1F1000 Developing stem Medicago ... 32 8.9
 emb|AW309484|AW309484 sf20a10.x1 Gm-c1028 Glycine max cDNA clone... 32 8.9
 emb|AI442542|AI442542 sa32h01.y1 Gm-c1004 Glycine max cDNA clone... 32 8.9
 emb|X55347|LPHSF24 Tomato mRNA for heat stress transcription fac... 32 8.9
 10 emb|X54488|CRCAH2 Chlamydomonas reinhardtii CAH2 gene for carbon... 32 8.9
 emb|A85864|A85864 Sequence 523 from Patent EP0866129. 32 8.9
 emb|AF020814|AF020814 Pisum sativum glucose-6-phosphate/phosphat... 32 8.9
 emb|AW184970|AW184970 se84g02.y1 Gm-c1023 Glycine max cDNA clone... 32 8.9
 emb|Z46871|SOEXG1 S.occidentalis gene for exo-1,3-beta-glucanase... 32 8.9
 15 emb|AI163250|AI163250 A038p15u Hybrid aspen plasmid library Popu... 32 8.9
 emb|AL023592|SPCC550 S.pombe chromosome III cosmid c550. 32 8.9
 emb|AW668371|AW668371 GA__Ea0013L20 Gossypium arboreum 7-10 dpa ... 26 9.3
 emb|AW255363|AW255363 ML376 peppermint glandular trichome Menth... 26 9.5
 gb|C96116|C96116 C96116 Marchantia polymorpha immature sex organ... 27 9.6
 20 emb|AW255126|AW255126 ML1418 peppermint glandular trichome Menth... 26 9.8

Query= AC000348.23_at 14443_at /id_source genbank /description
 gb|aab61498.1| (ac000348) t7n9.22 [arabidopsis thaliana] /blast_score
 0 /ec_number /family /chip nova /gb_link
 25 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000348|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000348|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000348|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac000348>
 (1869 letters)

- 30 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

- 35 Score E
 Sequences producing significant alignments: (bits) Value
- emb|AW622865|AW622865 EST306935 tomato flower buds 3-8 mm, Corne... 246 3e-64
 emb|AW907167|AW907167 EST343290 potato stolon, Cornell Universit... 152 7e-36
 40 emb|AW596038|AW596038 si97b04.y1 Gm-c1032 Glycine max cDNA clone... 98 4e-28
 emb|AW774367|AW774367 EST333518 KV3 Medicago truncatula cDNA clo... 101 1e-25
 emb|AW459521|AW459521 sh42e12.y1 Gm-c1017 Glycine max cDNA clone... 96 5e-24
 emb|AW777159|AW777159 Str2-E4 Sugar Beet germination cDNA librar... 82 1e-20
 emb|AW694460|AW694460 NF076E10ST1F1082 Developing stem Medicago ... 95 1e-18
 45 emb|AW651335|AW651335 EST329789 tomato germinating seedlings, TA... 82 8e-15
 gb|BE052602|BE052602 GA__Ea0032J02f Gossypium arboreum 7-10 dpa ... 50 2e-13
 emb|AW928691|AW928691 EST337479 tomato flower buds 8 mm to pre-a... 50 2e-09
 emb|AW226419|AW226419 ST82B05 Pine TriplEx shoot tip library Pin... 62 2e-08
 emb|AW398212|AW398212 EST298059 L. pennellii trichome, Cornell U... 60 4e-08
 50 emb|AT002124|AT002124 AT002124 Flower bud cDNA Brassica rapa sub... 44 0.004
 emb|AW666214|AW666214 sk33g11.y1 Gm-c1028 Glycine max cDNA clone... 40 0.040
 gb|U51033|YSCP9513 Saccharomyces cerevisiae chromosome XVI cosmi... 38 0.19
 emb|AI725302|AI725302 1168 PtIFG2 Pinus taeda cDNA clone 9253r, ... 38 0.19
 emb|AB035928|AB035928 Malus transitoria mRNA for St-RNase, compl... 36 0.50
 55 emb|Z48618|SCCHVII35 S.cerevisiae genes for RAD54, ACE1(CUP2), P... 36 0.68
 emb|Z72673|SCYGL151W S.cerevisiae chromosome VII reading frame O... 36 0.68
 emb|AF126872|AF126872 Magnaporthe grisea magnaporin mRNA, comple... 36 0.68
 emb|AF044679|AF044679 Leishmania major thiol specific antioxidan... 31 1.0
 emb|AC011617|AC011617 Leishmania major chromosome 35 clone L2993... 36 1.3
 60 emb|AB002141|AB002141 Pyrus pyrifolia mRNA for S5-RNase, complet... 35 1.3
 dbj|D88282|D88282 Pyrus serotina mRNA for S5-RNase, complete cds. 35 1.3

- emb|AB025421|AB025421 *Pyrus pyrifolia* gene for S3-RNase, complet... 35 1.3
 emb|AB002140|AB002140 *Pyrus pyrifolia* mRNA for S3-RNase, complet... 35 1.3
 emb|AL357592|LMFL5856 *Leishmania major* Friedlin chromosome 5 cos... 35 1.3
 5 emb|AW180136|AW180136 MgA0212f MgA Library *Mycosphaerella gramin...* 35 1.8
 emb|AW677734|AW677734 WS1_10_E07.g1_A002 Water-stressed 1 (WS1) ... 35 1.8
 emb|AI780435|AI780435 EST261314 tomato susceptible, Cornell Lyco... 34 2.4
 emb|AL355928|NCB1D4 *Neurospora crassa* DNA linkage group II BAC c... 34 2.4
 emb|AF188714|AF188714 *Emericella nidulans* chromosome VIII cosmid... 34 2.4
 emb|AF138284|AF138284 *Emericella nidulans* molybdopterin synthase... 34 2.4
 10 gb|M23080|BLYHORA *Hordeum vulgare* alpha-hordothionin (Hth-1) gen... 26 3.3
 emb|AQ989014|AQ989014 35C1D04NE.R1 *C. parvum* Lambda Zap Express ... 34 3.3
 emb|X55685|LEEXTENS Tomato extensin mRNA (clone uG-18). 34 3.3
 emb|AB001337|AB001337 *Saccharum officinarum* mRNA for Sucrose-Pho... 34 3.3
 emb|AW565301|AW565301 LG1_342_G03.g1_A002 Light Grown 1 (LG1) So... 34 3.3
 15 emb|AL035064|SPAC1687 *S.pombe* chromosome I cosmid c1687. 34 3.3
 emb|AJ223010|SCP223010 *Schizosaccharomyces pombe* pmt2 gene. 34 3.3
 emb|AL356456|LMFLUNK01 *Leishmania major* Friedlin cosmid clones L... 34 3.3
 emb|AW683291|AW683291 NF010B07LF1F1060 Developing leaf *Medicago* ... 34 3.3
 emb|X63357|HVNREHTH *H.vulgare* Hth-1 gene (promoter region). 26 3.3
 20 emb|AW710511|AW710511 e4c05ne.fl *Neurospora crassa* evening cDNA ... 34 4.4
 emb|AQ411888|AQ411888 CpG0892A CpIOWAgDNA1 *Cryptosporidium parvu...* 34 4.4
 emb|AB036808|AB036808 *Saccharomyces cerevisiae* DNA, plasmid pTLU... 33 4.6
 emb|AA901701|AA901701 NCP2A2T7 Perithecial *Neurospora crassa* cDN... 33 4.6
 emb|AF128526|AF128526 *Theileria lestoquardi* sporozoite antigen S... 33 4.6
 25 gb|M76671|TOMEXTENB *L.esculentum* extensin (class II) gene, compl... 33 4.6
 emb|AL049181|PFMAL13P4 *Plasmodium falciparum* chromosome 13 strai... 33 4.6
 emb|AB036809|AB036809 *Saccharomyces cerevisiae* DNA, plasmid pTLU... 33 4.6
 emb|AC004145|AC004145 *Leishmania major* chromosome 3 clone L5801 ... 32 4.8
 gb|L12467|YSCGCN1A *Saccharomyces cerevisiae* translational activa... 33 6.1
 30 emb|AW725958|AW725958 GA__Ea0020E02 *Gossypium arboreum* 7-10 dpa ... 33 6.1
 emb|X91837|SCCHVIEU *S.cerevisiae* G1301, G1304, G1307, G1315, G1... 33 6.1
 emb|Z72717|SCYGL195W *S.cerevisiae* chromosome VII reading frame O... 33 6.1
 emb|X55694|LEEXTEN14 Tomato extensin mRNA (clone w10-1 L). 33 6.3
 emb|X55693|LEEXTEN13 Tomato mRNA for a glycine-rich protein (clo... 33 6.3
 35 emb|AV427911|AV427911 AV427911 *Lotus japonicus* young plants (two... 33 6.3
 emb|AI897079|AI897079 EST266522 tomato ovary, TAMU *Lycopersicon* ... 33 6.3
 emb|AW690872|AW690872 NF039H07ST1F1000 Developing stem *Medicago* ... 33 6.3
 emb|AW688252|AW688252 NF005C01ST1F1000 Developing stem *Medicago* ... 33 6.3
 gb|L38908|TOBEXTE *Nicotiana tabacum* extensin gene, complete cds. 33 6.3
 40 dbj|D13951|TOBEXTS Tobacco gene for extensin, complete cds. 33 6.3
 dbj|E05393|E05393 DNA sequence encoding *Nicotiana tabacum* extensin. 33 6.3
 emb|AA901958|AA901958 NCC2C12T7 *Conidial Neurospora crassa* cDNA ... 33 8.3
 emb|AW704352|AW704352 sk18c03.y1 Gm-cl028 Glycine max cDNA clone... 33 8.3
 emb|AF085735|AF085735 *Trypanosoma triglae* kinetoplast minicircle... 33 8.3
 45 emb|AW457944|AW457944 sh97h02.y1 Gm-cl016 Glycine max cDNA clone... 33 8.3
 emb|AW714167|AW714167 h6d08ne.fl *Neurospora crassa* evening cDNA ... 33 8.3
 emb|AI320172|AI320172 clf06nm.fl *Neurospora crassa* morning cDNA ... 33 8.3
 emb|AQ941354|AQ941354 Sheared DNA-19O3.TR Sheared DNA *Trypanosom...* 32 8.6
 emb|AF046120|AF046120 *Candida glabrata* ATP-binding cassette tran... 32 8.6
 50 emb|AW725268|AW725268 GA__Ea0015L23 *Gossypium arboreum* 7-10 dpa ... 32 8.6
 emb|X77955|NCERG3 *N.crassa* (74-OR23-1VA) erg3 gene. 27 8.8

Query= AL022605.63_at 14882_at /id_source genbank /description
 emb|caa18753.1| (al022605) putative protein [arabidopsis thaliana]
 55 /blast_score 1.00e-103 /ec_number /family /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022605|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022605|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022605|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?al022605>
 (645 letters)

60

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5	Score	E
Sequences producing significant alignments:		(bits) Value
	emb AW398164 AW398164 EST298047 L. pennellii trichome, Cornell U...	101 1e-44
	emb AW351246 AW351246 GM210011A20F7R Gm-r1021 Glycine max cDNA 3...	114 3e-43
10	emb AW222063 AW222063 EST298874 tomato fruit red ripe, TAMU Lyco...	103 4e-40
	emb AW218145 AW218145 EST303326 tomato radicle, 5 d post-imbibit...	103 1e-39
	emb AW398260 AW398260 EST298107 L. pennellii trichome, Cornell U...	101 3e-39
	emb AW477271 AW477271 ga44c12.y1 Moss EST library PPU Physcomitr...	94 1e-38
	emb AW568049 AW568049 si56g06.y1 Gm-r1030 Glycine max cDNA clone...	102 1e-36
15	emb AW565775 AW565775 LG1_349_D04.g1_A002 Light Grown 1 (LG1) So...	108 5e-35
	emb AW218146 AW218146 EST303327 tomato radicle, 5 d post-imbibit...	108 5e-26
	emb AI488047 AI488047 EST246369 tomato ovary, TAMU Lycopersicon ...	78 3e-24
	emb AW671633 AW671633 LG1_349_D04.b1_A002 Light Grown 1 (LG1) So...	111 4e-24
	emb AI495965 AI495965 sb18d07.y1 Gm-c1004 Glycine max cDNA clone...	102 3e-21
20	emb AT002115 AT002115 AT002115 Flower bud cDNA Brassica rapa sub...	52 1e-09
	emb AT001714 AT001714 AT001714 Flower bud cDNA Brassica rapa sub...	52 3e-09
	emb AW621058 AW621058 sj95d05.y1 Gm-c1023 Glycine max cDNA clone...	52 3e-08
	emb AW099304 AW099304 sd38a08.y1 Gm-c1016 Glycine max cDNA clone...	33 0.092
	emb AI774719 AI774719 EST255819 tomato resistant, Cornell Lycope...	35 0.12
25	emb AW040524 AW040524 EST283484 tomato mixed elicitor, BTI Lycop...	35 0.12
	emb AB003068 AB003068 Trypanosoma cruzi clone TcCE5-9-1 mRNA, pa...	36 0.22
	emb AI781680 AI781680 EST262559 tomato susceptible, Cornell Lyco...	33 0.29
	emb AI778418 AI778418 EST259297 tomato susceptible, Cornell Lyco...	33 0.29
	emb AI775731 AI775731 EST256831 tomato resistant, Cornell Lycope...	35 0.78
30	emb AF047694 AF047694 Vernicia fordii glutaredoxin mRNA, complet...	34 1.1
	emb AW599677 AW599677 ga91d04.y1 Moss EST library PPN Physcomitr...	34 1.1
	emb AW039130 AW039130 EST281103 tomato mixed elicitor, BTI Lycop...	31 1.3
	emb AB003073 AB003073 Trypanosoma cruzi clone CE5-9-5 mRNA, part...	34 1.5
	emb AI899521 AI899521 EST268964 tomato susceptible, Cornell Lyco...	30 1.8
35	emb AI055583 AI055583 coau0004G11 Cotton Boll Abscission Zone cD...	33 2.0
	emb AI776180 AI776180 EST257280 tomato resistant, Cornell Lycope...	30 2.4
	emb AL110509 SPAC1250 S.pombe chromosome I cosmid c1250.	33 2.8
	emb Z74775 SCYOL033W S.cerevisiae chromosome XV reading frame OR...	33 2.8
	gb BE034215 BE034215 MH01C08 MH Mesembryanthemum crystallinum cD...	33 2.8
40	emb AZ220957 AZ220957 Sheared DNA-94E5.TR Sheared DNA Trypanosom...	33 2.8
	gb L39015 YSCMSE1G Saccharomyces cerevisiae nuclear-encoded mito...	33 2.8
	emb AI398391 AI398391 NCSM1H10T7 Subtracted Mycelial Neurospora ...	33 2.8
	emb AI898738 AI898738 EST268181 tomato ovary, TAMU Lycopersicon ...	32 3.8
	emb AI487645 AI487645 EST245967 tomato ovary, TAMU Lycopersicon ...	32 3.8
45	emb AW929266 AW929266 EST338054 tomato flower buds 8 mm to pre-a...	32 3.8
	emb AQ911385 AQ911385 LMAJFV1_in03f07.x1 Leishmania major FV1 ra...	32 3.8
	emb AW677168 AW677168 DG1_5_E01.b1_A002 Dark Grown 1 (DG1) Sorgh...	32 3.8
	emb AI486591 AI486591 EST244912 tomato ovary, TAMU Lycopersicon ...	32 3.8
	emb AU011071 AU011071 AU011071 Schizosaccharomyces pombe late lo...	32 3.8
50	emb AI776382 AI776382 EST257482 tomato resistant, Cornell Lycope...	29 4.3
	emb AW760067 AW760067 sl57f01.y1 Gm-c1027 Glycine max cDNA clone...	28 4.7
	emb AW570039 AW570039 si85h08.y1 Gm-c1031 Glycine max cDNA clone...	32 5.3
	emb Z36045 SCYBR176W S.cerevisiae chromosome II reading frame OR...	32 5.3
	emb AB012577 AB012577 Saccharomyces cerevisiae EHT1 gene for alc...	32 5.3
55	emb AQ952955 AQ952955 Sheared DNA-52J12.TR Sheared DNA Trypanoso...	32 5.3
	emb AW704696 AW704696 sk39d04.y1 Gm-c1028 Glycine max cDNA clone...	31 7.2
	emb AF091835 AF091835 Trypanosoma cruzi strain CL beta tubulin a...	31 7.2
	gb M96849 TRBBEALTUB Trypanosoma cruzi beta and alpha tubulin ge...	31 7.2
	gb M97956 TRBBEALTU Trypanosoma cruzi beta tubulin and alpha tub...	31 7.2
60	emb AW686835 AW686835 NF043H11NR1F1000 Nodulated root Medicago t...	31 9.9
	emb AI304976 AI304976 EST00081 mRNP Lambda ZapII Express Library...	31 9.9

emb|AF026421|AF026421 Chlamydomonas reinhardtii clone CD191 star... 31 9.9
 emb|AV391990|AV391990 AV391990 Chlamydomonas reinhardtii C9 Chla... 31 9.9
 emb|AW624834|AW624834 EST313651 tomato radicle, 5 d post-imbibit... 31 9.9
 gb|L34658|FSOGAGPOL Fusarium oxysporum gag polypeptide (gag) gen... 31 9.9
 5 emb|X64601|ANNIMTMR A.nidulans nimT mRNA for tyrosine phosphatase. 31 9.9

Query= U93215.38_at 15366_at /id_source genbank /description
 gb|aab63077.1| (u93215) unknown protein [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link
 10 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|u93215| /ncgi
 http://www.ncgr.org/cgi-bin/ff?u93215
 (1761 letters)

15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

20 Score E
 Sequences producing significant alignments: (bits) Value

emb|AV411445|AV411445 AV411445 Lotus japonicus young plants (two... 198 1e-49
 emb|AV415235|AV415235 AV415235 Lotus japonicus young plants (two... 190 3e-47
 25 emb|AV415282|AV415282 AV415282 Lotus japonicus young plants (two... 190 3e-47
 emb|AW906097|AW906097 EST342218 potato stolon, Cornell Universit... 162 8e-39
 emb|AV413830|AV413830 AV413830 Lotus japonicus young plants (two... 161 1e-38
 emb|AV419573|AV419573 AV419573 Lotus japonicus young plants (two... 82 5e-36
 emb|AA660119|AA660119 EST00006 watermelon lambda zap express lib... 148 7e-36
 30 emb|AI507855|AI507855 sa88a07.y1 Gm-c1004 Glycine max cDNA clone... 91 2e-35
 emb|AW160273|AW160273 EST290131 L. pennellii trichome, Cornell U... 146 4e-34
 emb|AV428532|AV428532 AV428532 Lotus japonicus young plants (two... 80 3e-30
 emb|AV424557|AV424557 AV424557 Lotus japonicus young plants (two... 128 1e-28
 emb|AW668007|AW668007 GA_Ea0012E04 Gossypium arboreum 7-10 dpa ... 117 2e-25
 35 emb|AW922981|AW922981 DGI_48_B03.b1_A002 Dark Grown 1 (DGI) Sorg... 105 8e-22
 emb|AW432282|AW432282 sh71f09.y1 Gm-c1015 Glycine max cDNA clone... 100 3e-20
 emb|AW621610|AW621610 EST312408 tomato root during/after fruit s... 100 5e-20
 emb|AV419981|AV419981 AV419981 Lotus japonicus young plants (two... 95 2e-18
 emb|AI937949|AI937949 sc06a10.y1 Gm-c1012 Glycine max cDNA clone... 88 3e-16
 40 emb|AV406642|AV406642 AV406642 Lotus japonicus young plants (two... 67 6e-10
 emb|AW497095|AW497095 ga53g06.y1 Moss EST library PPU Physcomitr... 42 3e-06
 emb|AW289850|AW289850 NXNV006F04F Nsf Xylem Normal wood Vertical... 40 4e-05
 emb|AW279534|AW279534 sf90g12.y1 Gm-c1019 Glycine max cDNA clone... 46 7e-04
 emb|AQ911817|AQ911817 LMAJFV1_in03b09.y1 Leishmania major FV1 ra... 46 7e-04
 45 emb|AW689523|AW689523 NF021G01ST1F1000 Developing stem Medicago ... 39 0.007
 emb|AW218923|AW218923 EST301405 tomato root during/after fruit s... 41 0.030
 emb|AW695963|AW695963 NF101A10ST1F1072 Developing stem Medicago ... 40 0.041
 emb|AW931531|AW931531 EST357374 tomato fruit mature green, TAMU ... 40 0.041
 emb|AW691108|AW691108 NF041C09ST1F1000 Developing stem Medicago ... 39 0.14
 50 emb|AA791402|AA791402 L0-136M13R Ice plant Lambda Uni-Zap XR exp... 38 0.20
 emb|AI001408|AI001408 L0-330M13R Ice plant Lambda Uni-Zap XR exp... 38 0.20
 emb|AI731457|AI731457 BNLGHi9807 Six-day Cotton fiber Gossypium ... 38 0.27
 emb|AQ161167|AQ161167 mgxb0007I01r CUGI Rice Blast BAC Library P... 35 1.3
 emb|AW690030|AW690030 NF027E08ST1F1000 Developing stem Medicago ... 35 1.8
 55 gb|BE124825|BE124825 EST393860 GVN Medicago truncatula cDNA clon... 35 1.8
 emb|AW684862|AW684862 NF022D06NR1F1000 Nodulated root Medicago t... 35 1.8
 emb|AW686248|AW686248 NF039F10NR1F1000 Nodulated root Medicago t... 35 1.8
 emb|AW696000|AW696000 NF100H02ST1F1026 Developing stem Medicago ... 35 1.8
 emb|AW686364|AW686364 NF037B05NR1F1000 Nodulated root Medicago t... 35 1.8
 60 emb|AW926002|AW926002 HVSMEg0006A15 Hordeum vulgare pre-anthesis... 35 2.5
 emb|AA660722|AA660722 00613 MtRHE Medicago truncatula cDNA 5', m... 34 3.5

	emb AI054829 AI054829 coau0002E06 Cotton Boll Abscission Zone cD...	34	3.5
	emb AW719283 AW719283 LjNEST2b8r Lotus japonicus nodule library,...	34	3.5
	emb AW677540 AW677540 DG1_8_H03.b1_A002 Dark Grown 1 (DG1) Sorgh...	34	4.8
	emb X78996 CSTETFP C.sativus mRNA for tetrafunctional protein.	33	6.6
5	emb AQ654502 AQ654502 Sheared DNA-25C14.TR Sheared DNA Trypanoso...	33	6.6
	emb AW981113 AW981113 EST392266 GVN Medicago truncatula cDNA clo...	33	6.6
	gb L40389 YSAERG11X Candida glabrata ERG11 gene, complete cds.	33	6.6
	emb X79365 CSMFPB C.sativus MFP-b mRNA.	33	6.6
	gb U05612 CSU05612 Colysis sintenensis chloroplast large subunit...	28	6.8
10	emb X02433 MIPSCOX2 Pea mitochondrial gene for cytochrome oxidas...	24	6.9
	emb AQ654503 AQ654503 Sheared DNA-25C15.TR Sheared DNA Trypanoso...	33	9.0
	emb AI163319 AI163319 A039P66U Hybrid aspen plasmid library Popu...	33	9.0
	emb AQ641986 AQ641986 RPCI93-EcoRI-6N23.TJ RPCI93-EcoRI Trypanos...	33	9.0
	emb AL034558 PFMAL3P2 Plasmodium falciparum MAL3P2, complete seq...	33	9.0
15	emb AQ649633 AQ649633 Sheared DNA-17K4.TF Sheared DNA Trypanosom...	33	9.0
	emb AI728749 AI728749 BNLGHi11499 Six-day Cotton fiber Gossypium...	33	9.0
	emb AQ940463 AQ940463 Sheared DNA-33A23.TR Sheared DNA Trypanoso...	33	9.0
	emb AQ647492 AQ647492 RPCI93-EcoRI-6G10.TJ RPCI93-EcoRI Trypanos...	33	9.0
	emb AW443117 AW443117 EST308047 tomato mixed elicitor, BTI Lycop...	33	9.0
20	emb AA231646 AA231646 CDO328.F cDNA from oat Avena sativa cDNA c...	33	9.0
Query= AF000657.28_at 15415_at /id_source genbank /description			
gb aab72169.1 (af000657) hypothetical protein [arabidopsis thaliana]			
/blast_score 9.00e-96 /ec_number /family /chip nova /gb_link			
25	http://www3.ncbi.nlm.nih.gov/htbin-		
	post/entrez/query?db=n&form=6&dopt=g&uid=gb af000657 /ncgi		
	http://www.ncgr.org/cgi-bin/ff?af000657		
	(564 letters)		
30	Database: plantfungal		
	661,018 sequences; 426,114,510 total letters		
	Searching.....done		
35	Score E		
	Sequences producing significant alignments: (bits) Value		
	emb AW622665 AW622665 EST313465 tomato root during/after fruit s...	166	8e-42
	emb AW625889 AW625889 EST319892 tomato radicle, 5 d post-imbibit...	166	1e-41
40	emb AI776839 AI776839 EST257939 tomato resistant, Cornell Lycopersicon...	166	2e-40
	emb AI898331 AI898331 EST267774 tomato ovary, TAMU Lycopersicon ...	166	2e-40
	emb AI772887 AI772887 EST253987 tomato resistant, Cornell Lycopersicon...	166	2e-40
	emb AI782639 AI782639 EST263518 tomato susceptible, Cornell Lycopersicon...	161	2e-40
	emb AW035141 AW035141 EST280403 tomato callus, TAMU Lycopersicon...	162	3e-40
45	emb AW559773 AW559773 EST314821 DSIR Medicago truncatula cDNA cl...	136	4e-40
	emb AI488935 AI488935 EST247274 tomato ovary, TAMU Lycopersicon ...	162	1e-39
	emb AW626015 AW626015 EST319922 tomato radicle, 5 d post-imbibit...	161	4e-39
	emb AW035118 AW035118 EST280380 tomato callus, TAMU Lycopersicon...	159	1e-38
	emb AI442841 AI442841 sa27e02.x1 Gm-c1004 Glycine max cDNA clone...	131	2e-38
50	gb BE057238 BE057238 sm99d06.y1 Gm-c1015 Glycine max cDNA clone ...	133	4e-37
	gb BE021888 BE021888 sm63g06.y1 Gm-c1028 Glycine max cDNA clone ...	151	4e-36
	emb AW782173 AW782173 sm02d12.y1 Gm-c1027 Glycine max cDNA clone...	151	4e-36
	emb AW981240 AW981240 EST392330 DSIL Medicago truncatula cDNA cl...	127	5e-36
	emb AW624844 AW624844 EST313673 tomato radicle, 5 d post-imbibit...	150	6e-36
55	emb AW348098 AW348098 GM210001A11F3R Gm-r1021 Glycine max cDNA 3...	121	1e-35
	emb AW348956 AW348956 GM210004A12C2R Gm-r1021 Glycine max cDNA 3...	127	2e-35
	gb BE058374 BE058374 sn15b11.y1 Gm-c1016 Glycine max cDNA clone ...	127	2e-35
	emb AW570563 AW570563 sj63f09.y1 Gm-c1033 Glycine max cDNA clone...	127	2e-35
60	emb AW568265 AW568265 si69f02.y1 Gm-r1030 Glycine max cDNA clone...	127	2e-35
	emb AW666011 AW666011 sk31a06.y1 Gm-c1028 Glycine max cDNA clone...	127	2e-35

	emb AW306271 AW306271 se48e06.y1 Gm-c1017 Glycine max cDNA clone...	125 6e-35
	emb AI772066 AI772066 EST253166 tomato resistant, Cornell Lycopersicon...	146 1e-34
	emb AW395160 AW395160 sh40f10.y1 Gm-c1017 Glycine max cDNA clone...	124 1e-34
	emb AW306309 AW306309 se49a06.y1 Gm-c1017 Glycine max cDNA clone...	124 1e-34
5	gb BE022272 BE022272 sm73a07.y1 Gm-c1028 Glycine max cDNA clone ...	146 1e-34
	gb BE021996 BE021996 sm65c01.y1 Gm-c1028 Glycine max cDNA clone ...	146 1e-34
	emb AW706543 AW706543 sj57h02.y1 Gm-c1033 Glycine max cDNA clone...	146 1e-34
	emb AW620987 AW620987 sj50d09.y1 Gm-c1033 Glycine max cDNA clone...	146 1e-34
10	emb AW349990 AW349990 GM210006B20G11R Gm-r1021 Glycine max cDNA ...	146 1e-34
	emb AW706119 AW706119 sj52a11.y1 Gm-c1033 Glycine max cDNA clone...	146 1e-34
	emb AW311107 AW311107 sg33a02.y1 Gm-c1025 Glycine max cDNA clone...	124 2e-34
	emb AW200806 AW200806 se93g05.y1 Gm-c1027 Glycine max cDNA clone...	123 3e-34
	emb AW830450 AW830450 sm27b08.y1 Gm-c1028 Glycine max cDNA clone...	145 3e-34
15	emb AW458429 AW458429 sh09b05.y1 Gm-c1016 Glycine max cDNA clone...	127 4e-34
	emb AW559537 AW559537 EST314585 DSIR Medicago truncatula cDNA cl...	79 5e-34
	emb AW559584 AW559584 EST314632 DSIR Medicago truncatula cDNA cl...	79 5e-34
	emb AI939020 AI939020 sc64e06.y1 Gm-c1016 Glycine max cDNA clone...	144 7e-34
	emb AW234019 AW234019 sf33b10.y1 Gm-c1028 Glycine max cDNA clone...	143 1e-33
20	emb AW011055 AW011055 ST16B07 Pine TriplEx shoot tip library Pin...	142 2e-33
	emb AW687043 AW687043 NF005D02RT1F1016 Developing root Medicago ...	133 2e-33
	gb BE022312 BE022312 sm73c09.y1 Gm-c1028 Glycine max cDNA clone ...	142 3e-33
	emb AW620826 AW620826 sj47a07.y1 Gm-c1033 Glycine max cDNA clone...	119 3e-33
	emb AW666225 AW666225 sk34a04.y1 Gm-c1028 Glycine max cDNA clone...	140 9e-33
25	emb AI494896 AI494896 sb06g10.y1 Gm-c1004 Glycine max cDNA clone...	140 9e-33
	emb AI443387 AI443387 sa31d11.x1 Gm-c1004 Glycine max cDNA clone...	139 1e-32
	emb AW203753 AW203753 sf37h02.y1 Gm-c1028 Glycine max cDNA clone...	139 2e-32
	emb AW559725 AW559725 EST314717 DSIR Medicago truncatula cDNA cl...	78 4e-32
	emb AW289859 AW289859 NXNV007A04F Nsf Xylem Normal wood Vertical...	137 4e-32
30	emb AW234737 AW234737 sf18f10.y1 Gm-c1028 Glycine max cDNA clone...	136 2e-31
	emb AW351059 AW351059 GM210010B10G3R Gm-r1021 Glycine max cDNA 3...	136 2e-31
	emb AW684772 AW684772 NF021H06NR1F1000 Nodulated root Medicago t...	120 5e-31
	emb AW775144 AW775144 EST334295 KV3 Medicago truncatula cDNA clo...	76 9e-31
35	emb AI495113 AI495113 sb03f02.y1 Gm-c1004 Glycine max cDNA clone...	133 1e-30
	emb AW472306 AW472306 si23e07.y1 Gm-c1029 Glycine max cDNA clone...	117 2e-30
	emb AW035139 AW035139 EST280401 tomato callus, TAMU Lycopersicon...	131 5e-30
	emb AI496590 AI496590 sb13g02.y1 Gm-c1004 Glycine max cDNA clone...	129 2e-29
	emb AW351151 AW351151 GM210011A10E12R Gm-r1021 Glycine max cDNA ...	81 2e-29
40	emb AW460064 AW460064 si08g11.y1 Gm-c1029 Glycine max cDNA clone...	105 4e-29
	emb AW432674 AW432674 sh83h05.y1 Gm-c1016 Glycine max cDNA clone...	126 1e-28
	emb AW507521 AW507521 si53a07.y1 Gm-r1030 Glycine max cDNA clone...	106 1e-28
	emb AI461088 AI461088 sa73g10.y1 Gm-c1004 Glycine max cDNA clone...	123 8e-28
	emb AI461045 AI461045 sa73c04.y1 Gm-c1004 Glycine max cDNA clone...	123 8e-28
45	emb AW010003 AW010003 ST01B12 Pine TriplEx shoot tip library Pin...	123 8e-28
	gb BE021390 BE021390 sm48e04.y1 Gm-c1028 Glycine max cDNA clone ...	122 2e-27
	gb BE022539 BE022539 sm86c09.y1 Gm-c1015 Glycine max cDNA clone ...	121 4e-27
	emb AW559258 AW559258 EST306094 DSIR Medicago truncatula cDNA cl...	118 3e-26
	emb AW760707 AW760707 sl36a09.y1 Gm-c1027 Glycine max cDNA clone...	95 8e-26
50	emb AI941013 AI941013 sb83c06.y1 Gm-c1010 Glycine max cDNA clone...	95 8e-26
	emb AW745074 AW745074 LG1_386_D11.b1_A002 Light Grown 1 (LG1) So...	91 3e-25
	emb AI900284 AI900284 sc03d11.y1 Gm-c1012 Glycine max cDNA clone...	111 4e-25
	emb AW666457 AW666457 sk36g12.y1 Gm-c1028 Glycine max cDNA clone...	114 7e-25
	emb AI522845 AI522845 sa74e03.y1 Gm-c1004 Glycine max cDNA clone...	114 7e-25
55	emb AW350289 AW350289 GM210008A10D4R Gm-r1021 Glycine max cDNA 3...	113 9e-25
	emb AW233771 AW233771 sf26e08.y1 Gm-c1028 Glycine max cDNA clone...	105 1e-24
	gb BE021431 BE021431 sm49a02.y1 Gm-c1028 Glycine max cDNA clone ...	111 4e-24
	emb AW495792 AW495792 NXNV_065_D12_FF Nsf Xylem Normal wood Vert...	110 8e-24
60	emb AI441701 AI441701 sa60b06.y1 Gm-c1004 Glycine max cDNA clone...	110 8e-24
	emb AW686910 AW686910 NF003H08RT1F1000 Developing root Medicago ...	79 9e-24

emb|AW310235|AW310235 sf33b10.x1 Gm-c1028 Glycine max cDNA clone... 110 1e-23
 emb|AI495196|AI495196 sa89d04.y1 Gm-c1004 Glycine max cDNA clone... 100 4e-23
 emb|AI442650|AI442650 sa43f05.y1 Gm-c1004 Glycine max cDNA clone... 106 1e-22
 emb|AW926095|AW926095 HVSMEg0006F02 Hordeum vulgare pre-anthesis... 106 1e-22
 5 emb|AW309915|AW309915 sf26e08.x1 Gm-c1028 Glycine max cDNA clone... 105 2e-22
 emb|AI812367|AI812367 1E2 Pine Lambda Zap Xylem library Pinus ta... 104 5e-22
 gb|BE022988|BE022988 sm69b05.y1 Gm-c1028 Glycine max cDNA clone... 103 1e-21
 emb|AI748713|AI748713 sb61a02.y1 Gm-c1010 Glycine max cDNA clone... 82 1e-21
 gb|BE020169|BE020169 sm39e04.y1 Gm-c1028 Glycine max cDNA clone... 103 1e-21
 10 gb|BE021658|BE021658 sm60g09.y1 Gm-c1028 Glycine max cDNA clone... 101 3e-21
 emb|AI855670|AI855670 sc32f08.y1 Gm-c1014 Glycine max cDNA clone... 100 2e-20
 emb|AI920195|AI920195 1725 Pine Lambda Zap Xylem library Pinus t... 73 2e-20
 emb|AW686987|AW686987 NF004G02RT1F1018 Developing root Medicago ... 99 2e-20
 emb|AW684941|AW684941 NF023D03NR1F1000 Nodulated root Medicago t... 88 1e-19
 15 emb|AI494665|AI494665 sb18f10.y1 Gm-c1004 Glycine max cDNA clone... 89 1e-19
 emb|AW277935|AW277935 sf87g05.y1 Gm-c1019 Glycine max cDNA clone... 97 1e-19
 gb|BE023344|BE023344 sm70f11.y1 Gm-c1028 Glycine max cDNA clone... 78 2e-19
 emb|AV422621|AV422621 AV422621 Lotus japonicus young plants (two... 60 2e-19
 emb|AW127416|AW127416 M110599 DSIL Medicago truncatula cDNA clon... 95 4e-19

20

Query= AL030978.64_at 15431_at /id_source genbank /description
 emb|caa19722.1| (al030978) putative protein [arabidopsis thaliana]
 /blast_score 2.00e-51 /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 25 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al030978|/ncgi
 http://www.ncgr.org/cgi-bin/ff?al030978
 (393 letters)

Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 35 Sequences producing significant alignments: (bits) Value

emb|AW218792|AW218792 EST301272 tomato root during/after fruit s... 104 2e-30
 emb|AW218791|AW218791 EST301271 tomato root during/after fruit s... 104 2e-30
 emb|AI781536|AI781536 EST262415 tomato susceptible, Cornell Lyco... 104 2e-30
 40 emb|AI894486|AI894486 EST263929 tomato callus, TAMU Lycopersicon... 100 3e-29
 emb|AW255546|AW255546 ML580 peppermint glandular trichome Mentha... 96 4e-25
 emb|AW781055|AW781055 sl88d08.y1 Gm-c1037 Glycine max cDNA clone... 95 5e-25
 emb|AW980335|AW980335 EST391488 GVN Medicago truncatula cDNA clo... 94 1e-24
 emb|AW982334|AW982334 HVSMEg0002O20f Hordeum vulgare pre-anthesi... 86 1e-24
 45 gb|H74448|H74448 150 Standard Brassica napus cDNA clone R29F, mR... 92 4e-24
 emb|AI960943|AI960943 sc93a04.y1 Gm-c1019 Glycine max cDNA clone... 92 5e-24
 emb|AU036790|AU036790 AU036790 Cryptomeria japonica seedling lea... 88 5e-24
 emb|AW598247|AW598247 sj42f01.y1 Gm-c1008 Glycine max cDNA clone... 80 3e-23
 emb|AW100651|AW100651 sd58b12.y1 Gm-c1008 Glycine max cDNA clone... 89 4e-23
 50 emb|AW208200|AW208200 M110845e GVSN Medicago truncatula cDNA clo... 88 5e-23
 emb|AW559726|AW559726 EST314718 DSIR Medicago truncatula cDNA cl... 83 2e-22
 emb|AW101120|AW101120 sd74c08.y1 Gm-c1008 Glycine max cDNA clone... 94 2e-22
 emb|AW926990|AW926990 HVSMEg0009D05 Hordeum vulgare pre-anthesis... 103 8e-22
 gb|BE124173|BE124173 EST394298 DSIL Medicago truncatula cDNA clo... 94 1e-21
 55 emb|AT000903|AT000903 AT000903 Brassica rapa guard cell Brassica... 54 2e-20
 emb|AW690635|AW690635 NF031H11ST1F1000 Developing stem Medicago ... 75 6e-20
 emb|AW126039|AW126039 N100235e rootphos(-) Medicago truncatula c... 75 6e-20
 emb|AW126127|AW126127 N100324e rootphos(-) Medicago truncatula c... 75 7e-20
 emb|AI812959|AI812959 2A11 Pine Lambda Zap Xylem library Pinus t... 75 2e-19
 60 emb|AI043565|AI043565 L30-578T3 Ice plant Lambda Uni-Zap XR expr... 75 3e-19
 emb|AW396602|AW396602 sg80b06.y1 Gm-c1026 Glycine max cDNA clone... 95 3e-19

	gb BE059263 BE059263 sn28d04.y1 Gm-cl016 Glycine max cDNA clone ...	95	3e-19
	emb AW736823 AW736823 NXNV_083_D01_F Nsf Xylem Normal wood Verti...	73	3e-19
	emb AW461253 AW461253 NXNV060C05F Nsf Xylem Normal wood Vertical...	70	7e-18
	emb AW126244 AW126244 N100089e rootphos(-) Medicago truncatula c...	53	2e-17
5	emb AW683890 AW683890 NF003A10NR1F1000 Nodulated root Medicago t...	49	4e-17
	emb AW922806 AW922806 DG1_46_G06.g1_A002 Dark Grown 1 (DG1) Sorg...	84	4e-17
	emb AW290613 AW290613 NXNV044B04F Nsf Xylem Normal wood Vertical...	65	9e-17
	emb AW567768 AW567768 si54f04.y1 Gm-r1030 Glycine max cDNA clone...	64	7e-16
	emb AW568036 AW568036 si56f04.y1 Gm-r1030 Glycine max cDNA clone...	64	7e-16
10	emb AW461226 AW461226 NXNV048H05F Nsf Xylem Normal wood Vertical...	74	9e-15
	emb AW720025 AW720025 LjNEST15c3r Lotus japonicus nodule library...	78	2e-14
	emb AI812590 AI812590 13F9 Pine Lambda Zap Xylem library Pinus t...	54	1e-13
	emb AW350351 AW350351 GM210008A10G1R Gm-r1021 Glycine max cDNA 3...	73	1e-12
	emb AI779006 AI779006 EST259885 tomato susceptible, Cornell Lyco...	73	1e-12
15	emb AA557075 AA557075 917 Loblolly pine N Pinus taeda cDNA clone...	70	2e-12
	emb AI899615 AI899615 EST269058 tomato susceptible, Cornell Lyco...	72	2e-12
	emb AW394975 AW394975 sh37h12.y1 Gm-cl017 Glycine max cDNA clone...	69	1e-11
	emb AU036851 AU036851 AU036851 Cryptomeria japonica seedling lea...	69	1e-11
	emb AW394753 AW394753 sh34h05.y1 Gm-cl017 Glycine max cDNA clone...	68	2e-11
20	emb AI965467 AI965467 sc72c05.y1 Gm-cl018 Glycine max cDNA clone...	68	3e-11
	emb AI495151 AI495151 sa88f06.y1 Gm-cl004 Glycine max cDNA clone...	67	6e-11
	gb BE034744 BE034744 ML03G11 ML Mesembryanthemum crystallinum cD...	44	2e-10
	emb AI771301 AI771301 EST252317 tomato ovary, TAMU Lycopersicon ...	64	6e-10
	emb AW424128 AW424128 sh61c09.y1 Gm-cl015 Glycine max cDNA clone...	63	8e-10
25	emb AI736289 AI736289 sb26d05.y1 Gm-cl008 Glycine max cDNA clone...	59	1e-08
	emb AW888120 AW888120 NXNV_129_D10_F Nsf Xylem Normal wood Verti...	56	2e-08
	emb AW784020 AW784020 NXNV_103_A11_F Nsf Xylem Normal wood Verti...	54	8e-08
	emb AI938510 AI938510 sb46e12.y1 Gm-cl015 Glycine max cDNA clone...	55	2e-07
	emb AT000179 AT000179 AT000179 Apple young fruit cDNA library Ma...	41	0.004
30	emb AW234162 AW234162 sf22a01.y1 Gm-cl028 Glycine max cDNA clone...	40	0.006
	gb BE033785 BE033785 MF06D08 MF Mesembryanthemum crystallinum cD...	40	0.006
	gb BE034795 BE034795 ML04D08 ML Mesembryanthemum crystallinum cD...	40	0.008
	emb AW309614 AW309614 sf22a01.x1 Gm-cl028 Glycine max cDNA clone...	40	0.008
	gb L01433 SOYSCAM4X Soybean calmodulin (SCaM-4) mRNA, complete cds.	40	0.008
35	gb U20292 STU20292 Solanum tuberosum clone PCM3 calmodulin gene,...	40	0.008
	emb AW458431 AW458431 sh09b07.y1 Gm-cl016 Glycine max cDNA clone...	40	0.012
	emb AW704882 AW704882 sk40g04.y1 Gm-cl019 Glycine max cDNA clone...	39	0.016
	emb AW706736 AW706736 sk02d02.y1 Gm-cl023 Glycine max cDNA clone...	39	0.022
	gb M88307 BNACALM Brassica juncea calmodulin mRNA, complete cds.	38	0.030
40	gb U10150 BNU10150 Brassica napus Naehan calmodulin (bcm1) mRNA,...	38	0.030
	emb AW266313 AW266313 L30-3052T3 Ice plant Lambda Uni-Zap XR exp...	38	0.041
	emb AW317381 AW317381 sg48f11.y1 Gm-cl025 Glycine max cDNA clone...	38	0.041
	emb AI973796 AI973796 sd10d10.y1 Gm-cl020 Glycine max cDNA clone...	37	0.078
	emb AW704342 AW704342 sk18b05.y1 Gm-cl028 Glycine max cDNA clone...	36	0.15
45	gb U13736 PSU13736 Pisum sativum Alaska calmodulin-like protein ...	35	0.20
	emb AI080805 AI080805 TENU3514 T. cruzi epimastigote normalized ...	35	0.28
	emb AW696965 AW696965 NF110H11ST1F1095 Developing stem Medicago ...	34	0.52
	emb AW695301 AW695301 NF093G03ST1F1023 Developing stem Medicago ...	34	0.52
	emb AW776108 AW776108 EST335173 DSIL Medicago truncatula cDNA cl...	34	0.52
50	emb AW691424 AW691424 NF044G02ST1F1000 Developing stem Medicago ...	34	0.52
	emb AW559907 AW559907 EST314955 DSIR Medicago truncatula cDNA cl...	34	0.52
	emb AW689882 AW689882 NF026C01ST1F1000 Developing stem Medicago ...	34	0.52
	emb AW267797 AW267797 EST305925 DSIR Medicago truncatula cDNA cl...	34	0.52
	emb AA660947 AA660947 00844 MtrHE Medicago truncatula cDNA 5' si...	34	0.52
55	emb AW696479 AW696479 NF106F05ST1F1046 Developing stem Medicago ...	34	0.52
	emb AW693088 AW693088 NF060A07ST1F1052 Developing stem Medicago ...	34	0.52
	emb AW687985 AW687985 NF001G08ST1F1000 Developing stem Medicago ...	34	0.52
	emb AW692657 AW692657 NF057H03ST1F1000 Developing stem Medicago ...	34	0.52
	emb AW559906 AW559906 EST314954 DSIR Medicago truncatula cDNA cl...	34	0.52
60	emb AI075569 AI075569 TENU3146 T. cruzi epimastigote normalized ...	33	0.99
	emb AQ656273 AQ656273 Sheared DNA-25J5.TF Sheared DNA Trypanosom...	33	1.4

emb|AQ643265|AQ643265 RPCI93-DpnII-30O24.TJ RPCI93-DpnII Trypano... 33 1.4
emb|AW145395|AW145395 gal9g01.y1 Moss EST library PPU Physcomitr... 33 1.4
emb|AF216527|AF216527 Dunaliella tertiolecta calcium-dependent p... 33 1.4
5 emb|AF137317|AF137317 Pariana radiciflora phytochrome B (PHYB) g... 32 1.9
gb|U25841|YSCP9677 Saccharomyces cerevisiae chromosome XVI cosmi... 32 2.6
emb|AL354107|L2187X Leishmania major Friedlin cosmid L2187 t3Hyg... 31 3.5
emb|Y10156|BNMYAP12 B.napus for myrosinase-associated protein, c... 31 3.5
emb|AA901634|AA901634 NCM7H7T7 Mycelial Neurospora crassa cDNA c... 31 3.5
emb|AA519327|AA519327 TgESTzz40d01.s1 TgME49 invivo Bradyzoite c... 31 3.5
10 emb|AL109820|SPAC1952 S.pombe chromosome I cosmid c1952. 31 4.8
emb|AV388698|AV388698 AV388698 Chlamydomonas reinhardtii C9 Chla... 31 4.8
emb|AQ852174|AQ852174 LMAJFV1_lm62c09.x1 Leishmania major FV1 ra... 31 4.8
emb|AW772887|AW772887 925001C07.y1 C. reinhardtii CC-2290, norma... 31 4.8
gb|BE024237|BE024237 894001F07.y1 C. reinhardtii CC-1690, normal... 31 4.8
15
Query= AC006067.63_at 15846_at /id_source genbank /description
gb|aad15461.1| (ac006067) unknown protein [arabidopsis thaliana]
/blast_score 1.00e-117 /ec_number /family /chip nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-
20 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006067|/ncgi
http://www.ncgr.org/cgi-bin/ff?ac006067
(777 letters)

Database: plantfungal
25 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
30 Sequences producing significant alignments: (bits) Value

emb|AI938176|AI938176 sc40e07.y1 Gm-c1014 Glycine max cDNA clone... 226 1e-58
emb|AI938151|AI938151 sc40a07.y1 Gm-c1014 Glycine max cDNA clone... 226 2e-58
emb|AW348772|AW348772 GM210003A22G1R Gm-r1021 Glycine max cDNA 3... 222 3e-
35 57
gb|BE057559|BE057559 sn04a01.y1 Gm-c1015 Glycine max cDNA clone ... 210 1e-53
emb|AW133238|AW133238 se16b04.y1 Gm-c1013 Glycine max cDNA clone... 200 8e-51
emb|AW219398|AW219398 EST301976 tomato root during/after fruit s... 190 9e-48
emb|AW930095|AW930095 EST340552 tomato fruit mature green, TAMU ... 190 9e-48
40 emb|AW399412|AW399412 EST309912 L. pennellii trichome, Cornell U... 189 2e-47
emb|AW399345|AW399345 EST309845 L. pennellii trichome, Cornell U... 189 2e-47
emb|AI896756|AI896756 EST266199 tomato callus, TAMU Lycopersicon... 188 4e-47
emb|AW030559|AW030559 EST273814 tomato callus, TAMU Lycopersicon... 188 4e-47
emb|AI773854|AI773854 EST254954 tomato resistant, Cornell Lycope... 133 2e-44
45 emb|AW832123|AW832123 sm30h02.y1 Gm-c1028 Glycine max cDNA clone... 178 3e-44
emb|AI894447|AI894447 EST263902 tomato callus, TAMU Lycopersicon... 177 9e-44
emb|AI778651|AI778651 EST259530 tomato susceptible, Cornell Lyco... 177 9e-44
emb|AI487153|AI487153 EST245475 tomato ovary, TAMU Lycopersicon ... 166 3e-40
emb|AW568464|AW568464 si59b03.y1 Gm-r1030 Glycine max cDNA clone... 163 2e-39
50 emb|AW153022|AW153022 se33h12.y1 Gm-c1015 Glycine max cDNA clone... 158 6e-38
emb|AI896759|AI896759 EST266202 tomato callus, TAMU Lycopersicon... 157 8e-38
emb|AW094322|AW094322 EST287502 tomato mixed elicitor, BTI Lycop... 128 5e-29
gb|BE125244|BE125244 DG1_18_B07.b1_A002 Dark Grown 1 (DG1) Sorgh... 127 1e-28
emb|AW922420|AW922420 DG1_18_B07.g1_A002 Dark Grown 1 (DG1) Sorg... 123 2e-27
55 gb|BE024006|BE024006 sm95c09.y1 Gm-c1015 Glycine max cDNA clone ... 122 2e-27
gb|T14912|T14912 crs394 lambdaZAPST Ricinus communis cDNA clone ... 72 3e-27
emb|AI898070|AI898070 EST267513 tomato ovary, TAMU Lycopersicon ... 119 2e-26
emb|AW030966|AW030966 EST274273 tomato callus, TAMU Lycopersicon... 96 1e-25
emb|AI938035|AI938035 sc40e07.x1 Gm-c1014 Glycine max cDNA clone... 116 3e-25
60 emb|AI771551|AI771551 EST252651 tomato ovary, TAMU Lycopersicon ... 111 7e-24
emb|AI938013|AI938013 sc40a07.x1 Gm-c1014 Glycine max cDNA clone... 110 1e-23

	emb AI776842 AI776842 EST257942 tomato resistant, Cornell Lycopersicon...	110	2e-23
	emb AA556663 AA556663 518 Loblolly pine CA Pinus taeda cDNA clone...	61	2e-20
	emb AI736542 AI736542 sb30b04.y1 Gm-c1009 Glycine max cDNA clone...	68	2e-17
	emb AI899328 AI899328 EST268771 tomato ovary, TAMU Lycopersicon ...	82	6e-15
5	gb BE021003 BE021003 sm54e07.y1 Gm-c1028 Glycine max cDNA clone ...	55	1e-12
	emb AW217201 AW217201 EST295915 tomato callus, TAMU Lycopersicon...	73	2e-12
	emb AI443600 AI443600 sa42b08.y1 Gm-c1004 Glycine max cDNA clone...	72	5e-12
	gb BE123900 BE123900 EST394025 DSIL Medicago truncatula cDNA clo...	58	7e-08
	gb BE022589 BE022589 sm86h09.y1 Gm-c1015 Glycine max cDNA clone ...	57	2e-07
10	gb BE022911 BE022911 sm89a12.y1 Gm-c1015 Glycine max cDNA clone ...	55	6e-07
	emb AW184959 AW184959 se84d10.y1 Gm-c1023 Glycine max cDNA clone...	52	6e-06
	emb AW185963 AW185963 se61h02.y1 Gm-c1019 Glycine max cDNA clone...	52	6e-06
	emb AW153055 AW153055 se34d02.y1 Gm-c1015 Glycine max cDNA clone...	45	7e-04
	emb AI727849 AI727849 BNLGH9260 Six-day Cotton fiber Gossypium ...	39	0.056
15	emb AI965877 AI965877 sc79a11.y1 Gm-c1018 Glycine max cDNA clone...	30	0.082
	emb AF157837 AF157837 Trypanosoma cruzi putative 90 kDa surface ...	35	0.52
	emb AL049182 PFMAL13P5 Plasmodium falciparum chromosome 13 strai...	35	0.98
	emb AL112108 CNS019UC Botrytis cinerea strain T4 cDNA library un...	34	1.4
	emb AF101023 AF101023 Picea abies clone PAA12E3 family 2 repetit...	34	1.4
20	emb AA520766 AA520766 TgESTzz67g11.r1 TgME49 invivo Bradyzoite c...	34	1.4
	emb AA519752 AA519752 TgESTzz28f05.r1 TgME49 invivo Bradyzoite c...	34	1.4
	emb AA785314 AA785314 g6d11a1.fl Aspergillus nidulans 24hr asexu...	34	1.9
	emb AQ367507 AQ367507 toxb0002H01r CUGI Tomato BAC Library Lycop...	34	1.9
	emb AW348996 AW348996 GM210003B22A1R Gm-r1021 Glycine max cDNA 3...	33	2.6
25	emb AW348959 AW348959 GM210004A12C6R Gm-r1021 Glycine max cDNA 3...	33	2.6
	emb AL034559 PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq...	33	2.6
	emb AW348503 AW348503 GM210002B12C1R Gm-r1021 Glycine max cDNA 3...	33	2.6
	emb AW398499 AW398499 EST308999 L. pennellii trichome, Cornell U...	33	2.6
	emb AW349705 AW349705 GM210005B21C6R Gm-r1021 Glycine max cDNA 3...	33	2.6
30	emb AW596289 AW596289 sj01e09.y1 Gm-c1032 Glycine max cDNA clone...	33	3.5
	emb AF199419 AF199419 Trypanosoma cruzi 90 kDa surface protein (...)	33	3.5
	emb AW102268 AW102268 sd85e07.y1 Gm-c1009 Glycine max cDNA clone...	33	3.5
	emb AI441442 AI441442 sa86a02.y1 Gm-c1004 Glycine max cDNA clone...	33	3.5
	emb X78037 MIOB250 O.berteriana mitochondrial DNA for orf250.	33	3.5
35	emb AC004688 AC004688 Plasmodium falciparum chromosome 12 clone ...	32	4.8
	emb AW719534 AW719534 LjNEST5c5rW Lotus japonicus nodule library...	32	4.8
	emb AC004709 AC004709 Plasmodium falciparum chromosome 12, *** S...	32	4.8
	emb AF119172 AF119172 Cyanophora paradoxa alpha-tubulin (atub) g...	32	4.8
	emb AW101722 AW101722 sd69d02.y1 Gm-c1008 Glycine max cDNA clone...	32	4.8
40	gb U56098 AOU56098 Aspergillus oryzae putative DNA binding prote...	32	4.8
	emb AI507866 AI507866 sa88b06.y1 Gm-c1004 Glycine max cDNA clone...	32	4.8
	gb BE125213 BE125213 DG1_16_E11.b1_A002 Dark Grown 1 (DG1) Sorgh...	32	4.8
	emb AA785315 AA785315 g6d11a1.r1 Aspergillus nidulans 24hr asexu...	32	4.8
	gb BE059192 BE059192 sn27d12.y1 Gm-c1016 Glycine max cDNA clone ...	32	4.8
45	emb Z71334 SCYNL058C S.cerevisiae chromosome XIV reading frame O...	32	6.6
	emb AW219947 AW219947 EST302430 tomato root during/after fruit s...	32	6.6
	emb X56235 SCHYP1 Yeast (S.cerevisiae) HYP1 gene for hypusine co...	32	6.6
	emb AL121851 LMFL2581 Leishmania major Friedlin chromosome 23 co...	32	6.6
	emb AW686452 AW686452 NF041F08NR1F1000 Nodulated root Medicago t...	32	6.6
50	emb Z67961 SPAC30D11 S.pombe chromosome I cosmid c30D11.	32	6.6
	emb AW395281 AW395281 sh46b07.y1 Gm-c1017 Glycine max cDNA clone...	32	6.6
	emb AL034563 SPBC660 S.pombe chromosome II cosmid c660.	32	6.6
	emb AW667846 AW667846 GA_Ea0010O22 Gossypium arboreum 7-10 dpa ...	32	6.6
	emb AI043302 AI043302 TENU0942 T. cruzi epimastigote normalized ...	32	6.6
55	emb AI043452 AI043452 TENU1011 T. cruzi epimastigote normalized ...	32	6.6
	emb AW773882 AW773882 EST332868 KV3 Medicago truncatula cDNA clo...	32	6.6
	emb AW219946 AW219946 EST302429 tomato root during/after fruit s...	32	6.6
	gb UI2141 SCU12141 Saccharomyces cerevisiae chromosome XIV left ...	32	6.6
	emb AQ653810 AQ653810 Sheared DNA-8B13.TF Sheared DNA Trypanosom...	32	6.6
60	emb AW219759 AW219759 EST302241 tomato root during/after fruit s...	32	6.6
	emb AI069155 AI069155 mgae0005dA02f Magnaporthe grisea Appressor...	27	7.0

emb|AC023488|AC023488 Trypanosoma brucei chromosome IV clone RPC... 31 9.1
 emb|AW509230|AW509230 sh92h07.y1 Gm-c1016 Glycine max cDNA clone... 31 9.1
 emb|AW932541|AW932541 EST358384 tomato fruit mature green, TAMU ... 31 9.1
 emb|AF206700|AF206700 Neurospora crassa heterokaryon incompatibi... 31 9.1
 5 emb|AW621293|AW621293 EST312091 tomato root during/after fruit s... 31 9.1
 dbj|D15051|BLYIDS2NK Hordeum vulgare gene for ids2, complete cds. 31 9.1
 gb|BE021558|BE021558 sm49e02.y1 Gm-c1028 Glycine max cDNA clone ... 31 9.1
 emb|AW442607|AW442607 EST307537 tomato mixed elicitor, BTI Lycop... 31 9.1
 emb|AL049181|PFMAL13P4 Plasmodium falciparum chromosome 13 strai... 31 9.1
 10 emb|AI780125|AI780125 EST261004 tomato susceptible, Cornell Lyco... 31 9.1

Query= AC006067.63_g_at 15847_g_at /id_source genbank /description
 gb|aad15461.1| (ac006067) unknown protein [arabidopsis thaliana]
 /blast_score 1.00e-117 /ec_number /family /chip nova /gb_link /ncgi

15

(777 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

20

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

25

emb|AI938176|AI938176 sc40e07.y1 Gm-c1014 Glycine max cDNA clone... 226 1e-58
 emb|AI938151|AI938151 sc40a07.y1 Gm-c1014 Glycine max cDNA clone... 226 2e-58
 emb|AW348772|AW348772 GM210003A22G1R Gm-r1021 Glycine max cDNA 3... 222 3e-57

30

gb|BE057559|BE057559 sn04a01.y1 Gm-c1015 Glycine max cDNA clone ... 210 1e-53
 emb|AW133238|AW133238 se16b04.y1 Gm-c1013 Glycine max cDNA clone... 200 8e-51

emb|AW219398|AW219398 EST301976 tomato root during/after fruit s... 190 9e-48
 emb|AW930095|AW930095 EST340552 tomato fruit mature green, TAMU ... 190 9e-48
 emb|AW399412|AW399412 EST309912 L. pennellii trichome, Cornell U... 189 2e-47

35

emb|AW399345|AW399345 EST309845 L. pennellii trichome, Cornell U... 189 2e-47

emb|AI896756|AI896756 EST266199 tomato callus, TAMU Lycopersicon... 188 4e-47
 emb|AW030559|AW030559 EST273814 tomato callus, TAMU Lycopersicon... 188 4e-47

emb|AI773854|AI773854 EST254954 tomato resistant, Cornell Lycope... 133 2e-44

emb|AW832123|AW832123 sm30h02.y1 Gm-c1028 Glycine max cDNA clone... 178 3e-44

40

emb|AI894447|AI894447 EST263902 tomato callus, TAMU Lycopersicon... 177 9e-44

emb|AI778651|AI778651 EST259530 tomato susceptible, Cornell Lyco... 177 9e-44

emb|AI487153|AI487153 EST245475 tomato ovary, TAMU Lycopersicon ... 166 3e-40

emb|AW568464|AW568464 si59b03.y1 Gm-r1030 Glycine max cDNA clone... 163 2e-39

emb|AW153022|AW153022 se33h12.y1 Gm-c1015 Glycine max cDNA clone... 158 6e-38

45

emb|AI896759|AI896759 EST266202 tomato callus, TAMU Lycopersicon... 157 8e-38

emb|AW094322|AW094322 EST287502 tomato mixed elicitor, BTI Lycop... 128 5e-29

gb|BE125244|BE125244 DG1_18_B07.b1_A002 Dark Grown 1 (DG1) Sorgh... 127 1e-28

emb|AW922420|AW922420 DG1_18_B07.g1_A002 Dark Grown 1 (DG1) Sorg... 123 2e-27

gb|BE024006|BE024006 sm95c09.y1 Gm-c1015 Glycine max cDNA clone ... 122 2e-27

50

gb|T14912|T14912 crs394 lambdaZAPST Ricinus communis cDNA clone ... 72 3e-27

emb|AI898070|AI898070 EST267513 tomato ovary, TAMU Lycopersicon ... 119 2e-26

emb|AW030966|AW030966 EST274273 tomato callus, TAMU Lycopersicon... 96 1e-25

emb|AI938035|AI938035 sc40e07.x1 Gm-c1014 Glycine max cDNA clone... 116 3e-25

emb|AI771551|AI771551 EST252651 tomato ovary, TAMU Lycopersicon ... 111 7e-24

55

emb|AI938013|AI938013 sc40a07.x1 Gm-c1014 Glycine max cDNA clone... 110 1e-23

emb|AI776842|AI776842 EST257942 tomato resistant, Cornell Lycope... 110 2e-23

emb|AA556663|AA556663 518 Loblolly pine CA Pinus taeda cDNA clon... 61 2e-20

emb|AI736542|AI736542 sb30b04.y1 Gm-c1009 Glycine max cDNA clone... 68 2e-17

emb|AI899328|AI899328 EST268771 tomato ovary, TAMU Lycopersicon ... 82 6e-15

60

gb|BE021003|BE021003 sm54e07.y1 Gm-c1028 Glycine max cDNA clone ... 55 1e-12

emb|AW217201|AW217201 EST295915 tomato callus, TAMU Lycopersicon... 73 2e-12

	emb AI443600 AI443600 sa42b08.y1 Gm-c1004 Glycine max cDNA clone...	72	5e-12
	gb BE123900 BE123900 EST394025 DSIL Medicago truncatula cDNA clo...	58	7e-08
	gb BE022589 BE022589 sm86h09.y1 Gm-c1015 Glycine max cDNA clone ...	57	2e-07
	gb BE022911 BE022911 sm89a12.y1 Gm-c1015 Glycine max cDNA clone ...	55	6e-07
5	emb AW184959 AW184959 se84d10.y1 Gm-c1023 Glycine max cDNA clone...	52	6e-06
	emb AW185963 AW185963 se61h02.y1 Gm-c1019 Glycine max cDNA clone...	52	6e-06
	emb AW153055 AW153055 se34d02.y1 Gm-c1015 Glycine max cDNA clone...	45	7e-04
	emb AI727849 AI727849 BNLGHi9260 Six-day Cotton fiber Gossypium ...	39	0.056
	emb AI965877 AI965877 sc79a11.y1 Gm-c1018 Glycine max cDNA clone...	30	0.082
10	emb AF157837 AF157837 Trypanosoma cruzi putative 90 kDa surface ...	35	0.52
	emb AL049182 PFMAL13P5 Plasmodium falciparum chromosome 13 strai...	35	0.98
	emb AL112108 CNS019UC Botrytis cinerea strain T4 cDNA library un...	34	1.4
	emb AF101023 AF101023 Picea abies clone PAA12E3 family 2 repetit...	34	1.4
	emb AA520766 AA520766 TgESTzz67g11.r1 TgME49 invivo Bradyzoite c...	34	1.4
15	emb AA519752 AA519752 TgESTzz28f05.r1 TgME49 invivo Bradyzoite c...	34	1.4
	emb AA785314 AA785314 g6d11a1.fl Aspergillus nidulans 24hr asexu...	34	1.9
	emb AQ367507 AQ367507 toxb0002H01r CUGI Tomato BAC Library Lycop...	34	1.9
	emb AW348996 AW348996 GM210003B22A1R Gm-r1021 Glycine max cDNA 3...	33	2.6
	emb AW348959 AW348959 GM210004A12C6R Gm-r1021 Glycine max cDNA 3...	33	2.6
20	emb AL034559 PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq...	33	2.6
	emb AW348503 AW348503 GM210002B12C1R Gm-r1021 Glycine max cDNA 3...	33	2.6
	emb AW398499 AW398499 EST308999 L. pennellii trichome, Cornell U...	33	2.6
	emb AW349705 AW349705 GM210005B21C6R Gm-r1021 Glycine max cDNA 3...	33	2.6
	emb AW596289 AW596289 sj01e09.y1 Gm-c1032 Glycine max cDNA clone...	33	3.5
25	emb AF199419 AF199419 Trypanosoma cruzi 90 kDa surface protein (...	33	3.5
	emb AW102268 AW102268 sd85e07.y1 Gm-c1009 Glycine max cDNA clone...	33	3.5
	emb AI441442 AI441442 sa86a02.y1 Gm-c1004 Glycine max cDNA clone...	33	3.5
	emb X78037 MIOB250 O.berteriana mitochondrial DNA for orf250.	33	3.5
	emb AC004688 AC004688 Plasmodium falciparum chromosome 12 clone ...	32	4.8
30	emb AW719534 AW719534 LjNEST5c5rW Lotus japonicus nodule library...	32	4.8
	emb AC004709 AC004709 Plasmodium falciparum chromosome 12, *** S...	32	4.8
	emb AF119172 AF119172 Cyanophora paradoxa alpha-tubulin (atub) g...	32	4.8
	emb AW101722 AW101722 sd69d02.y1 Gm-c1008 Glycine max cDNA clone...	32	4.8
	gb U56098 AOU56098 Aspergillus oryzae putative DNA binding prote...	32	4.8
35	emb AI507866 AI507866 sa88b06.y1 Gm-c1004 Glycine max cDNA clone...	32	4.8
	gb BE125213 BE125213 DG1_16_E11.b1_A002 Dark Grown 1 (DG1) Sorgh...	32	4.8
	emb AA785315 AA785315 g6d11a1.r1 Aspergillus nidulans 24hr asexu...	32	4.8
	gb BE059192 BE059192 sn27d12.y1 Gm-c1016 Glycine max cDNA clone ...	32	4.8
	emb Z71334 SCYNL058C S.cerevisiae chromosome XIV reading frame O...	32	6.6
40	emb AW219947 AW219947 EST302430 tomato root during/after fruit s...	32	6.6
	emb X56235 SCHYP1 Yeast (S.cerevisiae) HYP1 gene for hypusine co...	32	6.6
	emb AL121851 LMFL2581 Leishmania major Friedlin chromosome 23 co...	32	6.6
	emb AW686452 AW686452 NF041F08NR1F1000 Nodulated root Medicago t...	32	6.6
	emb Z67961 SPAC30D11 S.pombe chromosome I cosmid c30D11.	32	6.6
45	emb AW395281 AW395281 sh46b07.y1 Gm-c1017 Glycine max cDNA clone...	32	6.6
	emb AL034563 SPBC660 S.pombe chromosome II cosmid c660.	32	6.6
	emb AW667846 AW667846 GA_Ea0010O22 Gossypium arboreum 7-10 dpa ...	32	6.6
	emb AI043302 AI043302 TENU0942 T. cruzi epimastigote normalized ...	32	6.6
	emb AI043452 AI043452 TENU1011 T. cruzi epimastigote normalized ...	32	6.6
50	emb AW773882 AW773882 EST332868 KV3 Medicago truncatula cDNA clo...	32	6.6
	emb AW219946 AW219946 EST302429 tomato root during/after fruit s...	32	6.6
	gb U12141 SCU12141 Saccharomyces cerevisiae chromosome XIV left ...	32	6.6
	emb AQ653810 AQ653810 Sheared DNA-8B13.TF Sheared DNA Trypanosom...	32	6.6
	emb AW219759 AW219759 EST302241 tomato root during/after fruit s...	32	6.6
55	emb AI069155 AI069155 mgae0005dA02f Magnaporthe grisea Appressor...	27	7.0
	emb AC023488 AC023488 Trypanosoma brucei chromosome IV clone RPC...	31	9.1
	emb AW509230 AW509230 sh92h07.y1 Gm-c1016 Glycine max cDNA clone...	31	9.1
	emb AW932541 AW932541 EST358384 tomato fruit mature green, TAMU ...	31	9.1
	emb AF206700 AF206700 Neurospora crassa heterokaryon incompatibi...	31	9.1
60	emb AW621293 AW621293 EST312091 tomato root during/after fruit s...	31	9.1
	dbj D15051 BLYIDS2NK Hordeum vulgare gene for ids2, complete cds.	31	9.1

gb|BE021558|BE021558 sm49e02.y1 Gm-c1028 Glycine max cDNA clone ... 31 9.1
 emb|AW442607|AW442607 EST307537 tomato mixed elicitor, BTI Lycop... 31 9.1
 emb|AL049181|PFMAL13P4 Plasmodium falciparum chromosome 13 strai... 31 9.1
 emb|AI780125|AI780125 EST261004 tomato susceptible, Cornell Lyco... 31 9.1

5

Query= AC006587.164_at 15859_at /id_source genbank /description
 gb|aad21491.1| (ac006587) unknown protein [arabidopsis thaliana]
 /blast_score 4.00e-17 /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 10 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006587| /ncgi
 http://www.ncgr.org/cgi-bin/ff?ac006587
 (504 letters)

Database: plantfungal

15 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E

20 Sequences producing significant alignments: (bits) Value

emb|AC006279|AC006279 Plasmodium falciparum chromosome 12 clone ... 36 0.16
 emb|AW932996|AW932996 EST358839 tomato fruit mature green, TAMU ... 36 0.16
 emb|AC005140|AC005140 Plasmodium falciparum chromosome 12 clone ... 36 0.22
 25 emb|AC005139|AC005139 Plasmodium falciparum chromosome 12, *** S... 36 0.22
 gb|M73214|TETH3H4A Tetrahymena vorax histone H3 (histone H3II) g... 36 0.22
 emb|AL034559|PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq... 35 0.30
 gb|M17221|YSCRNR2 S.cerevisiae ribonucleotide reductase (RNR2) s... 35 0.30
 emb|AE001384|AE001384 Plasmodium falciparum chromosome 2, sectio... 35 0.30
 30 gb|BE034256|BE034256 MH02B11 MH Mesembryanthemum crystallinum cD... 35 0.41
 emb|AC004688|AC004688 Plasmodium falciparum chromosome 12 clone ... 35 0.41
 emb|AL031748|PFMAL1P5 Plasmodium falciparum chromosome 1 strain ... 35 0.41
 emb|AE001383|AE001383 Plasmodium falciparum chromosome 2, sectio... 35 0.41
 gb|BE023268|BE023268 sm80b05.y1 Gm-c1015 Glycine max cDNA clone... 35 0.41
 35 emb|Z97348|PFMAL3P1 Plasmodium falciparum MAL3P1, complete seque... 35 0.41
 emb|X56950|PFCALM P. falciparum gene for calmodulin. 35 0.41
 gb|M59349|PFACALMOD Plasmodium falciparum calmodulin gene; compl... 35 0.41
 emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, *** S... 35 0.41
 emb|AL049184|PFMAL13P3 Plasmodium falciparum chromosome 13 strai... 35 0.56
 40 gb|M37892|TETRPROL21 Tetrahymena thermophila ribosomal protein L... 35 0.56
 gb|T09806|T09806 0387m7 gmbPfHB3.1, G. Roman Reddy Plasmodium fa... 35 0.56
 gb|T09805|T09805 0387m3 gmbPfHB3.1, G. Roman Reddy Plasmodium fa... 35 0.56
 emb|AE001399|AE001399 Plasmodium falciparum chromosome 2, sectio... 34 0.77
 emb|AQ501167|AQ501167 V26E6 mTn-3xHA/lacZ Insertion Library Sacc... 34 0.77
 45 emb|AQ934965|AQ934965 CpG2344B CpIOWAgDNA1 Cryptosporidium parvu... 34 0.77
 emb|AQ934964|AQ934964 CpG2344A CpIOWAgDNA1 Cryptosporidium parvu... 34 0.77
 emb|AL111484|CNS019D0 Botrytis cinerea strain T4 cDNA library un... 28 0.94
 emb|AQ942015|AQ942015 Sheared DNA-41C1.TR Sheared DNA Trypanosom... 34 1.1
 emb|AL035476|PFMAL4P3 Plasmodium falciparum chromosome 4 strain ... 34 1.1
 50 emb|AC005507|AC005507 Plasmodium falciparum chromosome 12 clone ... 34 1.1
 emb|AL031745|PFMAL1P2 Plasmodium falciparum chromosome 1 strain ... 34 1.1
 gb|N98036|N98036 2094C3 czapPFDd2.1, Debopam Chakrabarti Plasmod... 34 1.1
 gb|L27838|PFARHPR Plasmodium yoelii rhoptry protein, complete cds. 29 1.1
 emb|AW686975|AW686975 NF004F02RT1F1025 Developing root Medicago ... 28 1.3
 55 gb|U84395|PFU84395 Plasmodium falciparum sarcalumenin/eps15 homo... 33 1.5
 emb|AQ657627|AQ657627 Sheared DNA-24C13.TR Sheared DNA Trypanoso... 33 1.5
 emb|AW286528|AW286528 LG1_334_A05.g1_A002 Light Grown 1 (LG1) So... 33 1.5
 emb|AV427431|AV427431 AV427431 Lotus japonicus young plants (two... 33 1.5
 emb|AL034557|PFMAL4P1 Plasmodium falciparum chromosome 4 strain ... 33 1.5
 60 emb|AA550506|AA550506 1663m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 33 1.5
 emb|AW286549|AW286549 LG1_334_C05.g1_A002 Light Grown 1 (LG1) So... 33 1.5

	emb AQ023572 AQ023572 CpGR0492A <i>Cryptosporidium parvum</i> genomic r...	33	1.5
	emb AL035477 PFMAL4P4 <i>Plasmodium falciparum</i> chromosome 4 strain ...	33	1.5
	gb U36927 PYU36927 <i>Plasmodium yoelii</i> rhoptry protein gene, compl...	33	1.5
	emb AC006281 AC006281 <i>Plasmodium falciparum</i> chromosome 12 clone ...	33	1.5
5	emb AL034556 PFMAL3P5 <i>Plasmodium falciparum</i> MAL3P5, complete seq...	33	1.5
	emb AJ002233 PFJ002233 <i>Plasmodium falciparum</i> genomic gene for su...	29	1.6
	emb AC005505 AC005505 <i>Plasmodium falciparum</i> chromosome 12 clone ...	33	2.0
	emb AC005308 AC005308 <i>Plasmodium falciparum</i> chromosome 12 clone ...	33	2.0
	emb AL049180 PFMAL13P1 <i>Plasmodium falciparum</i> chromosome 13 strai...	33	2.0
10	emb AV419396 AV419396 AV419396 <i>Lotus japonicus</i> young plants (two...	33	2.0
	gb U49822 SDU49822 <i>Saccharomyces douglasii</i> mitochondrial tRNA-Se...	33	2.0
	emb AV412618 AV412618 AV412618 <i>Lotus japonicus</i> young plants (two...	33	2.0
	emb AW458882 AW458882 sh16a07.y1 Gm-cl016 <i>Glycine max</i> cDNA clone...	33	2.0
	emb AV428274 AV428274 AV428274 <i>Lotus japonicus</i> young plants (two...	33	2.0
15	emb AL096783 PFMAL13P9 <i>Plasmodium falciparum</i> chromosome 13 strai...	33	2.0
	gb M35612 YSCMTARSA Yeast (<i>S.cerevisiae</i>) mitochondrial autonomou...	33	2.0
	emb AL031744 PFMAL1P1 <i>Plasmodium falciparum</i> chromosome 1 strain ...	32	2.8
	emb AF093584 AF093584 <i>Plasmodium vivax</i> merozoite surface protein...	32	2.8
	emb AC006280 AC006280 <i>Plasmodium falciparum</i> chromosome 12 clone ...	32	2.8
20	emb AC004710 AC004710 <i>Plasmodium falciparum</i> chromosome 12, *** S...	32	2.8
	emb AE001410 AE001410 <i>Plasmodium falciparum</i> chromosome 2, sectio...	32	2.8
	emb X74069 SCALP1 <i>S.cerevisiae</i> APL1 gene for basic-amino-acid pe...	32	2.8
	emb AC005504 AC005504 <i>Plasmodium falciparum</i> chromosome 12, *** S...	32	2.8
	emb AW727908 AW727908 GA__Ea0028M15 <i>Gossypium arboreum</i> 7-10 dpa ...	32	2.8
25	emb AE001395 AE001395 <i>Plasmodium falciparum</i> chromosome 2, sectio...	32	2.8
	emb AF030694 AF030694 <i>Plasmodium falciparum</i> strain Dd2 heat shoc...	32	2.8
	emb AQ647469 AQ647469 RPCI93-EcoRI-6E20.TJ RPCI93-EcoRI <i>Trypanos...</i>	32	2.8
	emb Z38061 SC9168 <i>S.cerevisiae</i> chromosome IX cosmid 9168.	32	2.8
	emb AL110675 CNS018QK <i>Botrytis cinerea</i> strain T4 cDNA library un...	32	2.8
30	emb AL008970 PFMAL3P4 <i>Plasmodium falciparum</i> MAL3P4, complete seq...	31	2.9
	emb AW035978 AW035978 EST282837 tomato callus, TAMU <i>Lycopersicon...</i>	32	3.8
	emb AF126285 AF126285 <i>Pleurotus ostreatus</i> linear mitochondrial p...	32	3.8
	emb AL049181 PFMAL13P4 <i>Plasmodium falciparum</i> chromosome 13 strai...	32	3.8
	emb AW691746 AW691746 NF043G06ST1F1000 Developing stem <i>Medicago ...</i>	32	3.8
35	emb Z98551 PFMAL3P6 <i>Plasmodium falciparum</i> MAL3P6, complete seque...	32	3.8
	emb AW030017 AW030017 EST273272 tomato callus, TAMU <i>Lycopersicon...</i>	32	3.8
	emb AL049183 PFMAL13P6 <i>Plasmodium falciparum</i> chromosome 13 strai...	32	3.8
	emb AC018661 AC018661 <i>Leishmania major</i> chromosome 35 clone L3836...	32	3.8
	emb AQ909783 AQ909783 GSSTc08262 <i>Trypanosome cruzi</i> random genomi...	32	3.8
40	emb AQ906056 AQ906056 GSSTc07178 <i>Trypanosome cruzi</i> random genomi...	32	3.8
	emb AQ905917 AQ905917 GSSTc010600 <i>Trypanosome cruzi</i> random genom...	32	3.8
	emb X16104 SBKAFGK1 <i>Sorghum</i> DNA for kafirin, pGK1.	32	3.8
	emb AW684444 AW684444 NF017A07NR1F1000 Nodulated root <i>Medicago t...</i>	32	3.8
	emb AC011016 AC011016 <i>Leishmania major</i> chromosome 35 clone L218 ...	32	3.8
45	emb AL033503 CAC49C4 <i>C.albicans</i> cosmid Ca49C4.	32	3.8
	emb AW761381 AW761381 sl66g01.y1 Gm-cl027 <i>Glycine max</i> cDNA clone...	32	3.8
	emb AW220823 AW220823 EST297292 tomato fruit mature green, TAMU ...	32	3.8
	emb AC007863 AC007863 <i>Trypanosoma brucei</i> chromosome VI clone RPC...	32	3.8
	dbj D83006 D83006 <i>Saccharomyces cerevisiae</i> MNN4 gene, complete cds.	32	3.8
50	emb AA557046 AA557046 888 Loblolly pine N <i>Pinus taeda</i> cDNA clone...	32	3.8
	emb AW692198 AW692198 NF048F08ST1F1000 Developing stem <i>Medicago ...</i>	32	3.8
	emb AQ935320 AQ935320 CpG2407A CpIOWAgDNA1 <i>Cryptosporidium parvu...</i>	31	5.2
	emb Z68144 SPAC3H1 <i>S. pombe</i> chromosome I cosmid c3H1.	31	5.2
	emb AE001422 AE001422 <i>Plasmodium falciparum</i> chromosome 2, sectio...	31	5.2
55	emb AE001401 AE001401 <i>Plasmodium falciparum</i> chromosome 2, sectio...	31	5.2
	emb AE001380 AE001380 <i>Plasmodium falciparum</i> chromosome 2, sectio...	31	5.2
	emb AC004157 AC004157 <i>Plasmodium falciparum</i> chromosome 12 clone ...	31	5.2
	emb AE001376 AE001376 <i>Plasmodium falciparum</i> chromosome 2, sectio...	31	5.2
	emb AQ941118 AQ941118 Sheared DNA-35E12.TF Sheared DNA <i>Trypanoso...</i>	31	5.2
60	emb AQ949411 AQ949411 Sheared DNA-38N10.TF Sheared DNA <i>Trypanoso...</i>	31	5.2

Query= AL021890.71_at 16298_at /id_source genbank /description
 emb|caal7152.1| (al021890) putative protein [arabidopsis thaliana]
 /blast_score 1.00e-68 /ec_number /family /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021890|/ncgi)
 5 [post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021890|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021890|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?al021890>
 (375 letters)

Database: plantfungal
 10 661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	
		(bits)	Value	
15	Sequences producing significant alignments:			
	emb AW685341 AW685341 NF026D08NR1F1000 Nodulated root Medicago t...	162	1e-39	
	gb BE124622 BE124622 EST393657 GVN Medicago truncatula cDNA clon...	162	1e-39	
	emb AI943438 AI943438 MF02E10 MF Mesembryanthemum crystallinum c...	158	2e-38	
20	gb BE033541 BE033541 MF02E10 MF Mesembryanthemum crystallinum cD...	158	2e-38	
	emb AW667752 AW667752 GA__Ea0010I06 Gossypium arboreum 7-10 dpa ...	155	1e-37	
	emb AW747419 AW747419 WS1_68_E10.b1_A002 Water-stressed 1 (WS1) ...	155	2e-37	
	emb AW981480 AW981480 EST392633 DSIL Medicago truncatula cDNA cl...	154	4e-37	
	emb AW441269 AW441269 EST310665 tomato fruit red ripe, TAMU Lyco...	153	5e-37	
25	emb AW223703 AW223703 EST300514 tomato fruit red ripe, TAMU Lyco...	153	5e-37	
	emb AW034892 AW034892 EST279121 tomato callus, TAMU Lycopersicon...	153	5e-37	
	emb AW224013 AW224013 EST300824 tomato fruit red ripe, TAMU Lyco...	153	5e-37	
	emb AW907232 AW907232 EST343355 potato stolon, Cornell Universit...	153	7e-37	
	emb AW747501 AW747501 WS1_68_E10.g1_A002 Water-stressed 1 (WS1) ...	152	9e-37	
30	emb AW730496 AW730496 GA__Ea0026O23 Gossypium arboreum 7-10 dpa ...	152	9e-37	
	emb AW760599 AW760599 sl52d09.y1 Gm-c1027 Glycine max cDNA clone...	151	2e-36	
	emb AI960575 AI960575 sc86c01.y1 Gm-c1018 Glycine max cDNA clone...	151	2e-36	
	emb AW706639 AW706639 sj62h07.y1 Gm-c1033 Glycine max cDNA clone...	151	2e-36	
	emb AI166395 AI166395 xylem.est.231 Poplar xylem Lambda ZAPII li...	150	5e-36	
35	emb AI443884 AI443884 sa44f06.y1 Gm-c1004 Glycine max cDNA clone...	149	6e-36	
	emb AW568285 AW568285 si69g11.y1 Gm-r1030 Glycine max cDNA clone...	149	6e-36	
	emb AW186193 AW186193 se64g04.y1 Gm-c1019 Glycine max cDNA clone...	149	6e-36	
	emb AI855496 AI855496 sc16h05.y1 Gm-c1013 Glycine max cDNA clone...	149	1e-35	
	gb BE020351 BE020351 sm43b05.y1 Gm-c1028 Glycine max cDNA clone ...	148	2e-35	
40	emb AW132618 AW132618 se06f04.y1 Gm-c1013 Glycine max cDNA clone...	148	2e-35	
	emb AI777814 AI777814 EST258693 tomato susceptible, Cornell Lyco...	146	8e-35	
	emb AV408412 AV408412 AV408412 Lotus japonicus young plants (two...	141	2e-33	
	emb AW156084 AW156084 ga24f11.y1 Moss EST library PPU Physcomitr...	131	3e-30	
	emb AV398027 AV398027 AV398027 Chlamydomonas reinhardtii C9 Chla...	126	7e-29	
45	emb AI965929 AI965929 sc79h07.y1 Gm-c1018 Glycine max cDNA clone...	123	6e-28	
	emb AV427426 AV427426 AV427426 Lotus japonicus young plants (two...	108	2e-23	
	emb AL160493 LMFLCHR26 Leishmania major Friedlin assembled chrom...	102	1e-21	
	emb AW738874 AW738874 gb03e09.y1 Moss EST library PPN Physcomitr...	99	2e-20	
	emb AW476911 AW476911 ga38h10.y1 Moss EST library PPU Physcomitr...	95	2e-19	
50	emb AL049558 SPBC216 S.pombe chromosome II cosmid c216.	67	2e-19	
	emb AW335287 AW335287 S45D10 AGS-1 Pneumocystis carinii f. sp. c...	71	3e-19	
	emb AI822525 AI822525 L0-1030T3 Ice plant Lambda Uni-Zap XR expr...	95	3e-19	
	emb AI730110 AI730110 BNLGHi6160 Six-day Cotton fiber Gossypium ...	94	6e-19	
	emb AW933218 AW933218 EST359061 tomato fruit mature green, TAMU ...	90	5e-18	
55	emb AW933878 AW933878 EST359721 tomato fruit mature green, TAMU ...	90	5e-18	
	emb AW222361 AW222361 EST299172 tomato fruit red ripe, TAMU Lyco...	90	5e-18	
	emb AW617209 AW617209 EST323620 L. hirsutum trichome, Cornell Un...	90	5e-18	
	emb AW222638 AW222638 EST299449 tomato fruit red ripe, TAMU Lyco...	90	5e-18	
	emb AW094164 AW094164 EST287344 tomato mixed elicitor, BTI Lycop...	90	5e-18	
60	emb AW220746 AW220746 EST297215 tomato fruit mature green, TAMU ...	90	5e-18	
	emb AI939238 AI939238 sc68h11.y1 Gm-c1016 Glycine max cDNA clone...	90	7e-18	

- gb|BE060018|BE060018 sn39h09.y1 Gm-c1027 Glycine max cDNA clone ... 90 7e-18
 emb|AW775277|AW775277 EST334342 DSIL Medicago truncatula cDNA cl... 88 4e-17
 emb|AW127596|AW127596 M110327 DSLC Medicago truncatula cDNA clon... 86 9e-17
 emb|AI026521|AI026521 TENU0733 T. cruzi epimastigote normalized ... 73 1e-16
 5 emb|X59720|SCCHRII S.cerevisiae chromosome III complete DNA seq... 85 2e-16
 gb|T36700|T36700 EST101687 S. cerevisiae strain X2180-1A Sacchar... 79 1e-14
 emb|AW650769|AW650769 EST329223 tomato germinating seedlings, TA... 79 1e-14
 emb|AW739119|AW739119 gb26a12.y1 Moss EST library PPN Physcomitr... 79 1e-14
 emb|AT000681|AT000681 AT000681 Brassica rapa guard cell Brassica... 62 4e-14
 10 gb|N81594|N81594 TgESTzy60e01.r1 TgRH Tachyzoite cDNA Toxoplasma... 55 1e-12
 emb|AA740047|AA740047 812 PtiFG2 Pinus taeda cDNA clone 9275M 3'... 62 4e-12
 emb|AW907238|AW907238 EST343361 potato stolon, Cornell Universit... 68 2e-11
 emb|AA948748|AA948748 L0-267M13R Ice plant Lambda Uni-Zap XR exp... 66 1e-10
 emb|AA842826|AA842826 CFB57 Floral bud cDNA library of Hot peppe... 63 1e-09
 15 emb|AW351206|AW351206 GM210011A20E12R Gm-r1021 Glycine max cDNA ... 61 5e-09
 emb|AI495735|AI495735 sb15f07.y1 Gm-c1004 Glycine max cDNA clone... 61 5e-09
 emb|AW597401|AW597401 si92d06.y1 Gm-c1031 Glycine max cDNA clone... 60 9e-09
 emb|AW094112|AW094112 EST287292 tomato mixed elicitor, BTI Lycop... 58 2e-08
 emb|AV412908|AV412908 AV412908 Lotus japonicus young plants (two... 54 6e-07
 20 emb|AW931744|AW931744 EST357587 tomato fruit mature green, TAMU ... 46 9e-05
 emb|AW459770|AW459770 sh91h03.y1 Gm-c1016 Glycine max cDNA clone... 42 0.002
 emb|AI483073|AI483073 EST242396 tomato shoot, Cornell Lycopersic... 35 0.19
 emb|AW686356|AW686356 NF040G07NR1F1000 Nodulated root Medicago t... 35 0.36
 emb|AV389829|AV389829 AV389829 Chlamydomonas reinhardtii C9 Chla... 34 0.49
 25 emb|Z71549|SCYNL273W S.cerevisiae chromosome XIV reading frame O... 34 0.68
 emb|AQ845543|AQ845543 LMAJFV1_lm26g12.y1 Leishmania major FV1 ra... 33 0.93
 emb|AW692037|AW692037 NF046H05ST1F1000 Developing stem Medicago ... 30 1.1
 emb|AW329632|AW329632 N200892e rootphos(-) Medicago truncatula c... 30 1.2
 emb|AL136235|SPAC664 S.pombe chromosome I cosmid c664. 32 1.8
 30 emb|AU013634|AU013634 AU013634 Schizosaccharomyces pombe late lo... 32 1.8
 emb|AF152203|AF152203 Metasequoia glyptostroboides maturase (mat... 32 1.8
 emb|AU013588|AU013588 AU013588 Schizosaccharomyces pombe late lo... 32 1.8
 emb|X83998|CPEAPB C.parasitica eapB gene. 32 2.4
 gb|BE049708|BE049708 NXNV_142_E09_F Nsf Xylem Normal wood Vertic... 31 3.3
 35 emb|AW310022|AW310022 sf28e03.x1 Gm-c1028 Glycine max cDNA clone... 31 3.3
 emb|AI813025|AI813025 2H4 Pine Lambda Zap Xylem library Pinus ta... 31 3.3
 emb|AQ399658|AQ399658 mgxb0002B08f CUGI Rice Blast BAC Library P... 31 3.3
 emb|AW349850|AW349850 GM210005B21F11R Gm-r1021 Glycine max cDNA ... 31 3.3
 emb|AI440691|AI440691 sa67h01.y1 Gm-c1004 Glycine max cDNA clone... 31 3.3
 40 emb|AW497050|AW497050 ga53b08.y1 Moss EST library PPU Physcomitr... 31 3.3
 emb|AW278010|AW278010 sf89d09.y1 Gm-c1019 Glycine max cDNA clone... 30 3.6
 emb|AW496915|AW496915 ga50a09.y1 Moss EST library PPU Physcomitr... 31 4.6
 emb|AZ048302|AZ048302 LMAJFV1_lm76d06.x1 Leishmania major FV1 ra... 31 4.6
 emb|AQ398363|AQ398363 mgxb0014B01f CUGI Rice Blast BAC Library P... 31 4.6
 45 emb|X90948|ANRNAHSP7 A.nodosum mRNA for HSP70 protein. 31 4.6
 emb|AW509671|AW509671 ga62c03.y1 Moss EST library PPU Physcomitr... 31 4.6
 emb|AW561529|AW561529 ga81h08.y1 Moss EST library PPU Physcomitr... 31 4.6
 emb|AW738897|AW738897 gb03h02.y1 Moss EST library PPN Physcomitr... 31 4.6
 emb|X79095|FTPDKG F.trinervia pdk gene for pyruvate,orthophospha... 30 6.3
 50 emb|Z99262|SPAC9E9 S.pombe chromosome I cosmid c9E9. 30 6.3
 emb|X79192|FBPDK F.brownii pdk gene. 30 6.3
 emb|AI164197|AI164197 A056p02u Hybrid aspen plasmid library Popu... 30 6.3
 emb|AW156147|AW156147 se20b05.y1 Gm-c1015 Glycine max cDNA clone... 30 6.3
 emb|X75516|FPPDK F.pringlei mRNA for pyruvate, orthophosphate di... 30 6.3
 55 gb|U08399|FBU08399 Flaveria brownii cold stable pyruvate, orthop... 30 6.3

Query= AL024486.185_at 16299_at /id_source genbank /description
 emb|caa19705.1| (al024486) putative protein [arabidopsis thaliana]
 /blast_score 1.00e-170 /ec_number /family /chip nova /gb_link
 60 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al024486|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al024486|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al024486|/ncgi)

<http://www.ncgr.org/cgi-bin/ff?al024486>
(844 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E		(bits)	Value
10	Sequences producing significant alignments:				
	emb AI489421 AI489421	EST247760	tomato ovary, TAMU Lycopersicon ...	336	1e-91
	emb AW329288 AW329288	N200509e	rootphos(-) Medicago truncatula c...	307	9e-83
	emb AW733754 AW733754	sk77g11.y1	Gm-cl016 Glycine max cDNA clone...	290	9e-78
15	emb AW561007 AW561007	EST316055	DSIR Medicago truncatula cDNA cl...	287	8e-77
	emb AI489189 AI489189	EST247528	tomato ovary, TAMU Lycopersicon ...	273	1e-72
	emb AI488043 AI488043	EST246365	tomato ovary, TAMU Lycopersicon ...	269	2e-71
	emb AW625207 AW625207	EST319114	tomato radicle, 5 d post-imbibit...	258	5e-68
	emb AW559910 AW559910	EST314958	DSIR Medicago truncatula cDNA cl...	258	5e-68
20	emb AW559909 AW559909	EST314957	DSIR Medicago truncatula cDNA cl...	245	4e-64
	emb AI487722 AI487722	EST246044	tomato ovary, TAMU Lycopersicon ...	241	5e-63
	emb AW218466 AW218466	EST303649	tomato radicle, 5 d post-imbibit...	238	3e-62
	emb AW624963 AW624963	EST313792	tomato radicle, 5 d post-imbibit...	234	8e-61
	emb AW774997 AW774997	EST334148	KV3 Medicago truncatula cDNA clo...	217	1e-55
25	emb AA495616 AA495616	c425	Zhou and Ragan 1993 Gracilaria gracil...	118	3e-52
	emb AW678376 AW678376	WS1_15_G07.g1_A002	Water-stressed 1 (WS1) ...	175	5e-50
	emb AW760767 AW760767	sl36g03.y1	Gm-cl027 Glycine max cDNA clone...	194	8e-49
	emb AI416755 AI416755	sa18h08.x1	Gm-cl005 Glycine max cDNA clone...	175	5e-44
	gb BE020624 BE020624	sm51d11.y1	Gm-cl028 Glycine max cDNA clone ...	175	4e-43
30	emb AW218418 AW218418	EST303601	tomato radicle, 5 d post-imbibit...	174	9e-43
	emb AW684921 AW684921	NF023B02NR1F1000	Nodulated root Medicago t...	138	8e-40
	emb AL035218 SPCC1281	S.pombe	chromosome III cosmid c1281.	81	3e-37
	emb AW222782 AW222782	EST299593	tomato fruit red ripe, TAMU Lyco...	149	4e-35
	emb AW098211 AW098211	ga07f10.y1	Moss EST library CPU Ceratodon ...	147	9e-35
35	emb Z48639 SC9920	S.cerevisiae	chromosome XIII cosmid 9920.	67	2e-34
	emb AA660525 AA660525	00411	MtRHE Medicago truncatula cDNA 5', m...	104	1e-33
	emb Z28301 SCYKR076W	S.cerevisiae	chromosome XI reading frame OR...	77	5e-32
	emb AW931289 AW931289	EST357132	tomato fruit mature green, TAMU ...	123	1e-27
	emb X85807 SCCVIIRA	S.cerevisiae	chromosome VII 27kbp right arm ...	51	2e-23
40	emb Z72939 SCYGR154C	S.cerevisiae	chromosome VII reading frame O...	51	2e-23
	emb AA788015 AA788015	r4b01a1.r1	Aspergillus nidulans 24hr asexu...	90	1e-22
	emb AW931288 AW931288	EST357131	tomato fruit mature green, TAMU ...	106	2e-22
	emb AW686971 AW686971	NF004E10RT1F1082	Developing root Medicago ...	104	1e-21
	emb AI416795 AI416795	sa18h08.y1	Gm-cl005 Glycine max cDNA clone...	98	7e-20
45	emb AI327824 AI327824	j0c06a1.r1	Aspergillus nidulans 24hr asexu...	77	1e-17
	emb AI212279 AI212279	x1e09a1.r1	Aspergillus nidulans 24hr asexu...	90	2e-17
	emb AI165879 AI165879	B002P45U	Hybrid aspen plasmid library Popu...	84	2e-15
	emb AA966531 AA966531	w5h12a1.r1	Aspergillus nidulans 24hr asexu...	82	5e-15
	emb AW931345 AW931345	EST357188	tomato fruit mature green, TAMU ...	82	7e-15
50	emb AW442112 AW442112	EST311508	tomato fruit red ripe, TAMU Lyco...	80	2e-14
	emb AW704348 AW704348	sk18b11.y1	Gm-cl028 Glycine max cDNA clone...	77	2e-13
	emb AW221318 AW221318	EST297787	tomato fruit mature green, TAMU ...	68	9e-11
	emb AQ875035 AQ875035	V120D9	mTn-3xHA/lacZ Insertion Library, st...	67	2e-10
	emb AW934230 AW934230	EST360073	tomato fruit mature green, TAMU ...	66	3e-10
55	emb AA787150 AA787150	m8a03a1.r1	Aspergillus nidulans 24hr asexu...	58	1e-07
	emb AQ492097 AQ492097	V111F10	mTn-3xHA/lacZ Insertion Library Sa...	55	9e-07
	emb AA788014 AA788014	r4b01a1.fl	Aspergillus nidulans 24hr asexu...	35	4e-04
	emb AA787149 AA787149	m8a03a1.fl	Aspergillus nidulans 24hr asexu...	46	5e-04
	emb AC007865 AC007865	Trypanosoma	brucei chromosome II clone RPC...	38	0.12
60	emb AA788490 AA788490	l3a06a1.fl	Aspergillus nidulans 24hr asexu...	35	0.58
	emb AV420850 AV420850	AV420850	Lotus japonicus young plants (two...	29	1.0

emb|AF041468|AF041468 Guillardia theta complete plastid genome. 35 1.1
 emb|AW037453|AW037453 EST279002 tomato mixed elicitor, BTI Lycop... 35 1.1
 emb|Z34288|SCXCDNA S.cerevisiae (S288C) X chromosome DNA (17137bp). 34 1.5
 emb|Z49346|SCYJL071W S.cerevisiae chromosome X reading frame ORF... 34 1.5
 5 emb|X71362|HVDHN7 H.vulgare gene for dehydrin 7. 34 1.5
 emb|X88851|SCESTGENE S.cerevisiae DNA for hypothetical proteins a... 34 1.5
 emb|AF043087|AF043087 Hordeum vulgare dehydrin 1 (dhn1) gene, co... 34 1.5
 emb|AI988341|AI988341 sc99e11.y1 Gm-c1020 Glycine max cDNA clone... 34 2.1
 emb|Y10224|CMAO1 C.melo aol gene, partial. 34 2.1
 10 emb|AI900471|AI900471 sc11b06.y1 Gm-c1012 Glycine max cDNA clone... 34 2.1
 emb|AQ874584|AQ874584 V111B3 mTn-3xHA/lacZ Insertion Library, st... 34 2.1
 emb|AW279161|AW279161 sf67b09.y1 Gm-c1013 Glycine max cDNA clone... 34 2.1
 emb|Z99531|SPAC19D5 S.pombe chromosome I cosmid c19D5. 33 2.8
 emb|AJ273736|AJ273736 AJ273736 Metarhizium anisopliae ARSEF 2575... 33 2.8
 15 emb|AW730699|AW730699 GA_Ea0027C11 Gossypium arboreum 7-10 dpa ... 33 3.9
 emb|AW982536|AW982536 HVSMEdg0003I12f Hordeum vulgare pre-anthesi... 33 3.9
 emb|AJ229614|KLAJ9614 Kluyveromyces lactis DNA fragment for sequ... 33 3.9
 emb|Z49625|SCYJR125C S.cerevisiae chromosome X reading frame ORF... 33 3.9
 emb|Z49624|SCYJR124C S.cerevisiae chromosome X reading frame ORF... 33 3.9
 20 emb|Z98547|PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque... 25 5.2
 emb|Z35776|SCYBL015W S.cerevisiae chromosome II reading frame OR... 32 5.3
 emb|AZ214742|AZ214742 Sheared DNA-68E9.TR Sheared DNA Trypanosom... 32 5.3
 emb|AW691304|AW691304 NF040B04ST1F1000 Developing stem Medicago ... 32 5.3
 emb|X68577|SC114 S. cerevisiae 11.4kb segment of chromosome II. 32 5.3
 25 gb|M31036|YSCACH1A S.cerevisiae acetyl-CoA hydrolase (ACH1) mRNA... 32 5.3
 emb|AJ243754|SAL243754 Sinapis alba chloroplast rpoB operon (rpo... 32 5.3
 emb|AL110506|SPBC577 S.pombe chromosome II cosmid c577. 26 5.9
 emb|AU010645|AU010645 AU010645 Schizosaccharomyces pombe late lo... 32 7.3
 emb|AI966191|AI966191 sc35a11.y1 Gm-c1014 Glycine max cDNA clone... 32 7.3
 30 emb|AL022244|SPBC3B8 S.pombe chromosome II cosmid c3B8. 32 7.3
 emb|AU012735|AU012735 AU012735 Schizosaccharomyces pombe late lo... 32 7.3
 emb|AE001394|AE001394 Plasmodium falciparum chromosome 2, sectio... 32 7.3

Query= AF149413.38_at 16357_at /id_source genbank /description
 35 "gb|aad40144.1|af149413_25 (af149413) contains similarity to protein
 kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien
 rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis
 thaliana]" /blast_score 0 /ec_number /family kinase /chip nova
 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
 40 post/entrez/query?db=n&form=6&dopt=g&uid=gb|af149413|/ncgi
 http://www.ncgr.org/cgi-bin/ff?af149413
 (3018 letters)

Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	(bits)	Value
50	Sequences producing significant alignments:			
	emb AF053127 AF053127	Malus domestica leucine-rich receptor-like...	169	8e-99
	emb AW930866 AW930866	EST356709 tomato fruit mature green, TAMU ...	152	2e-83
	emb AF197947 AF197947	Glycine max receptor protein kinase-like p...	160	3e-83
55	emb AF197946 AF197946	Glycine max receptor protein kinase-like p...	154	8e-81
	emb AI897516 AI897516	EST266959 tomato ovary, TAMU Lycopersicon ...	133	2e-73
	emb AF053998 AF053998	Lycopersicon esculentum Hcr2-5D (Hcr2-5D) ...	143	2e-72
	emb A67434 A67434	Sequence 7 from Patent WO9743429.	143	2e-72
	emb AW650851 AW650851	EST329305 tomato germinating seedlings, TA...	123	4e-72
60	emb AF053995 AF053995	Lycopersicon esculentum Hcr2-0B (Hcr2-0B) ...	144	2e-71
	emb AF053993 AF053993	Lycopersicon esculentum disease resistance...	145	4e-71

	emb A67429 A67429 Sequence 2 from Patent WO9743429.	145 4e-71
	emb A67428 A67428 Sequence 1 from Patent WO9743429.	145 4e-71
	gb U42444 U42444 Lycopersicon pimpinellifolium leucine rich repe...	150 4e-70
	emb A57130 A57130 Sequence 1 from Patent WO9531564.	150 4e-70
5	gb U42445 U42445 Lycopersicon pimpinellifolium leucine rich repe...	150 4e-70
	emb A57133 A57133 Sequence 4 from Patent WO9531564.	150 4e-70
	emb AW034426 AW034426 EST277997 tomato callus, TAMU Lycopersicon...	252 1e-65
	emb AW560797 AW560797 EST315845 DSIR Medicago truncatula cDNA cl...	240 5e-62
	emb AF053997 AF053997 Lycopersicon esculentum Hcr2-5B (Hcr2-5B) ...	144 7e-60
10	emb A67432 A67432 Sequence 5 from Patent WO9743429.	144 7e-60
	emb AW033860 AW033860 EST277431 tomato callus, TAMU Lycopersicon...	117 2e-59
	gb U77888 INU77888 Ipomoea nil receptor-like protein kinase (inr...	136 1e-55
	emb AI486612 AI486612 EST244933 tomato ovary, TAMU Lycopersicon ...	133 2e-53
	emb AW979740 AW979740 EST341365 tomato root deficiency, Cornell ...	105 5e-53
15	emb AF053996 AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr...	142 2e-52
	emb AW726024 AW726024 GA__Ea0020G24 Gossypium arboreum 7-10 dpa ...	149 1e-51
	emb AF053994 AF053994 Lycopersicon esculentum Hcr2-0A (Hcr2-0A) ...	139 2e-51
	emb AB029327 AB029327 Nicotiana tabacum mRNA for elicitor-induci...	133 9e-51
	emb AW564182 AW564182 LG1_285_D10.b1_A002 Light Grown 1 (LG1) So...	193 3e-48
20	emb AW693988 AW693988 NF071C05ST1F1037 Developing stem Medicago ...	190 6e-47
	dbj D30049 BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti...	84 1e-45
	emb AW650232 AW650232 EST328686 tomato germinating seedlings, TA...	96 7e-45
	emb AI895242 AI895242 EST264685 tomato callus, TAMU Lycopersicon...	154 1e-44
	gb BE060160 BE060160 HVSMeg0011B12f Hordeum vulgare pre-anthesis...	90 4e-44
25	emb AW621923 AW621923 EST312721 tomato root during/after fruit s...	94 2e-43
	emb AW428824 AW428824 Ljirmp24-927-c5 Ljirmp Lambda HybriZap ...	120 8e-43
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	85 2e-42
	emb AI484701 AI484701 EST242962 tomato ovary, TAMU Lycopersicon ...	89 2e-41
	emb AW621706 AW621706 EST312504 tomato root during/after fruit s...	92 3e-41
30	emb AW668493 AW668493 GA__Ea0014C20 Gossypium arboreum 7-10 dpa ...	92 6e-41
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	83 7e-41
	emb AW929662 AW929662 EST338450 tomato flower buds 8 mm to pre-a...	92 8e-41
	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR...	128 1e-40
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	82 1e-40
35	emb Z73295 CRPK1 Croseus mRNA for receptor-like protein kinase.	136 1e-40
	emb AW684304 AW684304 NF015C05NR1F1000 Nodulated root Medicago t...	108 1e-40
	emb AW010219 AW010219 ST03E03 Pine TriplEx shoot tip library Pin...	144 2e-40
	gb U20948 ITU20948 Ipomoea trifida receptor protein kinase (IRK1...	129 2e-40
	emb AW287714 AW287714 LG1_271_E06.b1_A002 Light Grown 1 (LG1) So...	103 2e-40
40	emb AW036763 AW036763 EST252152 tomato ovary, TAMU Lycopersicon ...	85 2e-40
	emb AW092144 AW092144 EST285240 tomato mixed elicitor, BTI Lycop...	102 3e-40
	emb AW704459 AW704459 sk53c10.y1 Gm-c1019 Glycine max cDNA clone...	100 3e-40
	emb AW036762 AW036762 EST252151 tomato ovary, TAMU Lycopersicon ...	85 4e-40
	emb AV427160 AV427160 AV427160 Lotus japonicus young plants (two...	117 4e-39
45	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	84 4e-39
	emb AA557073 AA557073 915 Loblolly pine N Pinus taeda cDNA clone...	96 4e-39
	emb AW831515 AW831515 sm26h11.y1 Gm-c1028 Glycine max cDNA clone...	93 6e-39
	emb AW299180 AW299180 EST305990 KV2 Medicago truncatula cDNA clo...	122 7e-39
	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	85 3e-38
50	emb AW727470 AW727470 GA__Ea0012H16 Gossypium arboreum 7-10 dpa ...	93 3e-38
	emb AW039328 AW039328 EST281585 tomato mixed elicitor, BTI Lycop...	102 3e-38
	emb AW694732 AW694732 NF079D07ST1F1061 Developing stem Medicago ...	102 3e-38
	emb AI894931 AI894931 EST264374 tomato callus, TAMU Lycopersicon...	97 4e-38
	emb AW686018 AW686018 NF033E02NR1F1000 Nodulated root Medicago t...	122 4e-38
55	emb AW040672 AW040672 EST283536 tomato mixed elicitor, BTI Lycop...	102 4e-38
	emb AI967314 AI967314 Ljirmp00-017 Ljirmp Lambda HybriZap two...	90 7e-38
	emb AV418863 AV418863 AV418863 Lotus japonicus young plants (two...	112 9e-38
	emb AI485090 AI485090 EST243394 tomato ovary, TAMU Lycopersicon ...	85 3e-37
	gb BE059471 BE059471 sn32d11.y1 Gm-c1016 Glycine max cDNA clone ...	82 3e-37
60	emb AI771841 AI771841 EST252941 tomato ovary, TAMU Lycopersicon ...	85 3e-37
	emb AI485862 AI485862 EST244183 tomato ovary, TAMU Lycopersicon ...	85 3e-37

- emb|AW756743|AW756743 sl26f10.y1 Gm-c1027 Glycine max cDNA clone... 92 4e-37
 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 78 5e-37
 dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 78 5e-37
 emb|AB030083|AB030083 Populus nigra PnLPK mRNA for lectin-like p... 121 6e-37
 5 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 91 6e-37
 emb|AW746575|AW746575 WS1_54_G12.b1_A002 Water-stressed 1 (WS1) ... 150 8e-37
 emb|AW756409|AW756409 sl21a08.y1 Gm-c1036 Glycine max cDNA clone... 114 1e-36
 emb|AI725692|AI725692 BNLGHi12653 Six-day Cotton fiber Gossypium... 101 1e-36
 emb|AW458376|AW458376 sh87d06.y1 Gm-c1016 Glycine max cDNA clone... 74 2e-36
 10 emb|AW185015|AW185015 se85e10.y1 Gm-c1023 Glycine max cDNA clone... 100 2e-36
 dbj|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 84 3e-36
 emb|Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 100 4e-36
 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 78 8e-36
 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 83 8e-36
 15 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 85 8e-36
 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 77 1e-35
 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 84 2e-35
 emb|AW734633|AW734633 sk97d07.y1 Gm-c1035 Glycine max cDNA clone... 101 2e-35
 emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 82 3e-35
 20 emb|AW736597|AW736597 EST333089 KV3 Medicago truncatula cDNA clo... 91 4e-35
 emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 76 9e-35
 emb|AW774582|AW774582 EST333733 KV3 Medicago truncatula cDNA clo... 94 9e-35
 emb|AW219672|AW219672 EST302154 tomato root during/after fruit s... 124 1e-34
 gb|BE020963|BE020963 sm54a06.y1 Gm-c1028 Glycine max cDNA clone ... 80 1e-34
 25 emb|AW329560|AW329560 N200811e rootphos(-) Medicago truncatula c... 146 2e-34
 emb|AI771280|AI771280 EST252296 tomato ovary, TAMU Lycopersicon ... 87 2e-34
 emb|AF166121|AF166121 Hordeum vulgare Cf2/Cf5 disease resistance... 103 2e-34
 emb|AW694942|AW694942 NF081G02ST1F1018 Developing stem Medicago ... 141 3e-34
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 82 3e-34

30

Query= AL031187.126_at 16360_at /id_source genbank /description
 emb|caa20203.1| (al031187) receptor-like serine/threonine protein
 kinase ark3 [arabidopsis thaliana] /blast_score 0 /ec_number /family
 kinase /chip nova /gb_link
 35 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031187|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031187|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031187|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?al031187>
 (2553 letters)

40

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

45

Score E
 Sequences producing significant alignments: (bits) Value

- emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 820 0.0
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 549 0.0
 50 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 510 0.0
 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 505 0.0
 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 504 0.0
 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 501 0.0
 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 490 0.0
 55 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 489 0.0
 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 488 0.0
 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 485 0.0
 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 483 0.0
 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 461 0.0
 60 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 458 0.0
 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 455 0.0

- dbj|D38564|BOLRPKB *Brassica campestris* mRNA for receptor protein... 395 0.0
emb|AB032474|AB032474 *Brassica oleracea* SRK60 mRNA for S60 S-loc... 394 0.0
dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 374 0.0
emb|Y14286|BOY14286 *Brassica oleracea* SFR3 gene, partial. 292 0.0
5 emb|Y12530|BOARLKGEN *B.oleraceae* gene encoding serine/threonine ... 652 0.0
emb|AB000972|AB000972 *Brassica campestris* pseudogene for SLG-lik... 237 0.0
emb|AB000970|AB000970 *Brassica campestris* gene for receptor kina... 481 0.0
emb|AB024419|AB024419S1 *Brassica oleracea* SRK13 gene, exon 1. 495 0.0
emb|AB024421|AB024421S1 *Brassica oleracea* SRK13-b gene, exon 1. 494 0.0
10 emb|AB024418|AB024418 *Brassica oleracea* SLG13-b gene, partial cds. 506 0.0
emb|AB000971|AB000971 *Brassica campestris* pseudogene for recepto... 320 e-180
emb|X55275|BOSLG13 *B.oleracea* SLG-13 gene for S-locus glycoprotein. 499 e-179
emb|AB009680|AB009680 *Raphanus sativus* SLG(S4) gene for S glycop... 493 e-179
emb|AB024417|AB024417 *Brassica oleracea* SLG13 gene, partial cds. 498 e-178
15 dbj|D85206|D85206 *Brassica oleracea* DNA for S blycoprotein, part... 406 e-177
dbj|D85215|D85215 *Brassica campestris* DNA for S glycoprotein, pa... 295 e-176
dbj|D85224|D85224 *Brassica campestris* DNA for S glycoprotein, pa... 486 e-176
dbj|D88765|D88765 *Brassica oleracea* DNA for S glycoprotein, part... 287 e-176
dbj|D85199|D85199 *Brassica oleracea* DNA for S glycoprotein, part... 485 e-176
20 emb|AB013719|AB013719 *Brassica oleracea* mRNA for SLG23Bol, compl... 404 e-175
dbj|D85219|D85219 *Brassica campestris* DNA for S glycoprotein, pa... 405 e-175
dbj|D85203|D85203 *Brassica oleracea* DNA for S glycoprotein, part... 409 e-175
dbj|D85198|D85198 *Brassica oleracea* DNA for S glycoprotein, part... 494 e-175
dbj|D85220|D85220 *Brassica campestris* DNA for S glycoprotein, pa... 410 e-175
25 emb|X55274|BCSLG8 *B.campestris* SLG-8 gene for S-locus glycoprotein. 482 e-175
emb|AB009682|AB009682 *Raphanus sativus* SLG(S6) gene for S glycop... 405 e-174
emb|Y00268|BOSLSG *Brassica oleracea* mRNA for S-locus specific gl... 408 e-174
emb|X03170|BOSLSGR *Brassica oleracea* mRNA 3' end for S-locus-spe... 408 e-174
dbj|D84468|BNASLG8A *Brassica campestris* mRNA for S-glycoprotein ... 478 e-173
30 emb|AB009681|AB009681 *Raphanus sativus* SLG(S5) gene for S glycop... 406 e-173
gb|S70937|S70937 self-incompatibility gene [*Brassica campestris*,... 283 e-173
dbj|D85218|D85218 *Brassica campestris* DNA for S glycoprotein, pa... 286 e-173
dbj|D85213|D85213 *Brassica campestris* DNA for S glycoprotein, pa... 283 e-173
emb|AB009683|AB009683 *Raphanus sativus* SLG(S8) gene for S glycop... 284 e-173
35 dbj|D85227|D85227 *Brassica campestris* DNA for S glycoprotein, pa... 293 e-172
dbj|D85211|D85211 *Brassica oleracea* DNA for S glycoprotein, part... 281 e-172
emb|X16123|BOS292 *B. oleracea* mRNA for S-locus specific glycopro... 397 e-172
gb|M36301|BNASLSGRA *B.campestris* S-locus-specific glycoprotein m... 402 e-172
dbj|D85225|D85225 *Brassica campestris* DNA for S glycoprotein, pa... 281 e-172
40 dbj|D85216|D85216 *Brassica campestris* DNA for S glycoprotein, pa... 409 e-171
dbj|D85204|D85204 *Brassica oleracea* DNA for S glycoprotein, part... 283 e-171
dbj|D85201|D85201 *Brassica oleracea* DNA for S glycoprotein, part... 490 e-171
emb|AB009684|AB009684 *Raphanus sativus* SLG(S7) gene for S glycop... 397 e-171
emb|X79432|BOSRK3 *B.oleracea* SRK3 gene. 396 e-171
45 dbj|D85208|D85208 *Brassica oleracea* DNA for S glycoprotein, part... 282 e-171
emb|AJ245479|BNA245479 *Brassica napus* SII3, slk, srk, CePP, Fmt,... 286 e-170
dbj|D84469|BNASLG12B *Brassica campestris* mRNA for S-glycoprotein... 287 e-170
emb|AB013717|AB013717S1 *Brassica rapa* gene for SRK46Bra, exon 1. 269 e-170
dbj|D85209|D85209 *Brassica oleracea* DNA for S glycoprotein, part... 286 e-170
50 dbj|D85205|D85205 *Brassica oleracea* DNA for S glycoprotein, part... 395 e-170
dbj|D85221|D85221 *Brassica campestris* DNA for S glycoprotein, pa... 348 e-170
emb|Z30211|BOSRK29G *B.oleracea* (alboglaba) srk29 gene. 288 e-169
emb|AB032471|AB032471 *Brassica oleracea* SLG pseudogene for S-loc... 398 e-169
gb|L08608|BNASLOCGLY *Brassica napus* S-locus glycoprotein mRNA, c... 477 e-168
55 emb|Z21608|BNESLOGPA *B.napus* mRNA for endogenous S-locus glycopr... 477 e-168
gb|L10736|BNASLGGA *Brassica napus* S-locus related glycoprotein (... 477 e-168
dbj|D85222|D85222 *Brassica campestris* DNA for S glycoprotein, pa... 243 e-166
dbj|D85229|D85229 *Brassica oleracea* DNA for S glycoprotein, part... 401 e-166
emb|AB009679|AB009679 *Raphanus sativus* SLG(S3) gene for S glycop... 285 e-166
60 dbj|D85212|D85212 *Brassica oleracea* DNA for S glycoprotein, part... 244 e-164
dbj|D85214|D85214 *Brassica campestris* DNA for S glycoprotein, pa... 395 e-163

- emb|AB009677|AB009677 *Raphanus sativus* SLG(S1) gene for S glycop... 266 e-163
 dbj|D85200|D85200 *Brassica oleracea* DNA for S glycoprotein, part... 204 e-163
 emb|AB008190|AB008190 *Brassica rapa* gene for SLG29, complete cds. 290 e-163
 emb|Y18261|BOY18261 *Brassica oleracea* SLGB gene, partial. 286 e-163
 5 emb|Z19548|BNSLGPII *B.napus* mRNA for S-locus glycoprotein type II. 286 e-163
 emb|Z11724|BNWSLGLP *B. napus* mRNA for S-locus glycoprotein. 278 e-160
 emb|AJ245480|BNA245480 *Brassica napus* slg gene for S-locus glyco... 380 e-160
 emb|AB024415|AB024415 *Brassica oleracea* SLG2-b mRNA, complete cds. 282 e-160
 dbj|D85226|D85226 *Brassica campestris* DNA for S glycoprotein, pa... 221 e-160
 10 dbj|D85223|D85223 *Brassica campestris* DNA for S glycoprotein, pa... 224 e-160
 emb|AB032472|AB032472 *Brassica oleracea* SLG60 pseudogene for S60... 160 e-159
 emb|Z18921|BOSRKL *B.oleracea* gene for S-receptor kinase-like pro... 198 e-158
 emb|AB012105|AB012105 *Brassica rapa* mRNA for SLG45; complete cds. 221 e-158
 dbj|D88193|D88193 *Brassica rapa* DNA for S-receptor kinase, compl... 160 e-158
 15 emb|X51637|BOSLSGA *B.oleracea* SLSG mRNA for self-incompatibility... 263 e-155
 dbj|D88192|D88192 *Brassica rapa* DNA for S-locus glycoprotein, co... 148 e-153
 dbj|D30050|BOLSRKB Turnip mRNA for S-glycoprotein SLG9, complete... 148 e-153
 emb|AF161333|AF161333 *Raphanus raphanistrum* subsp. *raphanistrum* ... 310 e-150
 emb|AF162908|AF162908 *Hirschfeldia incana* S-locus related (SLR) ... 261 e-150
 20 emb|Y12321|BOY12321 *Brassica oleracea* SLG-Sc and SLA-Sc genes an... 285 e-149
 emb|AB009872|AB009872 *Orychophragmus violaceus* gene for SLR1, pa... 413 e-149
 emb|X57673|BOSLR2RNA *B.oleracea* RNA for S-locus-related glycopr... 167 e-149
 emb|AB009873|AB009873 *Cheiranthus cheiri* gene for SLR1, partial ... 163 e-147
 emb|X58440|BCNS1 *B.campestris* NS1 mRNA for NS1 glycoprotein. 273 e-145
 25 emb|X52089|BOSLRG *Brassica* gene for S locus related glycoprotein. 272 e-143

Query= AC003974.136_at 16365_at /id_source genbank /description
 gb|aac04495.1| (ac003974) putative disease resistance protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family disease
 30 /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac003974|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac003974|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac003974|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac003974>
 (2673 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

	Score	E	
	Sequences producing significant alignments:		(bits) Value
	emb AF053998 AF053998 <i>Lycopersicon esculentum</i> Hcr2-5D (Hcr2-5D) ...	148	4e-74
45	emb A67434 A67434 Sequence 7 from Patent WO9743429.	148	4e-74
	emb AF053993 AF053993 <i>Lycopersicon esculentum</i> disease resistance...	148	4e-74
	emb A67429 A67429 Sequence 2 from Patent WO9743429.	148	4e-74
	emb A67428 A67428 Sequence 1 from Patent WO9743429.	148	4e-74
	emb AF053995 AF053995 <i>Lycopersicon esculentum</i> Hcr2-0B (Hcr2-0B) ...	150	4e-74
50	emb AF053997 AF053997 <i>Lycopersicon esculentum</i> Hcr2-5B (Hcr2-5B) ...	146	1e-72
	emb A67432 A67432 Sequence 5 from Patent WO9743429.	146	1e-72
	gb U42445 U42445 <i>Lycopersicon pimpinellifolium</i> leucine rich repe...	150	3e-71
	emb A57133 A57133 Sequence 4 from Patent WO9531564.	150	3e-71
	gb U42444 U42444 <i>Lycopersicon pimpinellifolium</i> leucine rich repe...	150	8e-71
55	emb A57130 A57130 Sequence 1 from Patent WO9531564.	150	8e-71
	emb AB029327 AB029327 <i>Nicotiana tabacum</i> mRNA for elicitor-induci...	97	4e-65
	emb AF053994 AF053994 <i>Lycopersicon esculentum</i> Hcr2-0A (Hcr2-0A) ...	149	6e-37
	emb AF119040 AF119040 <i>Lycopersicon esculentum</i> haplotype Northern...	143	3e-36
	emb AF053996 AF053996 <i>Lycopersicon pimpinellifolium</i> Hcr2-2A (Hcr...	144	3e-35
60	emb AF119041 AF119041 <i>Lycopersicon esculentum</i> haplotype Southern...	139	2e-33
	emb AJ002235 LHJ002235 <i>Lycopersicon hirsutum</i> Cf-4 resistance gen...	139	3e-33

- emb|AJ002236|LPJ002236 *Lycopersicon pimpinellifolium* Cf-9 resist... 140 4e-33
emb|AJ002237|LEJ002237 *Lycopersicon esculentum* haplotype of the ... 138 1e-32
emb|Y12640|LECF4A *L. esculentum* Cf-4A gene. 137 1e-32
emb|A58270|A58270 Sequence 1 from Patent WO9635790. 138 2e-31
5 gb|U15936|LPU15936 *Lycopersicon pimpinellifolium* Cf-9 precursor ... 138 2e-31
emb|AI778581|AI778581 EST259460 tomato susceptible, Cornell Lyco... 92 1e-29
emb|AW458587|AW458587 sh11a09.y1 Gm-c1016 Glycine max cDNA clone... 131 3e-29
emb|AW306725|AW306725 sf47e12.y1 Gm-c1009 Glycine max cDNA clone... 129 1e-28
emb|AF215729|AF215729 Glycine max RFLP clone A 45-10 sequence; a... 123 5e-27
10 emb|X81370|TAAWJL236 *T. aestivum* (subclone pAWJL236) AWJL236 gene. 115 8e-27
emb|AF140552|AF140552 *Lycopersicon esculentum* plant disease resi... 121 2e-26
emb|AI895949|AI895949 EST265392 tomato callus, TAMU *Lycopersicon*... 70 5e-25
emb|AW624314|AW624314 EST322175 tomato flower buds 3-8 mm, Corne... 113 5e-24
emb|X81369|TAAWJL218 *T. aestivum* (subclone pAWJL218) AWJL218 gene. 104 1e-23
15 emb|X81367|TAAWJL172 *T. aestivum* (subclone pAWJL172) AWJL172 gene. 99 7e-23
emb|X81368|TAAWJL175 *T. aestivum* (subclone pAWJL175) AWJL175 gene. 101 2e-22
emb|AW705275|AW705275 sk59a10.y1 Gm-c1019 Glycine max cDNA clone... 108 2e-22
emb|AF166121|AF166121 *Hordeum vulgare* Cf2/Cf5 disease resistance... 94 3e-22
emb|AI779817|AI779817 EST260696 tomato susceptible, Cornell Lyco... 100 1e-21
20 emb|AW888094|AW888094 NXNV_108_E11_F Nsf Xylem Normal wood Verti... 105 2e-21
emb|AQ917191|AQ917191 T233043b *Medicago truncatula* BAC library M... 93 1e-20
gb|U77888|INU77888 *Ipomoea nil* receptor-like protein kinase (inr... 79 2e-20
emb|AQ367638|AQ367638 toxb0002D20f CUGI Tomato BAC Library Lycop... 101 3e-20
emb|AZ044600|AZ044600 Gm_UMb001_116_G01.R UMN Soybean BAC Librar... 73 2e-19
25 emb|AW064561|AW064561 ST33A08 Pine TriplEx shoot tip library Pin... 98 3e-19
emb|AI484441|AI484441 EST242451 tomato ovary, TAMU *Lycopersicon* ... 98 3e-19
emb|AW279193|AW279193 sf67g09.y1 Gm-c1013 Glycine max cDNA clone... 98 4e-19
emb|AI900597|AI900597 sc13d11.y1 Gm-c1013 Glycine max cDNA clone... 97 5e-19
emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 82 1e-18
30 emb|AW032163|AW032163 EST275617 tomato callus, TAMU *Lycopersicon*... 64 1e-18
emb|AW979663|AW979663 EST341269 tomato root deficiency, Cornell ... 61 1e-18
emb|AW650508|AW650508 EST328962 tomato germinating seedlings, TA... 91 1e-18
emb|AI488023|AI488023 EST246345 tomato ovary, TAMU *Lycopersicon* ... 91 1e-18
emb|AI896676|AI896676 EST266119 tomato callus, TAMU *Lycopersicon*... 91 1e-18
35 emb|AW307311|AW307311 sf55d03.y1 Gm-c1009 Glycine max cDNA clone... 66 2e-18
emb|AV415568|AV415568 AV415568 *Lotus japonicus* young plants (two... 85 2e-18
emb|AI895309|AI895309 EST264752 tomato callus, TAMU *Lycopersicon*... 95 2e-18
emb|AI727073|AI727073 BNLGHi7256 Six-day Cotton fiber *Gossypium* ... 95 2e-18
emb|AW306675|AW306675 se53h08.y1 Gm-c1017 Glycine max cDNA clone... 95 3e-18
40 emb|X79130|TSLRRR *Triticum* sp. (pAWJL3) leucine rich repeat regi... 84 4e-18
emb|AW031498|AW031498 EST274952 tomato callus, TAMU *Lycopersicon*... 94 5e-18
emb|AW775087|AW775087 EST334238 KV3 *Medicago truncatula* cDNA clo... 94 6e-18
emb|AW690301|AW690301 NF029C05ST1F1000 Developing stem *Medicago* ... 81 7e-18
emb|AW267958|AW267958 EST306300 DSIR *Medicago truncatula* cDNA cl... 80 7e-18
45 emb|AI895893|AI895893 EST265336 tomato callus, TAMU *Lycopersicon*... 61 9e-18
emb|AW647847|AW647847 EST326301 tomato germinating seedlings, TA... 91 1e-17
emb|AW929189|AW929189 EST337977 tomato flower buds 8 mm to pre-a... 92 2e-17
emb|AW689506|AW689506 NF021E06ST1F1000 Developing stem *Medicago* ... 92 2e-17
emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 82 2e-17
50 emb|AW929854|AW929854 EST354124 tomato flower buds 8 mm to pre-a... 91 4e-17
emb|AW929780|AW929780 EST354050 tomato flower buds 8 mm to pre-a... 91 4e-17
emb|AW031218|AW031218 EST274756 tomato callus, TAMU *Lycopersicon*... 91 4e-17
emb|AW033367|AW033367 EST276938 tomato callus, TAMU *Lycopersicon*... 89 1e-16
emb|AI443128|AI443128 sa84f10.y1 Gm-c1004 Glycine max cDNA clone... 89 1e-16
55 emb|AI896313|AI896313 EST265756 tomato callus, TAMU *Lycopersicon*... 60 1e-16
emb|AW735867|AW735867 EST336635 tomato flower buds 0-3 mm, Corne... 89 2e-16
emb|AW980804|AW980804 EST391957 GVN *Medicago truncatula* cDNA clo... 69 2e-16
emb|AI488443|AI488443 EST246782 tomato ovary, TAMU *Lycopersicon* ... 88 3e-16
emb|AW033129|AW033129 EST276688 tomato callus, TAMU *Lycopersicon*... 78 3e-16
60 emb|AW127035|AW127035 ga20c02.y1 Moss EST library PPU *Physcomitr*... 88 4e-16
emb|AI895669|AI895669 EST265112 tomato callus, TAMU *Lycopersicon*... 88 4e-16

- emb|AW618685|AW618685 EST320671 *L. pennellii* trichome, Cornell U... 88 4e-16
 emb|AI894989|AI894989 EST264432 tomato callus, TAMU Lycopersicon... 88 4e-16
 emb|AI782076|AI782076 EST262955 tomato susceptible, Cornell Lyco... 87 5e-16
 emb|AW648795|AW648795 EST327249 tomato germinating seedlings, TA... 87 5e-16
 5 emb|AW694942|AW694942 NF081G02ST1F1018 Developing stem *Medicago* ... 78 6e-16
 emb|AV415057|AV415057 AV415057 *Lotus japonicus* young plants (two... 87 7e-16
 emb|AW399097|AW399097 EST309597 *L. pennellii* trichome, Cornell U... 63 8e-16
 emb|AW761367|AW761367 sl66e07.y1 Gm-cl027 *Glycine max* cDNA clone... 86 1e-15
 emb|AW649208|AW649208 EST327662 tomato germinating seedlings, TA... 86 1e-15
 10 emb|AV428126|AV428126 AV428126 *Lotus japonicus* young plants (two... 85 2e-15
 emb|AW290705|AW290705 NXNV045C11F Nsf Xylem Normal wood Vertical... 85 2e-15
 emb|AI352869|AI352869 MB70-4A PZ204.BNlib *Brassica napus* cDNA cl... 85 2e-15
 emb|AA661049|AA661049 00946 MtRHE *Medicago truncatula* cDNA 5' si... 85 2e-15
 emb|AW455303|AW455303 EST311841 tomato root during/after fruit s... 85 3e-15
 15 emb|AW869870|AW869870 NXNV_122_E02_F Nsf Xylem Normal wood Verti... 85 3e-15
 emb|AW398651|AW398651 EST309151 *L. pennellii* trichome, Cornell U... 84 4e-15
 emb|AW398661|AW398661 EST309161 *L. pennellii* trichome, Cornell U... 84 4e-15
 emb|AF049920|AF049920 *Petunia x hybrida* PGPS/D4 (PGPS/D4) mRNA, ... 84 4e-15
 emb|AW624634|AW624634 EST322579 tomato flower buds 3-8 mm, Corne... 59 4e-15
 20 emb|AW618879|AW618879 EST320865 *L. pennellii* trichome, Cornell U... 62 4e-15
 gb|BE035885|BE035885 MO11F02 *Mesembryanthemum crystallinum* cD... 84 5e-15

Query= AL096882.91_s_at 16817_s_at /id_source genbank /description

- 25 emb|cab51412.1| (al096882) acc synthase (atacs-6) [arabidopsis
 thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
 /ncgi
 (1488 letters)

- 30 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

- | | | Score | E | |
|----|--|--------|-------|--|
| | | (bits) | Value | |
| 35 | Sequences producing significant alignments: | | | |
| | emb X82273 BOACCS <i>B.oleracea</i> mRNA for ACC synthase. | 986 | 0.0 | |
| | emb X72676 BJMACC <i>B. juncea</i> mRNA for 1-Aminocyclopropane-1-carbo... | 875 | 0.0 | |
| | emb AF057563 AF057563 <i>Nicotiana glutinosa</i> 1-aminocyclopropane-1-... | 765 | 0.0 | |
| 40 | emb AJ005002 NTAJ5002 <i>Nicotiana tabacum</i> mRNA for 1-aminocyclopro... | 761 | 0.0 | |
| | emb AB034992 AB034992 <i>Malus domestica</i> MdACS-5A mRNA for 1-aminoc... | 754 | 0.0 | |
| | emb AB034993 AB034993 <i>Malus domestica</i> MdACS-5B mRNA for 1-aminoc... | 755 | 0.0 | |
| | gb U72389 LEU72389 <i>Lycopersicon esculentum</i> 1-aminocyclopropane-1... | 756 | 0.0 | |
| | gb U72390 LEU72390 <i>Lycopersicon esculentum</i> 1-aminocyclopropane-1... | 753 | 0.0 | |
| 45 | emb AB033503 AB033503 <i>Populus euramericana</i> peacs-2 mRNA for 1-am... | 741 | 0.0 | |
| | gb U68216 CPU68216 <i>Carica papaya</i> ACC synthase mRNA, complete cds. | 461 | 0.0 | |
| | emb AF061605 AF061605 <i>Nicotiana glutinosa</i> ACC synthase mRNA, com... | 742 | 0.0 | |
| | emb AB013100 AB013100 <i>Lycopersicon esculentum</i> LE-ACS6 mRNA for 1... | 741 | 0.0 | |
| | emb AJ012551 CSI012551 <i>Citrus sinensis</i> mRNA for ACC synthase. | 449 | 0.0 | |
| 50 | emb AB013346 AB013346 <i>Lycopersicon esculentum</i> mRNA for 1-aminocy... | 739 | 0.0 | |
| | emb AB033502 AB033502 <i>Populus euphratica</i> peacs-1 mRNA for 1-amin... | 620 | 0.0 | |
| | gb U88971 PHU88971 <i>Pelargonium hortorum</i> 1-aminocyclopropane-1-ca... | 455 | 0.0 | |
| | emb Z11613 VRACCSYNM <i>V.radiata</i> mRNA for ACC synthase. | 456 | 0.0 | |
| | emb X98492 NTACCS <i>Nicotiana tabacum</i> mRNA for ACC-synthase (clone... | 455 | 0.0 | |
| 55 | emb X67100 GMCACCS1 <i>G.max</i> mRNA for ACC synthase. | 454 | 0.0 | |
| | emb Z18952 DCAMCRBSY <i>D.caryophyllus</i> mRNA for 1-aminocyclopropane... | 716 | 0.0 | |
| | emb AJ012696 CSI012696 <i>Citrus sinensis</i> mRNA for ACC synthase (AC... | 449 | 0.0 | |
| | emb AJ011095 CSI011095 <i>Citrus sinensis</i> mRNA for ACC synthase (ac... | 452 | 0.0 | |
| | emb Z18953 PHAMCRBSY <i>P.hybrida</i> mRNA for 1-aminocyclopropane 1-ca... | 450 | 0.0 | |
| 60 | emb AB006804 AB006804 <i>Cucumis sativus</i> CS-ACS2 mRNA for ACC synth... | 451 | 0.0 | |
| | emb AF080258 AF080258 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo... | 711 | 0.0 | |

- emb|AF016459|AF016459 *Pisum sativum* 1-aminocyclopropane-1-carbox... 445 0.0
emb|AF109927|AF109927 *Musa acuminata* 1-aminocyclopropane-1-carbo... 707 0.0
dbj|D30805|CUS1A1CS Melon mRNA for 1-aminocyclopropane-1-carboxy... 705 0.0
emb|AB021906|AB021906 *Musa acuminata* MA-ACS1 mRNA for ACC syntha... 703 0.0
5 emb|AB006803|AB006803 *Cucumis sativus* CS-ACS1 mRNA for ACC synth... 703 0.0
emb|AF129508|AF129508 *Musa acuminata* 1-aminocyclopropane-1-carbo... 702 0.0
emb|X65982|NTXACCSYN *N.tabacum* mRNA for 1-aminocyclopropane-1-ca... 438 0.0
emb|AB031026|AB031026 *Prunus mume* PM-ACS1 mRNA for ACC synthase,... 434 0.0
emb|AB015625|AB015625 *Pyrus pyrifolia* pPPACS3 mRNA for 1-aminocy... 418 0.0
10 dbj|D01032|CUCACCW *Cucurbita maxima* mRNA for 1-aminocyclopropane... 695 0.0
dbj|E03724|E03724 cDNA encoding detriment induced type 1-aminocy... 695 0.0
gb|M58323|CUCACCSYN *Cucurbita pepo* 1-aminocyclopropane-1-carboxy... 692 0.0
emb|Y11357|CP1A1CS *C.papaya* mRNA for 1-aminocyclopropane-1-carbo... 430 0.0
emb|X62536|LEACC *L.esculentum* mRNA for ACC synthase. 327 0.0
15 emb|AF057562|AF057562 *Nicotiana glutinosa* 1-aminocyclopropane-1-... 437 0.0
emb|X59145|LEACC2MR *Lycopersicon esculentum* LE-ASCC2 mRNA (ptACC... 326 0.0
gb|U79999|MAU79999 *Musa acuminata* ACC synthase (acs3) mRNA, comp... 687 0.0
emb|Y15739|MAACSYNTH *Musa acuminata* mRNA for 1-aminocyclopropane... 687 0.0
gb|M34289|TOMACS *Tomato* 1-aminocyclopropane-1-carboxylate syntha... 327 0.0
20 gb|M63490|TOMACCS *Tomato* 1-aminocyclopropane-1-carboxylate synth... 682 0.0
emb|X59146|LEACC4MR *Lycopersicon esculentum* LE-ACC4 mRNA (ptACC4... 681 0.0
gb|U17229|PHU17229 *Pelargonium hortorum* clone pGAC-1 1-aminocycl... 438 0.0
gb|U17231|PHU17231 *Pelargonium hortorum* clone pGAC-2 1-aminocycl... 423 0.0
emb|AF038945|AF038945 *Rumex palustris* 1-aminocyclopropane-1-carb... 407 0.0
25 gb|L20634|POTACCSYN *Solanum tuberosum* 1-aminocyclopropane-1-carb... 403 0.0
emb|AJ276295|CSI276295 *Citrus sinensis* partial mRNA for ACC synt... 446 0.0
emb|AF239987|AF239987 *Prunus persica* ACC synthase ACS1 mRNA, par... 662 0.0
emb|AF178076|AF178076 *Carica papaya* 1-aminocyclopropane-1-carbox... 395 0.0
emb|X82265|CAACC1 *C.anuum* mRNA for 1-aminocyclopropane-1-carboxyl... 639 0.0
30 gb|U70842|STU70842 *Solanum tuberosum* 1-aminocyclopropane-1-carbo... 637 0.0
emb|AF144746|AF144746 *Solanum melongena* 1-aminocyclopropane-1-ca... 636 0.0
emb|AJ012577|CPA012577 *Carica papaya* mRNA for 1-aminocyclopropan... 387 e-180
gb|U73815|MDU73815 *Malus domestica* ACC synthase (MdACS-2) mRNA, ... 623 e-178
dbj|D37937|D37937 *Cucumis melo* mRNA for 1-aminocyclopropane-1-ca... 380 e-177
35 emb|Z11562|VRACCSYN *V.radiata* mRNA for 1-aminocyclopropane-1-car... 375 e-176
emb|AF177769|AF177769 *Carica papaya* 1-aminocyclopropane-1-carbox... 369 e-175
emb|AF083814|AF083814 *Antirrhinum majus* ACC synthase 1 (ACS1) mR... 605 e-172
emb|AF178077|AF178077 *Carica papaya* 1-aminocyclopropane-1-carbox... 316 e-172
emb|AF239989|AF239989 *Prunus persica* ACC synthase ACS25 mRNA, pa... 597 e-170
40 gb|U22523|MIU22523 *Mangifera indica* 1-aminocyclopropane-carboxyl... 359 e-169
emb|X66605|DCACCS *D.caryophyllus* mRNA for 1-aminocyclopropane-1-... 396 e-168
gb|L31347|MAUACCSYN *Malus domestica* 1-aminocyclopropane-1-carbox... 378 e-168
emb|AB015624|AB015624 *Pyrus pyrifolia* mRNA for 1-aminocyclopropa... 377 e-168
emb|AF049137|AF049137 *Dianthus caryophyllus* 1-aminocyclopropane-... 338 e-167
45 emb|AF170705|AF170705 *Mangifera indica* 1-aminocyclopropane-1-car... 290 e-167
gb|U03294|MSU03294 *Malus sylvestris* 1-aminocyclopropane-1-carbox... 372 e-166
emb|Z77854|PSPACS1 *Phalaenopsis species* mRNA for 1-aminocyclopro... 513 e-166
emb|AJ277160|CPA277160 *Carica papaya* partial paccs1A gene for 1-... 266 e-165
gb|U73816|MDU73816 *Malus domestica* ACC synthase (MdACS-3) mRNA, ... 505 e-164
50 emb|AB007449|AB007449 *Actinidia deliciosa* mRNA for 1-aminocyclop... 355 e-164
emb|AB007639|AB007639 *Pyrus pyrifolia* mRNA for 1-aminocyclopropa... 502 e-164
dbj|D01033|CUCACCA *Cucurbita maxima* mRNA for 1-aminocyclopropane... 366 e-164
emb|X87112|PCPCACS1G *P.communis* mRNA for 1-aminocyclopropane-1-c... 363 e-163
gb|U17972|LEU17972 *Lycopersicon esculentum* 1-aminocyclopropane-1... 362 e-163
55 emb|AB015495|AB015495 *Passiflora edulis* PE-ACS2 mRNA for ACC syn... 368 e-162
emb|AB006805|AB006805 *Cucumis sativus* CS-ACS3 mRNA for ACC synth... 360 e-160
emb|AB000679|AB000679 *Vigna radiata* mRNA for 1-aminocyclopropane... 365 e-158
gb|U34987|VRU34987 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 325 e-157
gb|M66619|DINCARACC *D.caryophyllus* 1-aminocyclopropane-1-carboxy... 496 e-156
60 gb|U34986|VRU34986 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 362 e-156
gb|U64031|DCU64031 *Dendrobium crumenatum* ACC synthase gene, comp... 259 e-154

emb|AF016458|AF016458 Pisum sativum 1-aminocyclopropane-1-carbox... 355 e-154
 emb|Z27233|STACCAS1 S.tuberosum (STAC1) gene for amino cycloprop... 237 e-152
 emb|Z27234|STACCAS2 S.tuberosum STACS2 gene for 1-Aminocycloprop... 232 e-152
 emb|AF043122|AF043122 Lycopersicon esculentum ACC synthase (LE-A... 236 e-150
 5 gb|U37774|CMU37774 Cucurbita maxima 1-aminocyclopropane-1-carbox... 234 e-150
 gb|L34171|TOMACS3A Lycopersicon esculentum 1-aminocyclopropane-1... 235 e-149
 gb|U18055|LEU18055 Lycopersicon esculentum 1-aminocyclopropane-1... 235 e-149
 emb|AF151961|AF151961 Vigna radiata 1-aminocyclopropane-1-carbox... 232 e-146
 emb|Z12135|VRACCSYN4 V.radiata gene for ACC synthase (pMAC-4). 376 e-145
 10 gb|L07883|DORAMICARB Moth orchid 1-aminocyclopropane-1-carboxyla... 243 e-144
 emb|AF074927|AF074927 Sinapis arvensis 1-aminocyclopropane-1-car... 330 e-142
 emb|AF083815|AF083815 Antirrhinum majus ACC synthase 2 (ACS2) mR... 482 e-141
 emb|AB021907|AB021907 Musa acuminata MA-ACS2 mRNA for ACC syntha... 310 e-140
 emb|AB021908|AB021908 Musa acuminata MA-ACS3 mRNA for ACC syntha... 298 e-138
 15 Query= AC000107.5_at 17278_at /id_source genbank /description
 gb|aad36959.1|ac000107_5 (ac000107) fl7f8.5.[arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000107|/ncgi
 20 http://www.ncgr.org/cgi-bin/ff?ac000107
 (1950 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

25

Searching.....done

		Score	E
	Sequences producing significant alignments:	(bits)	Value
30	gb U79958 PSU79958 Pisum sativum BP-80 vacuolar sorting receptor...	630	0.0
	emb AB006809 AB006809 Cucurbita sp. mRNA for PV72, complete cds.	606	0.0
	emb AW267745 AW267745 EST305873 DSIR Medicago truncatula cDNA cl...	350	e-124
	emb AW931583 AW931583 EST357426 tomato fruit mature green, TAMU ...	165	e-112
35	emb AW309187 AW309187 sg05d06.y1 Gm-cl019 Glycine max cDNA clone...	326	e-108
	emb AW622833 AW622833 EST306903 tomato flower buds 3-8 mm, Corne...	387	e-106
	emb AW774434 AW774434 EST333585 KV3 Medicago truncatula cDNA clo...	294	e-100
	emb AW689392 AW689392 NF018F12ST1F1000 Developing stem Medicago ...	338	e-100
	gb BE054150 BE054150 GA_Ea0034H17f Gossypium arboreum 7-10 dpa ...	195	2e-99
40	emb AI782787 AI782787 EST263666 tomato susceptible, Cornell Lyco...	332	6e-90
	emb AW737948 AW737948 EST339375 tomato flower buds, anthesis, Co...	225	1e-89
	emb AW615949 AW615949 EST325315 tomato flower buds 0-3 mm, Corne...	217	3e-86
	emb AW932529 AW932529 EST358372 tomato fruit mature green, TAMU ...	303	1e-83
	emb AW685785 AW685785 NF030C07NR1F1000 Nodulated root Medicago t...	157	2e-81
45	emb AW747297 AW747297 WS1_67_G06.b1_A002 Water-stressed 1 (WS1) ...	286	4e-76
	emb AI443067 AI443067 sa47a01.y1 Gm-cl004 Glycine max cDNA clone...	265	6e-76
	emb AI728635 AI728635 BNLGHI11276 Six-day Cotton fiber Gossypium...	135	1e-75
	emb AI484571 AI484571 EST242801 tomato ovary, TAMU Lycopersicon ...	278	1e-73
	emb AI727826 AI727826 BNLGHI9195 Six-day Cotton fiber Gossypium ...	135	9e-71
50	emb AW695542 AW695542 NF096C05ST1F1037 Developing stem Medicago ...	153	2e-65
	emb AV406766 AV406766 AV406766 Lotus japonicus young plants (two...	170	5e-65
	emb AW509740 AW509740 ga63h11.y1 Moss EST library PPU Physcomitr...	226	6e-63
	emb AW256542 AW256542 EST304679 KV2 Medicago truncatula cDNA clo...	181	8e-60
	emb AW397829 AW397829 sg68h03.y1 Gm-cl007 Glycine max cDNA clone...	225	1e-57
55	emb AW289687 AW289687 NXNV004E04F Nsf Xylem Normal wood Vertical...	182	7e-55
	emb AW690002 AW690002 NF026G04ST1F1000 Developing stem Medicago ...	143	4e-54
	emb AA660289 AA660289 00158 MtRHE Medicago truncatula cDNA 5', m...	138	2e-53
	emb AW064744 AW064744 ST35C06 Pine TripleEx shoot tip library Pin...	141	6e-53
	emb AV428420 AV428420 AV428420 Lotus japonicus young plants (two...	134	1e-51
60	emb AW623959 AW623959 EST321904 tomato flower buds 3-8 mm, Corne...	74	1e-49
	emb AW568619 AW568619 si60a11.y1 Gm-r1030 Glycine max cDNA clone...	165	2e-47

- emb|AI967865|AI967865 Ljirnp14-100-f3 Ljirnp Lambda HybriZap ... 180 5e-47
emb|AW309191|AW309191 sg05d10.y1 Gm-c1019 Glycine max cDNA clone... 105 2e-46
emb|AW398931|AW398931 EST309431 L. pennellii trichome, Cornell U... 132 2e-45
emb|AW737369|AW737369 EST338892 tomato flower buds, anthesis, Co... 182 6e-45
5 emb|AW096632|AW096632 EST289812 tomato mixed elicitor, BTI Lycop... 81 7e-45
emb|AF209910|AF209910 Prunus dulcis vacuolar sorting receptor pr... 76 8e-44
emb|AW056624|AW056624 ST53G07 Pine TriplEx shoot tip library Pin... 178 1e-43
emb|AW680054|AW680054 WS1_3_A01.g1_A002 Water-stressed 1 (WS1) S... 77 1e-41
emb|AW290400|AW290400 NXNV019G06F Nsf Xylem Normal wood Vertical... 170 4e-41
10 gb|BE125908|BE125908 DG1_59_E01.b1_A002 Dark Grown 1 (DG1) Sorgh... 164 2e-39
emb|AI161766|AI161766 A006P54U Hybrid aspen plasmid library Popu... 76 3e-39
emb|AI162330|AI162330 A016P01U Hybrid aspen plasmid library Popu... 130 2e-37
gb|BE049814|BE049814 NXNV_144_F04_F Nsf Xylem Normal wood Vertic... 156 4e-37
emb|AW508719|AW508719 si35f03.y1 Gm-r1030 Glycine max cDNA clone... 155 8e-37
15 gb|L38113|L38113 BNAF0628E Mustard flower buds Brassica rapa cDN... 153 4e-36
emb|AW616461|AW616461 EST322872 L. hirsutum trichome, Cornell Un... 102 4e-33
emb|AA660955|AA660955 00852 MtRHE Medicago truncatula cDNA 5' si... 72 4e-31
emb|AW774190|AW774190 EST333273 KV3 Medicago truncatula cDNA clo... 134 2e-30
emb|AW201441|AW201441 sf03b09.y1 Gm-c1027 Glycine max cDNA clone... 73 5e-30
20 emb|AW906386|AW906386 EST342508 potato stolon, Cornell Universit... 78 2e-27
emb|AW126100|AW126100 N100297e rootphos(-) Medicago truncatula c... 73 9e-27
emb|AW620693|AW620693 sj08d10.y1 Gm-c1032 Glycine max cDNA clone... 77 1e-26
emb|AW317388|AW317388 sg48g10.y1 Gm-c1025 Glycine max cDNA clone... 72 2e-26
emb|AW706755|AW706755 sk02f10.y1 Gm-c1023 Glycine max cDNA clone... 117 3e-25
25 emb|AW125944|AW125944 N100139e rootphos(-) Medicago truncatula c... 71 1e-23
emb|AW932524|AW932524 EST358367 tomato fruit mature green, TAMU ... 69 1e-22
emb|AW348825|AW348825 GM210003B11E6R Gm-r1021 Glycine max cDNA 3... 66 2e-22
emb|AW093844|AW093844 EST287024 tomato mixed elicitor, BTI Lycop... 98 3e-19
emb|AW691052|AW691052 NF037B05ST1F1000 Developing stem Medicago ... 79 6e-17
30 emb|AW119909|AW119909 sd54d08.y1 Gm-c1016 Glycine max cDNA clone... 88 2e-16
emb|AW685952|AW685952 NF036G09NR1F1000 Nodulated root Medicago t... 50 1e-15
emb|AW774852|AW774852 EST334003 KV3 Medicago truncatula cDNA clo... 83 9e-15
emb|AI794754|AI794754 sb68f11.y1 Gm-c1019 Glycine max cDNA clone... 82 1e-14
gb|BE060808|BE060808 HVSMEg0013H06f Hordeum vulgare pre-anthesis... 78 6e-14
35 emb|AW760128|AW760128 sl58d09.y1 Gm-c1027 Glycine max cDNA clone... 66 8e-14
emb|AW037563|AW037563 EST278890 tomato mixed elicitor, BTI Lycop... 77 6e-13
emb|AW256398|AW256398 EST304465 KV2 Medicago truncatula cDNA clo... 72 7e-13
emb|AW686287|AW686287 NF040A08NR1F1000 Nodulated root Medicago t... 67 6e-10
emb|AW443352|AW443352 EST308282 tomato mixed elicitor, BTI Lycop... 65 2e-09
40 emb|AW747372|AW747372 WS1_67_G06.g1_A002 Water-stressed 1 (WS1) ... 64 4e-09
emb|AW127457|AW127457 M110648 DSIL Medicago truncatula cDNA clon... 63 6e-09
emb|AI939286|AI939286 sc69h02.y1 Gm-c1016 Glycine max cDNA clone... 48 2e-04
emb|AQ652964|AQ652964 Sheared DNA-1M1.TR Sheared DNA Trypanosoma... 39 0.16
gb|C95899|C95899 C95899 Marchantia polymorpha immature sex organ... 38 0.31
45 gb|B67199|B67199 CpG0015B CpIOWAgDNA1 Cryptosporidium parvum gen... 38 0.31
emb|AW692657|AW692657 NF057H03ST1F1000 Developing stem Medicago ... 37 0.42
emb|AF083502|AF083502 Plasmodium vivax ookinete surface protein ... 37 0.42
emb|AW626172|AW626172 EST320079 tomato radicle, 5 d post-imbibit... 37 0.42
emb|AC008054|AC008054 Leishmania major chromosome 35 clone L8453... 36 0.55
50 emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 35 1.5
emb|AB033343|AB033343 Plasmodium vivax gene for ookinete surface... 35 1.5
emb|AB033342|AB033342 Plasmodium vivax gene for ookinete surface... 35 1.5
emb|AB033341|AB033341 Plasmodium vivax gene for ookinete surface... 35 1.5
emb|AB033340|AB033340 Plasmodium vivax gene for ookinete surface... 35 1.5
55 emb|AB033339|AB033339 Plasmodium vivax gene for ookinete surface... 35 1.5
emb|AV410215|AV410215 AV410215 Lotus japonicus young plants (two... 35 2.1
emb|AC007865|AC007865 Trypanosoma brucei chromosome II clone RPC... 35 2.8
emb|AQ649743|AQ649743 Sheared DNA-17O2.TR Sheared DNA Trypanoso... 35 2.8
emb|AW982863|AW982863 HVSMEg0004G15f Hordeum vulgare pre-anthesi... 35 2.8
60 emb|AZ216543|AZ216543 Sheared DNA-116G5.TR Sheared DNA Trypanoso... 35 2.8
emb|AC004157|AC004157 Plasmodium falciparum chromosome 12 clone ... 35 2.8

gb|U18916|SCE9781 *Saccharomyces cerevisiae* chromosome V cosmids ... 35 2.8
 dbj|D13340|CHL58S25S *Chlorella ellipsoidea* genes for 5.8S rRNA a... 35 2.8
 emb|AW648383|AW648383 EST326837 tomato germinating seedlings, TA... 33 3.3
 emb|AI778616|AI778616 EST259495 tomato susceptible, Cornell Lyco... 33 3.3
 5 emb|AA749476|AA749476 L30-23M13T3 Ice plant Lambda Uni-Zap XR ex... 31 3.3
 emb|AA938798|AA938798 L0-249M13R Ice plant Lambda Uni-Zap XR exp... 31 3.3
 emb|AI822187|AI822187 L0-664T3 Ice plant Lambda Uni-Zap XR expre... 31 3.3
 emb|AI822671|AI822671 L0-1192T3 Ice plant Lambda Uni-Zap XR expr... 31 3.3

 10 Query= AC004684.168_s_at 17744_s_at /id_source genbank /description
 gb|aac23646.1| (ac004684) putative alcohol dehydrogenase [*arabidopsis*
thaliana] /blast_score 1.00e-170 /ec_number /family /chip nova
 /gb_link /ncgi
 (885 letters)

 15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

 Searching.....done

 20

 Score E
 Sequences producing significant alignments: (bits) Value

 emb|X97606|MSRNAAAA *M.sativa* mRNA translated from abscisic activ... 306 e-115
 25 emb|AW666569|AW666569 GA_Ea0005J12 *Gossypium arboreum* 7-10 dpa ... 310 6e-91
 emb|AW692860|AW692860 NF056E06ST1F1000 Developing stem *Medicago* ... 309 2e-89
 gb|BE123903|BE123903 EST394028 DSIL *Medicago truncatula* cDNA clo... 304 7e-88
 emb|AW774316|AW774316 EST333467 KV3 *Medicago truncatula* cDNA clo... 308 5e-83
 emb|AW728361|AW728361 GA_Ea0016H09 *Gossypium arboreum* 7-10 dpa ... 306 2e-82
 30 emb|AW267789|AW267789 EST305917 DSIR *Medicago truncatula* cDNA cl... 169 4e-81
 emb|AW329160|AW329160 N200369e rootphos(-) *Medicago truncatula* c... 224 2e-80
 emb|AW696127|AW696127 NF102F09ST1F1078 Developing stem *Medicago* ... 298 4e-80
 emb|AI794650|AI794650 sb67a05.y1 Gm-c1019 *Glycine max* cDNA clone... 286 2e-76
 gb|BE037103|BE037103 MP15A03 MP *Mesembryanthemum crystallinum* cD... 139 8e-76
 35 emb|AW399617|AW399617 EST310117 L. pennellii trichome, Cornell U... 281 5e-75
 emb|AW564270|AW564270 LG1_289_E10.b1_A002 Light Grown 1 (LG1) So... 162 6e-72
 emb|AW756208|AW756208 sl17d10.y1 Gm-c1036 *Glycine max* cDNA clone... 264 5e-70
 emb|AW760494|AW760494 sl51a09.y1 Gm-c1027 *Glycine max* cDNA clone... 178 1e-69
 emb|AW831516|AW831516 sm27a02.y1 Gm-c1028 *Glycine max* cDNA clone... 261 4e-69
 40 emb|AJ223291|SRAJ3291 *Sesbania rostrata* mRNA for putative chalco... 115 2e-64
 emb|AW830327|AW830327 sm25f04.y1 Gm-c1028 *Glycine max* cDNA clone... 242 2e-63
 emb|AW688330|AW688330 NF006B06ST1F1000 Developing stem *Medicago* ... 169 6e-63
 gb|BE020597|BE020597 sm51b07.y1 Gm-c1028 *Glycine max* cDNA clone ... 239 2e-62
 emb|X82368|MSCHR2A *M.sativa* mRNA for chalcone reductase (1134 bp). 117 6e-61
 45 gb|U13925|MSU13925 *Medicago sativa* Apollo clone CHR7 chalcone re... 117 6e-61
 emb|X57526|HVALREDR *H.vulgare* gene for aldose reductase-related ... 92 1e-60
 emb|X82367|MSCHR1B *M.sativa* mRNA for chalcone reductase (1115 bp). 116 1e-60
 emb|X82366|MSCHR1A *M.sativa* mRNA for chalcone reductase (1202 bp). 116 2e-60
 emb|AF133841|AF133841 *Xerophyta viscosa* aldose reductase ALDRXV4... 97 2e-60
 50 gb|U13924|MSU13924 *Medicago sativa* Apollo clone CHR12 chalcone r... 114 8e-60
 emb|X55730|GMREDUC Soybean mRNA for reductase involved in deoxyc... 111 1e-59
 emb|AF108438|AF108438 *Papaver somniferum* putative NADPH-dependen... 154 1e-59
 gb|L12042|BMUSUSCUL *Bromus inermis* aldose reductase-related prot... 86 2e-59
 emb|AW694657|AW694657 NF078G04ST1F1035 Developing stem *Medicago* ... 164 3e-59
 55 emb|X59465|PSXYL1RE *P.stipitis* XYL1-gene for NAD(P)H-dependent X... 125 2e-58
 emb|AF020040|AF020040 *Pichia guilliermondii* xylose reductase mRN... 121 2e-58
 emb|AF039182|AF039182 *Fragaria x ananassa* probable aldo-keto red... 105 5e-58
 emb|AB002105|AB002105 *Candida tropicalis* DNA for D-xylose reduct... 127 6e-58
 emb|AW991001|AW991001 SsS0116 *Suaeda salsa* ZAP cDNA library Suae... 184 1e-57
 60 emb|AB002106|AB002106 *Candida tropicalis* DNA for D-xylose reduct... 124 2e-57
 emb|AW830449|AW830449 sm27b05.y1 Gm-c1028 *Glycine max* cDNA clone... 223 2e-57

- dbj|D83718|GYCPKR *Glycyrrhiza echinata* mRNA for polyketide reduc... 111 6e-57
 gb|U40706|PTU40706 *Pachysolen tannophilus* aldose reductase gene,... 123 8e-57
 dbj|D86559|D86559 *Glycyrrhiza glabra* mRNA for polyketide reducta... 110 1e-56
 dbj|D86558|D86558 *Glycyrrhiza glabra* mRNA for polyketide reducta... 110 1e-56
 5 emb|AF074484|AF074484 *Candida tenuis* xylose reductase (xylr) gen... 127 2e-54
 gb|L36993|YSKXYL *Kluyveromyces lactis* xylose reductase (XYL1) ge... 120 5e-53
 emb|Z73100|SPAC26F1 *S.pombe* chromosome I cosmid c26F1. 92 1e-51
 emb|AW730093|AW730093 GA_Ea0027M16 *Gossypium arboreum* 7-10 dpa ... 128 1e-51
 emb|AW186336|AW186336 sc66e01.y1 Gm-c1019 *Glycine max* cDNA clone... 127 2e-51
 10 gb|U83687|AGU83687 *Apium graveolens* NADPH-dependent mannose 6-ph... 80 2e-51
 emb|AF108432|AF108432 *Papaver somniferum* NADPH-dependent codeino... 141 4e-51
 gb|U00059|YSCH8263 *Saccharomyces cerevisiae* chromosome VIII cosm... 116 2e-50
 dbj|D11080|MAUS6PDH Apple S6PDH mRNA for NADP-dependent D-sorbit... 78 2e-49
 emb|AF219625|AF219625 *Aspergillus niger* D-xylose reductase (xylA... 86 6e-49
 15 emb|AF108435|AF108435 *Papaver somniferum* NADPH-dependent codeino... 85 1e-48
 emb|AF108434|AF108434 *Papaver somniferum* NADPH-dependent codeino... 83 1e-48
 emb|AW773597|AW773597 EST332583 KV3 *Medicago truncatula* cDNA clo... 161 2e-48
 emb|AF108433|AF108433 *Papaver somniferum* NADPH-dependent codeino... 85 2e-47
 emb|AW982655|AW982655 HVSMEg0003N17f *Hordeum vulgare* pre-anthesi... 156 2e-47
 20 emb|AL021815|SPBC8E4 *S.pombe* chromosome I cosmid c8E4. 84 3e-47
 gb|J04483|LEIP10011E *Leishmania major* reductase (P100/11E) mRNA,... 83 5e-47
 emb|AW266162|AW266162 L30-2855T3 Ice plant Lambda Uni-Zap XR exp... 185 7e-47
 emb|AW351113|AW351113 GM210010B20E10R Gm-r1021 *Glycine max* cDNA ... 122 2e-46
 emb|AW267703|AW267703 EST305831 DSIR *Medicago truncatula* cDNA cl... 114 3e-46
 25 emb|AL110661|CNS018Q6 *Botrytis cinerea* strain T4 cDNA library un... 108 2e-45
 emb|AB014493|AB014493 *Gibberella zeae* gene for reductase, partia... 91 5e-45
 emb|X94335|SC130KBXV *S.cerevisiae* 130kb DNA fragment from chromo... 57 2e-44
 emb|X90518|SCXVORFS *S.cerevisiae* DNA of 51 Kb from chromosome XV... 57 2e-44
 emb|Z75028|SCYOR120W *S.cerevisiae* chromosome XV reading frame OR... 57 2e-44
 30 emb|X13228|SCGCY Yeast GCY gene (homologous to vertebrate eye le... 57 2e-44
 emb|X96740|SCGCY1 *S.cerevisiae* GCY1 gene. 57 2e-44
 emb|AW775175|AW775175 EST334326 KV3 *Medicago truncatula* cDNA clo... 101 5e-44
 emb|AW776733|AW776733 EST335798 DSIL *Medicago truncatula* cDNA cl... 177 9e-44
 gb|BE036780|BE036780 MP05F01 MP *Mesembryanthemum crystallinum* cD... 84 9e-43
 35 gb|BE036644|BE036644 MP03B08 MP *Mesembryanthemum crystallinum* cD... 80 9e-43
 emb|AW706251|AW706251 sj54a08.y1 Gm-c1033 *Glycine max* cDNA clone... 106 2e-42
 emb|AW564750|AW564750 LG1_301_D05.b1_A002 Light Grown 1 (LG1) So... 155 3e-42
 gb|BE123887|BE123887 EST394012 DSIL *Medicago truncatula* cDNA clo... 114 3e-42
 emb|AW686854|AW686854 NF003B10RT1F1000 Developing root *Medicago* ... 114 4e-42
 40 gb|U21747|AFU21747 *Avena fatua* aldose reductase-related protein ... 91 4e-41
 emb|AW981220|AW981220 EST392310 DSIL *Medicago truncatula* cDNA cl... 83 5e-41
 emb|AW685322|AW685322 NF027B04NR1F1000 Nodulated root *Medicago t...* 93 6e-41
 emb|AW091709|AW091709 EST284805 tomato mixed elicitor, BTI Lycop... 166 2e-40
 emb|AW041447|AW041447 EST284311 tomato mixed elicitor, BTI Lycop... 166 2e-40
 45 emb|AW568008|AW568008 si56c03.y1 Gm-r1030 *Glycine max* cDNA clone... 166 3e-40
 emb|AW567986|AW567986 si56a03.y1 Gm-r1030 *Glycine max* cDNA clone... 166 3e-40
 emb|AW310318|AW310318 sf34d05.x1 Gm-c1028 *Glycine max* cDNA clone... 124 1e-38
 emb|AL115070|CNS01C4M *Botrytis cinerea* strain T4 cDNA library un... 90 2e-38
 emb|AW704367|AW704367 sk30b12.y1 Gm-c1028 *Glycine max* cDNA clone... 109 2e-38
 50 emb|AW306925|AW306925 sf50e02.y1 Gm-c1009 *Glycine max* cDNA clone... 93 2e-38
 emb|AW564756|AW564756 LG1_301_B12.b1_A002 Light Grown 1 (LG1) So... 147 6e-38
 emb|AW560687|AW560687 EST315735 DSIR *Medicago truncatula* cDNA cl... 93 3e-37
 emb|AW775758|AW775758 EST334823 DSIL *Medicago truncatula* cDNA cl... 89 1e-36
 emb|AA825062|AA825062 ETN380 *Trypanosoma brucei rhodesiense* ZAP ... 85 2e-36
 55 emb|AW728632|AW728632 GA_Ea0017G17 *Gossypium arboreum* 7-10 dpa ... 80 3e-36
 emb|AI441520|AI441520 sa87d08.y1 Gm-c1004 *Glycine max* cDNA clone... 126 3e-36
 emb|AW761087|AW761087 sl63a04.y1 Gm-c1027 *Glycine max* cDNA clone... 74 5e-36
 emb|AI939278|AI939278 sc69f11.y1 Gm-c1016 *Glycine max* cDNA clone... 150 1e-35
 emb|AW831528|AW831528 sm27e03.y1 Gm-c1028 *Glycine max* cDNA clone... 125 2e-35
 60 emb|AW756704|AW756704 sl26b12.y1 Gm-c1027 *Glycine max* cDNA clone... 79 2e-35
 gb|U26463|SSU26463 *Sporidiobolus salmonicolor* NADPH-dependent al... 86 3e-35

emb|AW234076|AW234076 sf34a01.y1 Gm-c1028 Glycine max cDNA clone... 111 7e-35

Query= AC004392.2_at 17775_at /id_source genbank /description

gb|aac28500.1| (ac004392) similar to

5 glucose-6-phosphate/phosphate-translocator (gpt) gb|af020814 from
pisum sativum. [arabidopsis thaliana] /blast_score 0 /ec_number

/family /chip nova /gb_link

http://www3.ncbi.nlm.nih.gov/htbin-

post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004392|/ncgi

10 http://www.ncgr.org/cgi-bin/ff?ac004392

(1233 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

20

emb|AF020814|AF020814 Pisum sativum glucose-6-phosphate/phosphat... 626 e-179

emb|AF020816|AF020816 Solanum tuberosum glucose-6-phosphate/phos... 359 e-167

emb|AW761153|AW761153 sl63h08.y1 Gm-c1027 Glycine max cDNA clone... 403 e-111

emb|AI973973|AI973973 sd14e11.y1 Gm-c1020 Glycine max cDNA clone... 387 e-106

25 emb|AW832261|AW832261 sm21g08.y1 Gm-c1027 Glycine max cDNA clone... 372 e-102

emb|AW507609|AW507609 si42a06.y1 Gm-r1030 Glycine max cDNA clone... 365 e-100

emb|AI974103|AI974103 sd16e09.y1 Gm-c1020 Glycine max cDNA clone... 202 9e-91

emb|AV421952|AV421952 AV421952 Lotus japonicus young plants (two... 304 1e-81

emb|AW509448|AW509448 si37c07.y1 Gm-r1030 Glycine max cDNA clone... 297 4e-81

30 emb|AW985263|AW985263 NXNV_135_B02_F Nsf Xylem Normal wood Verti... 209 5e-73

emb|AI352923|AI352923 MB73-9C PZ204.BNlib Brassica napus cDNA cl... 226 1e-70

gb|U13630|BOU13630 Brassica oleracea var. botrytis chloroplast p... 189 2e-69

emb|X75088|NTRNPHTR Nicotiana tabacum mRNA for phosphate translo... 185 8e-69

emb|X13754|SOPHTRAN Spinach mRNA for chloroplast phosphate trans... 186 8e-69

35 emb|X67045|STIPTMR S.tuberosum mRNA TPT for triose phosphate tra... 183 1e-67

emb|AW234628|AW234628 sf17d12.y1 Gm-c1028 Glycine max cDNA clone... 254 1e-66

gb|BE060177|BE060177 HVSMEg0011C12f Hordeum vulgare pre-anthesis... 249 3e-65

emb|AV413897|AV413897 AV413897 Lotus japonicus young plants (two... 229 3e-59

emb|AI894606|AI894606 EST264049 tomato callus, TAMU Lycopersicon... 228 6e-59

40 emb|AW926251|AW926251 HVSMEg0006L14 Hordeum vulgare pre-anthesis... 226 2e-58

emb|AW472436|AW472436 si25b11.y1 Gm-c1029 Glycine max cDNA clone... 221 2e-57

emb|AF173679|AF173679 Beta vulgaris phosphate translocator (pt) m... 135 2e-53

emb|AW560889|AW560889 EST315937 DSIR Medicago truncatula cDNA cl... 205 2e-53

emb|AI939281|AI939281 sc69g06.y1 Gm-c1016 Glycine max cDNA clone... 204 1e-51

45 emb|AW688995|AW688995 NF014B11ST1F1000 Developing stem Medicago ... 150 2e-50

emb|AW034833|AW034833 EST278941 tomato callus, TAMU Lycopersicon... 196 3e-49

emb|X54639|PSCIRP36 P. sativum mRNA for chloroplast import recep... 193 2e-48

emb|X68077|PSPTCPA P. sativum mRNA for phosphate translocator... 193 2e-48

emb|AW760040|AW760040 sl57c08.y1 Gm-c1027 Glycine max cDNA clone... 193 3e-48

50 emb|AW691966|AW691966 NF051A06ST1F1000 Developing stem Medicago ... 166 3e-47

emb|AI772801|AI772801 EST253901 tomato resistant, Cornell Lycope... 188 8e-47

emb|AW217547|AW217547 EST296261 tomato flower buds 3-8 mm, Corne... 188 8e-47

emb|X92656|LETPT L.esculentum mRNA for triose phosphate transloc... 188 8e-47

emb|Z26633|CHFCPT F.pringlei fpcpt mRNA for triose phosphate/ph... 188 1e-46

55 emb|AW758970|AW758970 sl33a11.y1 Gm-c1027 Glycine max cDNA clone... 187 2e-46

emb|Z26632|CHFTCPT F.trinervia ftcpt mRNA for triose phosphate/p... 184 1e-45

emb|AW031949|AW031949 EST275403 tomato callus, TAMU Lycopersicon... 184 1e-45

emb|AW564653|AW564653 LG1_297_C06.b1_A002 Light Grown 1 (LG1) So... 182 3e-45

emb|AI773418|AI773418 EST254518 tomato resistant, Cornell Lycope... 182 3e-45

60 emb|AI812950|AI812950 22G7 Pine Lambda Zap Xylem library Pinus t... 176 3e-43

emb|AI774019|AI774019 EST255119 tomato resistant, Cornell Lycope... 175 6e-43

	emb AW689300 AW689300 NF017F08ST1F1000 Developing stem Medicago ...	172	7e-43
	emb AW933284 AW933284 EST359127 tomato fruit mature green, TAMU ...	175	8e-43
	emb AW399333 AW399333 EST309833 L. pennellii trichome, Cornell U...	175	8e-43
	emb AW626582 AW626582 NXNV067A01 Nsf Xylem Normal wood Vertical ...	107	2e-42
5	emb AW671381 AW671381 LG1_335_G10.b1_A002 Light Grown 1 (LG1) So...	173	3e-42
	emb AW671933 AW671933 LG1_353_E03.b1_A002 Light Grown 1 (LG1) So...	173	3e-42
	emb AW559735 AW559735 EST314727 DSIR Medicago truncatula cDNA cl...	167	3e-42
	gb BE034606 BE034606 MK02F02 MK Mesembryanthemum crystallinum cD...	170	2e-41
	emb AW690541 AW690541 NF035G02ST1F1000 Developing stem Medicago ...	166	5e-41
10	gb U13632 BOU13632 Brassica oleracea var. botrytis non-green pla...	166	2e-40
	emb A93887 A93887 Sequence 1 from Patent WO9725346.	166	2e-40
	emb AW782182 AW782182 sm02e11.y1 Gm-c1027 Glycine max cDNA clone...	166	3e-40
	gb U66402 NTU66402 Nicotiana tabacum plastid phosphate/phosphoen...	165	6e-40
	emb AW666055 AW666055 sk31e07.y1 Gm-c1028 Glycine max cDNA clone...	160	2e-39
15	emb AW776623 AW776623 EST335688 DSIL Medicago truncatula cDNA cl...	162	4e-39
	gb U66401 NTU66401 Nicotiana tabacum plastid phosphate/phosphoen...	162	4e-39
	emb AF173656 AF173656 Beta vulgaris clone GPTII09UNI glucose-6-...	161	1e-38
	emb AW736423 AW736423 EST332437 KV3 Medicago truncatula cDNA clo...	153	6e-38
	emb AW038916 AW038916 EST280872 tomato mixed elicitor, BTI Lycop...	158	1e-37
20	emb AW930290 AW930290 EST340747 tomato fruit mature green, TAMU ...	157	2e-37
	emb AV415709 AV415709 AV415709 Lotus japonicus young plants (two...	153	2e-36
	emb AW201212 AW201212 se99c01.y1 Gm-c1027 Glycine max cDNA clone...	93	3e-36
	emb AI736196 AI736196 sb24f10.y1 Gm-c1008 Glycine max cDNA clone...	151	8e-36
	emb AV426398 AV426398 AV426398 Lotus japonicus young plants (two...	149	6e-35
25	emb AV422882 AV422882 AV422882 Lotus japonicus young plants (two...	147	2e-34
	emb AF173660 AF173660 Beta vulgaris clone GPTII09UNI glucose-6-p...	146	4e-34
	emb AI822397 AI822397 L0-856T3 Ice plant Lambda Uni-Zap XR expre...	125	7e-34
	emb AW040008 AW040008 EST282499 tomato mixed elicitor, BTI Lycop...	144	1e-33
	emb AW039997 AW039997 EST282488 tomato mixed elicitor, BTI Lycop...	144	1e-33
30	gb BE059998 BE059998 sn39f10.y1 Gm-c1027 Glycine max cDNA clone ...	143	3e-33
	emb AW671168 AW671168 LG1_330_E06.b1_A002 Light Grown 1 (LG1) So...	142	5e-33
	emb AW667825 AW667825 GA_Ea0010N10 Gossypium arboreum 7-10 dpa ...	141	9e-33
	emb AW760961 AW760961 sl61c01.y1 Gm-c1027 Glycine max cDNA clone...	138	8e-32
	emb AW832362 AW832362 sm08e01.y1 Gm-c1027 Glycine max cDNA clone...	138	8e-32
35	emb AW781979 AW781979 sl99a06.y1 Gm-c1027 Glycine max cDNA clone...	138	8e-32
	emb AV426209 AV426209 AV426209 Lotus japonicus young plants (two...	135	6e-31
	emb AW287694 AW287694 LG1_271_C05.b1_A002 Light Grown 1 (LG1) So...	135	8e-31
	emb AW041671 AW041671 EST284535 tomato mixed elicitor, BTI Lycop...	135	8e-31
	emb AW564618 AW564618 LG1_297_G09.b1_A002 Light Grown 1 (LG1) So...	134	1e-30
40	emb AW924990 AW924990 WS1_74_A05.b1_A002 Water-stressed 1 (WS1) ...	134	1e-30
	emb AW888070 AW888070 NXNV_126_H09_F Nsf Xylem Normal wood Verti...	134	1e-30
	emb AW694653 AW694653 NF078G03ST1F1023 Developing stem Medicago ...	108	2e-30
	emb AV425340 AV425340 AV425340 Lotus japonicus young plants (two...	132	5e-30
	emb AW030490 AW030490 EST273745 tomato callus, TAMU Lycopersicon...	132	7e-30
45	emb AW738715 AW738715 EST340142 tomato flower buds, anthesis, Co...	132	7e-30
	emb AW040512 AW040512 EST283472 tomato mixed elicitor, BTI Lycop...	131	1e-29
	emb AW780617 AW780617 sl73c03.y1 Gm-c1027 Glycine max cDNA clone...	131	1e-29
	emb AW287232 AW287232 LG1_268_C02.b1_A002 Light Grown 1 (LG1) So...	130	2e-29
	emb AV410940 AV410940 AV410940 Lotus japonicus young plants (two...	130	2e-29
50	emb AW286886 AW286886 LG1_222_F11.b1_A002 Light Grown 1 (LG1) So...	129	3e-29
	emb AW399232 AW399232 EST309732 L. pennellii trichome, Cornell U...	129	5e-29
	emb AW287673 AW287673 LG1_271_A05.b1_A002 Light Grown 1 (LG1) So...	129	5e-29
	emb AV412063 AV412063 AV412063 Lotus japonicus young plants (two...	128	7e-29
	emb AV421682 AV421682 AV421682 Lotus japonicus young plants (two...	128	7e-29
55	emb AW759175 AW759175 sl38a01.y1 Gm-c1027 Glycine max cDNA clone...	128	7e-29
	emb AW672543 AW672543 LG1_360_B12.b1_A002 Light Grown 1 (LG1) So...	128	7e-29
	emb AW596590 AW596590 sj14c04.y1 Gm-c1032 Glycine max cDNA clone...	128	9e-29
	emb AW694511 AW694511 NF077A11ST1F1084 Developing stem Medicago ...	128	9e-29
60	emb AV415908 AV415908 AV415908 Lotus japonicus young plants (two...	127	2e-28

Query= AC002333.223_s_at 17840_s_at /id_source genbank /description

gb|aab64049.1| (ac002333).putative endochitinase [arabidopsis
thaliana] /blast_score 1.00e-161 /ec_number /family /chip nova
/gb_link /ncgi
(834 letters)

5

Database: plantfungal
661,018 sequences; 426,114,510 total letters

10

Searching.....done

Score E
Sequences producing significant alignments: (bits) Value

15	gb U21848 BNU21848 Brassica napus chitinase class IV (LSC222) mR...	225	e-134
	emb X61488 BNCHITIN B.napus mRNA for chitinase.	156	7e-88
	gb U97521 VVU97521 Vitis vinifera class IV endochitinase (VvChi4...	173	3e-77
	gb U97522 VVU97522 Vitis vinifera class IV endochitinase (VvChi4...	174	2e-76
	emb X57187 PVCHITIN P.vulgaris mRNA for chitinase.	149	2e-74
	emb AF112966 AF112966 Triticum aestivum chitinase IV precursor (...)	157	5e-70
20	dbj D45181 D45181 Chenopodium amaranticolor mRNA for chitinase, ...	100	5e-67
	gb U52845 DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP...	114	7e-67
	gb U52846 DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP...	111	9e-66
	gb BE034166 BE034166 MG05H02 MG Mesembryanthemum crystallinum cD...	129	1e-65
	gb U52847 DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP...	110	8e-65
25	gb U52848 DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3...	111	2e-64
	gb BE034975 BE034975 ML07H10 ML Mesembryanthemum crystallinum cD...	125	2e-64
	gb BE034428 BE034428 MH04G02 MH Mesembryanthemum crystallinum cD...	123	2e-63
	gb BE034976 BE034976 ML07H11 ML Mesembryanthemum crystallinum cD...	120	6e-63
	dbj D45183 D45183 Chenopodium amaranticolor mRNA for chitinase, ...	96	1e-62
30	dbj D45184 D45184 Chenopodium amaranticolor mRNA for chitinase, ...	100	3e-62
	dbj D45182 D45182 Chenopodium amaranticolor mRNA for chitinase, ...	100	4e-60
	emb X75945 BVCH4RNA B.vulgaris Ch4 mRNA for chitinase.	92	6e-60
	emb A23392 A23392 B.vulgaris mRNA for chitinase 4 (B15).	92	6e-60
	emb X88803 VURNACHI4 V.unguiculata mRNA for chitinase clase 4 (p...	118	3e-59
35	emb AI897733 AI897733 EST267176 tomato ovary, TAMU Lycopersicon ...	110	1e-58
	gb BE034406 BE034406 MH04D10 MH Mesembryanthemum crystallinum cD...	105	2e-58
	gb L25826 BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds.	158	3e-58
	gb BE034497 BE034497 MH05H03 MH Mesembryanthemum crystallinum cD...	89	8e-58
	gb L42467 PLACHI Picea glauca chitinase (chi) mRNA, complete cds.	93	2e-57
40	emb AF090336 AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA...	166	2e-57
	emb AI897843 AI897843 EST267286 tomato ovary, TAMU Lycopersicon ...	103	1e-56
	emb AF112963 AF112963 Triticum aestivum chitinase II precursor (...)	149	9e-56
	gb BE035287 BE035287 MM04H04 MM Mesembryanthemum crystallinum cD...	162	4e-54
	emb AW680953 AW680953 WS1_9_A06.b1_A002 Water-stressed I (WS1) S...	178	3e-52
45	gb BE033502 BE033502 ME03F10-ME Mesembryanthemum crystallinum cD...	87	4e-50
	gb M94105 ALCCHITIN Allium sativum chitinase mRNA, 3' end.	100	6e-49
	emb AI898279 AI898279 EST267722 tomato ovary, TAMU Lycopersicon ...	83	1e-48
	gb U83592 MSU83592 Medicago sativa class I chitinase mRNA, compl...	109	1e-48
	gb U83591 MSU83591 Medicago sativa class I chitinase mRNA, compl...	109	1e-48
50	emb AW030814 AW030814 EST274069 tomato callus, TAMU Lycopersicon...	83	3e-48
	emb AW035013 AW035013 EST279284 tomato callus, TAMU Lycopersicon...	83	3e-48
	emb AW029733 AW029733 EST272988 tomato callus, TAMU Lycopersicon...	83	3e-48
	gb BE034481 BE034481 MH05F02 MH Mesembryanthemum crystallinum cD...	162	5e-48
	emb AW924422 AW924422 WS1_69_C06.b1_A002 Water-stressed I (WS1) ...	140	7e-48
55	emb AI485982 AI485982 EST244303 tomato ovary, TAMU Lycopersicon ...	83	1e-47
	emb AF061805 AF061805 Elaeagnus umbellata acidic chitinase mRNA,...	99	1e-47
	emb AW648023 AW648023 EST326477 tomato germinating seedlings, TA...	83	3e-47
	gb L37876 PEACHI2I Pisum sativum chitinase class I (chi2) gene, ...	109	3e-47
	gb BE034447 BE034447 MH05A08 MH Mesembryanthemum crystallinum cD...	87	5e-47
60	emb X15494 STCHITIN Potato endochitinase gene (EC 3.2.1.14).	95	6e-47
	emb X07130 STCHIT Solanum tuberosum mRNA for endochitinase (EC 3...	95	6e-47

- gb|M13968|PHVCHM *P.vulgaris* chitinase mRNA, complete cds. 106 1e-46
 emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 161 2e-46
 gb|S43926|S43926 CH5B=chitinase [*Phaseolus vulgaris*=beans, cv Sa... 106 5e-46
 emb|X88800|VURNACHI1 *V.unguiculata* mRNA for chitinase clase 1 (p... 105 1e-45
 5 emb|AJ012821|CAR012821 *Cicer arietinum* mRNA for class I chitinase. 108 6e-45
 emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem *Medicago* ... 78 8e-45
 emb|Y10373|MTCHITIN1 *M.truncatula* mRNA for chitinase. 109 8e-45
 emb|AW033122|AW033122 EST276681 tomato callus, TAMU *Lycopersicon*... 83 2e-44
 gb|M94106|ALCCHINTIA *Allium sativum* chitinase mRNA, 3' end. 102 3e-44
 10 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 170 3e-44
 emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 178 4e-44
 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 178 4e-44
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 95 5e-44
 gb|M15173|TOBECH Tobacco (*N.tabacum*) endochitinase mRNA, partial... 95 5e-44
 15 emb|AF061806|AF061806 *Elaeagnus umbellata* basic chitinase mRNA, ... 105 1e-43
 emb|Z54234|VVCHIT1MR *V.vinifera* mRNA for chitinase. 98 1e-43
 gb|S44869|S44869 basic chitinase [*Nicotiana tabacum*=tobacco, cv ... 95 2e-43
 emb|X16939|NTECHITR *Nicotiana tabacum* mRNA for endochitinase (EC... 95 2e-43
 emb|X76041|TACHIG *T.aestivum* (Chinese spring) chi gene for endoc... 93 4e-43
 20 emb|AB015655|AB015655 *Cucurbita* sp. mRNA for chitinase, complete... 97 6e-43
 emb|Z46948|SNCHJET15 *S.nigra* mRNA for chitinase, pathogenesis-re... 104 2e-42
 gb|U02605|STU02605 *Solanum tuberosum* chitinase (chtB1) mRNA, par... 95 3e-42
 gb|U02606|STU02606 *Solanum tuberosum* chitinase (chtB2) mRNA, par... 95 4e-42
 emb|Z46950|SNCHJET19 *S.nigra* mRNA chitinase class II, pathogenes... 104 6e-42
 25 gb|U78888|GHU78888 *Gossypium hirsutum* class I endochitinase mRNA... 102 1e-41
 gb|BE034450|BE034450 MH05B01 MH *Mesembryanthemum crystallinum* cD... 81 3e-41
 emb|Z15140|LECHI9 *L.esculentum* mRNA for chitinase. 95 3e-41
 gb|U02607|STU02607 *Solanum tuberosum* chitinase (chtB3) mRNA, par... 95 6e-41
 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 95 6e-41
 30 emb|AF034566|AF034566 *Gossypium hirsutum* class I chitinase mRNA,... 100 6e-41
 gb|BE033398|BE033398 ME01A01 ME *Mesembryanthemum crystallinum* cD... 165 7e-41
 gb|M25337|POPCHIB *Populus* sp. chitinase (win8) mRNA, complete cds. 89 8e-41
 gb|BE034267|BE034267 MH02D06 MH *Mesembryanthemum crystallinum* cD... 66 2e-40
 emb|AI897217|AI897217 EST266756 tomato ovary, TAMU *Lycopersicon* ... 110 4e-40
 35 emb|AF000965|AF000965 *Poa pratensis* chitinase (Chi3) pseudogene ... 91 4e-40
 emb|X95610|CSHITIB *C.sativa* mRNA for chitinase Ib. 88 9e-40
 gb|U48687|CSU48687 *Castanea sativa* endochitinase mRNA, complete ... 88 9e-40
 emb|AW676775|AW676775 DG1_14_C09.g1_A002 Dark Grown 1 (DG1) Sorg... 161 2e-39
 emb|Z78202|PACHI1 *Persea americana* mRNA for endochitinase. 96 2e-39
 40 emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed 1 (WS1) ... 163 2e-39
 emb|AW922596|AW922596 DG1_46_C01.b1_A002 Dark Grown 1 (DG1) Sorg... 94 2e-39
 gb|BE034616|BE034616 ML04B04 ML *Mesembryanthemum crystallinum* cD... 77 5e-39
 gb|L22032|ULMCHITIN *Ulmus americana* chitinase (pHS2) mRNA, compl... 106 6e-39
 emb|AW924229|AW924229 WS1_51_H04.b1_A002 Water-stressed 1 (WS1) ... 161 7e-39
 45 emb|AW560048|AW560048 EST315096 DSIR *Medicago truncatula* cDNA cl... 109 7e-39
 emb|AW267781|AW267781 EST305909 DSIR *Medicago truncatula* cDNA cl... 109 7e-39
 emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root *Medicago* t... 78 3e-38
 gb|U02287|HVVU02287 *Hordeum vulgare* cultivar NK1558 chitinase gen... 96 4e-38
 emb|AI897657|AI897657 EST267100 tomato ovary, TAMU *Lycopersicon* ... 101 1e-37
 50 emb|AF098302|AF098302 *Brassica juncea* chitinase mRNA, complete cds. 106 1e-37
 emb|AW746429|AW746429 WS1_53_G09.b1_A002 Water-stressed 1 (WS1) ... 97 4e-37
 emb|X74919|PVGEC9 *P.vulgaris* gene for endochitinase. 149 6e-37

Query= AC002391.150_s_at 17843_s_at /id_source genbank /description
 55 gb|aab87109.1| (ac002391) putative cytochrome p450 [*arabidopsis*
thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
 /ncgi

(1548 letters)

60 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	(bits)	Value
5	Sequences producing significant alignments:				
	emb AB001379 AB001379 Glycyrrhiza echinata CYP81E1 mRNA for cyto...	323	e-137		
	emb AJ238439 CAR238439 Cicer arietinum mRNA for a cytochrome P45...	328	e-136		
	emb AB022732 AB022732 Glycyrrhiza echinata CYP Ge-31 mRNA for cy...	322	e-136		
10	emb AB025016 AB025016 Lotus japonicus mRNA for cytochrome P450, ...	291	e-134		
	emb AJ012581 CAR012581 Cicer arietinum mRNA for cytochrome P450.	324	e-134		
	emb AJ000478 HTCYP81L Helianthus tuberosus mRNA for cytochrome P...	227	e-124		
	emb AJ000477 HTCYP81C Helianthus tuberosus mRNA for cytochrome P...	227	e-124		
	emb AJ239051 CAR239051 Cicer arietinum mRNA for cytochrome P450 ...	237	3e-82		
15	emb AJ249800 CAR249800 Cicer arietinum partial mRNA for cytochro...	290	3e-79		
	emb AW185361 AW185361 se90e02.y1 Gm-cl027 Glycine max cDNA clone...	280	3e-74		
	emb AW775904 AW775904 EST334969 DSIL Medicago truncatula cDNA cl...	228	1e-70		
	emb AF082028 AF082028 Hemerocallis hybrid cultivar senescence-as...	189	2e-70		
	emb AW234443 AW234443 sf25c03.y1 Gm-cl028 Glycine max cDNA clone...	264	1e-69		
20	emb AW307234 AW307234 sf54d12.y1 Gm-cl009 Glycine max cDNA clone...	258	1e-67		
	emb AW733691 AW733691 sk83g07.y1 Gm-cl016 Glycine max cDNA clone...	253	3e-66		
	emb AW171738 AW171738 N100632e rootphos(-) Medicago truncatula c...	251	1e-65		
	emb AJ249801 CAR249801 Cicer arietinum partial mRNA for cytochro...	242	5e-63		
	emb AI729126 AI729126 BNLGHi12694 Six-day Cotton fiber Gossypium...	180	4e-58		
25	emb AW329224 AW329224 N200436e rootphos(-) Medicago truncatula c...	224	1e-57		
	emb AI725744 AI725744 BNLGHi12803 Six-day Cotton fiber Gossypium...	180	4e-57		
	emb AI495626 AI495626 sb11c08.y1 Gm-cl004 Glycine max cDNA clone...	222	6e-57		
	emb AW100311 AW100311 sd22g12.y2 Gm-cl012 Glycine max cDNA clone...	206	5e-56		
	emb AW257188 AW257188 EST305325 KV2 Medicago truncatula cDNA clo...	177	6e-56		
30	emb AI774414 AI774414 EST255514 tomato resistant, Cornell Lycoper...	144	5e-54		
	emb AW171672 AW171672 N100566e rootphos(-) Medicago truncatula c...	212	7e-54		
	emb AW932147 AW932147 EST357990 tomato fruit mature green, TAMU ...	211	1e-53		
	emb AI731481 AI731481 BNLGHi9879 Six-day Cotton fiber Gossypium ...	168	3e-51		
	emb AI731081 AI731081 BNLGHi8648 Six-day Cotton fiber Gossypium ...	200	2e-50		
35	emb AI728374 AI728374 BNLGHi10609 Six-day Cotton fiber Gossypium...	163	9e-50		
	emb AF014802 AF014802 Eschscholzia californica (S)-N-methylcocla...	173	3e-48		
	emb AV412147 AV412147 AV412147 Lotus japonicus young plants (two...	185	7e-46		
	emb AF156976 AF156976 Gerbera hybrida flavone synthase II (CYP93...	100	8e-46		
	dbj E13663 E13663 cDNA encoding cytochrome P450 which is induced...	104	1e-45		
40	dbj D83968 SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)...	104	1e-45		
	emb Y10492 GMC450CP5 G.max mRNA for putative cytochrome P450, cl...	106	6e-44		
	emb AW695923 AW695923 NF100G02ST1F1018 Developing stem Medicago ...	170	9e-44		
	emb AW684707 AW684707 NF020A02NR1F1000 Nodulated root Medicago t...	178	1e-43		
	emb AB015762 AB015762 Nicotiana tabacum mRNA for cytochrome P450...	160	2e-43		
45	emb AI973839 AI973839 sd11c06.y1 Gm-cl020 Glycine max cDNA clone...	104	2e-43		
	emb AF155332 AF155332 Petunia x hybrida flavonoid 3'-hydroxylase...	158	2e-43		
	emb AW734404 AW734404 sk19f09.y1 Gm-cl028 Glycine max cDNA clone...	157	2e-43		
	gb U29333 PSU29333 Pisum sativum novel wound-inducible cytochrom...	160	5e-43		
	emb AF124372 AF124372 Nicotiana tabacum NT7 mRNA, partial cds.	134	6e-43		
50	gb U72654 EGU72654 Eustoma grandiflorum flavonoid 3'-hydroxyla...	149	2e-42		
	dbj D86351 D86351 Glycine max CYP93A2 mRNA for cytochrome P-450,...	102	2e-42		
	emb AW688601 AW688601 NF009D12ST1F1000 Developing stem Medicago ...	173	4e-42		
	emb AW616170 AW616170 EST307209 L. hirsutum trichome, Cornell Un...	148	5e-42		
	dbj D14589 D14589 Eustoma russellianum mRNA for flavonoid 3',5'-...	148	6e-42		
55	emb AJ011862 CRO011862 Catharanthus roseus mRNA for flavonoid 3'...	155	6e-42		
	emb Z22545 PHFLAHYDB P.hybrida flavonoid 3',5'-hydroxylase mRNA.	148	8e-42		
	dbj D14588 PETHF1 Petunia hybrida Hfl mRNA for flavonoid-3',5'-h...	148	8e-42		
	emb AW616482 AW616482 EST322893 L. hirsutum trichome, Cornell Un...	148	1e-41		
	emb AW617814 AW617814 EST324213 L. hirsutum trichome, Cornell Un...	148	1e-41		
60	emb AW309826 AW309826 sf25c03.x1 Gm-cl028 Glycine max cDNA clone...	166	1e-41		
	emb AB024931 AB024931 Lotus japonicus mRNA for cytochrome P450, ...	100	2e-41		

- emb|AW299084|AW299084 EST305758 KV2 Medicago truncatula cDNA clo... 171 2e-41
 emb|AW728587|AW728587 GA__Ea0017C12 Gossypium arboreum 7-10 dpa ... 170 2e-41
 emb|Z22544|PHFLAHYDA P.hybrida flavonoid 3',5'-hydroxylase mRNA. 146 3e-41
 emb|AW616075|AW616075 EST296834 L. hirsutum trichome, Cornell Un... 148 3e-41
 5 emb|AF195800|AF195800 Medicago sativa isoflavone synthase 1 (ifs... 99 4e-41
 emb|AW255096|AW255096 ML139 peppermint glandular trichome Menta... 157 5e-41
 emb|AI776121|AI776121 EST257209 tomato resistant, Cornell Lycop... 111 5e-41
 emb|AF135484|AF135484 Glycine max cytochrome P450 monooxygenase ... 98 6e-41
 emb|AF195811|AF195811 Trifolium pratense isoflavone synthase 2 (... 98 6e-41
 10 emb|AF195810|AF195810 Trifolium pratense isoflavone synthase 1 (... 98 6e-41
 emb|AF195809|AF195809 Vigna radiata isoflavone synthase 4 (ifs4)... 98 6e-41
 emb|AF195808|AF195808 Vigna radiata isoflavone synthase 3 (ifs3)... 98 6e-41
 emb|AF195807|AF195807 Vigna radiata isoflavone synthase 2 (ifs2)... 98 6e-41
 emb|AF195802|AF195802 Medicago sativa isoflavone synthase 3 (ifs... 98 6e-41
 15 emb|Y10982|GMP450CP6 Glycine max mRNA for cytochrome P450-like p... 149 7e-41
 emb|AF255014|AF255014 Citrus sinensis cinnamate 4-hydroxylase CY... 145 7e-41
 emb|AW651341|AW651341 EST329795 tomato germinating seedlings, TA... 148 7e-41
 emb|AF195798|AF195798 Glycine max isoflavone synthase 1 (ifs1) m... 98 8e-41
 dbj|D14590|D14590 Campanula medium mRNA for flavonoid 3',5'-hydr... 151 1e-40
 20 emb|AI782402|AI782402 EST263281 tomato susceptible, Cornell Lyco... 144 2e-40
 emb|AF195799|AF195799 Glycine max isoflavone synthase 2 (ifs2) m... 96 2e-40
 emb|AF022462|AF022462 Glycine max cytochrome P450 monooxygenase ... 96 2e-40
 emb|AF195806|AF195806 Vigna radiata isoflavone synthase 1 (ifs1)... 96 2e-40
 emb|AF195812|AF195812 Pisum sativum isoflavone synthase 1 (ifs1)... 98 2e-40
 25 emb|AF195817|AF195817 Beta vulgaris isoflavone synthase 2 (ifs2)... 97 2e-40
 emb|AW687247|AW687247 NF007E11RT1F1086 Developing root Medicago ... 167 2e-40
 emb|AF096998|AF096998 Pinus taeda trans-cinnamate 4-hydroxylase ... 143 2e-40
 emb|AF195815|AF195815 Trifolium repens isoflavone synthase 2 (if... 96 3e-40
 emb|AW278589|AW278589 sf46e01.y1 Gm-cl009 Glycine max cDNA clone... 97 3e-40
 30 emb|AW034115|AW034115 EST277610 tomato callus, TAMU Lycopersicon... 147 4e-40
 emb|AF081575|AF081575 Petunia x hybrida flavonoid 3',5'-hydroxyl... 142 5e-40
 emb|Z17369|HTTC4MMR H.tuberosus mRNA for trans-cinnamate 4-monoo... 143 5e-40
 emb|A74279|A74279 Sequence 1 from Patent WO9401564. 143 5e-40
 emb|AF195813|AF195813 Lupinus albus isoflavone synthase 1 (ifs1)... 96 5e-40
 35 emb|AW616066|AW616066 EST296823 L. hirsutum trichome, Cornell Un... 145 5e-40
 emb|AW728802|AW728802 GA__Ea0028I12 Gossypium arboreum 7-10 dpa ... 148 6e-40
 emb|AF195801|AF195801 Medicago sativa isoflavone synthase 2 (ifs... 98 7e-40
 gb|U47293|PTU47293 Populus tremuloides trans-cinnamate 4-hydroxy... 141 9e-40
 dbj|D87520|D87520 Glycyrrhiza echinata suspension-cultured cells... 141 9e-40
 40 gb|L07634|PHVC4HYDRO Phaseolus aureus cinnamate 4-hydroxylase mR... 141 9e-40
 emb|AF195814|AF195814 Trifolium repens isoflavone synthase 1 (if... 98 1e-39
 dbj|D82815|POPPCYP73D Populus kitakamiensis cyp73a mRNA for cinn... 140 1e-39
 emb|AJ243804|CAR243804 Cicer arietinum mRNA for cytochrome P450 ... 96 1e-39
 emb|AF195803|AF195803 Vicia villosa isoflavone synthase 1 (ifs1)... 96 1e-39
 45 emb|AF195816|AF195816 Beta vulgaris isoflavone synthase 1 (ifs1)... 97 1e-39

Query= AC005315.131_at 18844_at /id_source genbank /description
 gb|aac33239.1| (ac005315) putative ligand-gated ion channel protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 50 /gb_link [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005315|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005315|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005315|/ncgi)
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005315|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005315|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005315|/ncgi)
 (2805 letters)

55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

60 Score E
 Sequences producing significant alignments: (bits) Value

- emb|AF109392|AF109392 Brassica napus ligand gated channel-like p... 142 3e-57
emb|AW034636|AW034636 EST278320 tomato callus, TAMU Lycopersicon... 100 2e-26
emb|AI054890|AI054890 coau0002H02 Cotton Boll Abcission Zone cD... 90 1e-23
5 emb|AI759920|AI759920 sb66c06.y1 Gm-c1017 Glycine max cDNA clone... 84 4e-15
gb|BE022401|BE022401 sm85d03.y1 Gm-c1015 Glycine max cDNA clone ... 55 3e-13
emb|AW773978|AW773978 EST332964 KV3 Medicago truncatula cDNA clo... 53 1e-12
emb|AW982953|AW982953 HVSMEg0004K11f Hordeum vulgare pre-anthesi... 73 8e-12
gb|BE059628|BE059628 sn34g08.y1 Gm-c1016 Glycine max cDNA clone ... 58 5e-10
10 emb|AW928584|AW928584 EST337372 tomato flower buds 8 mm to pre-a... 66 1e-09
emb|AW622410|AW622410 EST313197 tomato root during/after fruit s... 40 3e-06
emb|AW160184|AW160184 EST290041 L. pennellii trichome, Cornell U... 40 4e-06
emb|AW933376|AW933376 EST359219 tomato fruit mature green, TAMU ... 52 2e-05
emb|AI441698|AI441698 sa60b02.y1 Gm-c1004 Glycine max cDNA clone... 49 2e-04
15 emb|AW925534|AW925534 HVSMEg0002H02 Hordeum vulgare pre-anthesis... 48 3e-04
emb|AW284671|AW284671 LG1_214_A11.g1_A002-Light Grown 1 (LG1) So... 47 8e-04
emb|AI054607|AI054607 coau0001I04 Cotton Boll Abcission Zone cD... 46 0.001
emb|AW933855|AW933855 EST359698 tomato fruit mature green, TAMU ... 31 0.42
emb|AW931421|AW931421 EST357264 tomato fruit mature green, TAMU ... 31 0.42
20 emb|AW034378|AW034378 EST277949 tomato callus, TAMU Lycopersicon... 31 0.42
emb|AW030398|AW030398 EST273653 tomato callus, TAMU Lycopersicon... 31 0.42
emb|AW625904|AW625904 EST319799 tomato radicle, 5 d post-imbibit... 31 0.42
emb|AI781375|AI781375 EST262242 tomato susceptible, Cornell Lyco... 31 0.42
emb|AW031815|AW031815 EST275269 tomato callus, TAMU Lycopersicon... 31 0.42
25 emb|AW443041|AW443041 EST307971 tomato mixed elicitor, BTI Lycop... 31 0.42
emb|AI489138|AI489138 EST247477 tomato ovary, TAMU Lycopersicon ... 31 0.42
emb|AW931241|AW931241 EST357084 tomato fruit mature green, TAMU ... 31 0.42
emb|AW931511|AW931511 EST357354 tomato fruit mature green, TAMU ... 31 0.42
emb|AW218030|AW218030 EST296745 tomato flower buds, anthesis, Co... 31 0.42
30 emb|AW224605|AW224605 EST303048 tomato root, plants pre-anthesis... 31 0.42
emb|AW441557|AW441557 EST310953 tomato fruit red ripe, TAMU Lyco... 31 0.42
emb|AI485565|AI485565 EST243886 tomato ovary, TAMU Lycopersicon ... 31 0.42
emb|AI490454|AI490454 EST248780 tomato ovary, TAMU Lycopersicon ... 31 0.42
emb|AW221704|AW221704 EST298515 tomato fruit red ripe, TAMU Lyco... 31 0.42
35 emb|AW455351|AW455351 EST311889 tomato root during/after fruit s... 31 0.42
emb|AW034104|AW034104 EST277599 tomato callus, TAMU Lycopersicon... 31 0.43
emb|AW038338|AW038338 EST280021 tomato mixed elicitor, BTI Lycop... 31 0.43
emb|AW222646|AW222646 EST299457 tomato fruit red ripe, TAMU Lyco... 31 0.43
emb|AW933318|AW933318 EST359161 tomato fruit mature green, TAMU ... 31 0.43
40 emb|AI487939|AI487939 EST246261 tomato ovary, TAMU Lycopersicon ... 31 0.43
emb|AW032107|AW032107 EST275561 tomato callus, TAMU Lycopersicon... 31 0.43
emb|AW221841|AW221841 EST298652 tomato fruit red ripe, TAMU Lyco... 31 0.43
emb|AW932038|AW932038 EST357881 tomato fruit mature green, TAMU ... 31 0.43
emb|AW039616|AW039616 EST282064 tomato mixed elicitor, BTI Lycop... 31 0.43
45 emb|AW222971|AW222971 EST299782 tomato fruit red ripe, TAMU Lyco... 31 0.59
emb|AW931586|AW931586 EST357429 tomato fruit mature green, TAMU ... 37 0.62
emb|AI812461|AI812461 11D11 Pine Lambda Zap Xylem library Pinus ... 26 0.73
emb|AI774678|AI774678 EST255778 tomato resistant, Cornell Lycope... 37 0.85
emb|AW982678|AW982678 HVSMEg0003O16f Hordeum vulgare pre-anthesi... 35 1.0
50 emb|AW933175|AW933175 EST359018 tomato fruit mature green, TAMU ... 36 1.6
emb|Z50171|TBBSLARN A T.brucei brucei SLA RNA gene. 36 1.6
emb|AI484282|AI484282 EST248834 tomato susceptible, Cornell Lyco... 31 2.0
emb|AW925473|AW925473 HVSMEg0001O11 Hordeum vulgare pre-anthesis... 35 2.2
emb|Z69727|SPAC4G9 S.pombe chromosome I cosmid c4G9. 35 2.2
55 emb|AB008750|AB008750 Schizosaccharomyces pombe gene for Alp11, ... 35 2.2
emb|AW983412|AW983412 HVSMEg0010I20f Hordeum vulgare pre-anthesi... 33 2.5
emb|AF110134|AF110134 Volvox carteri f. nagariensis GlsA (glsA) ... 35 3.0
emb|AJ011856|SCE011856 Saccharomyces cerevisiae complete mitocho... 35 3.0
emb|V00694|MISC13 Saccharomyces cerevisiae mitochondrion COX/OXI... 35 3.0
60 gb|L36897|YSCMTCG13 Saccharomyces cerevisiae mitochondrion oxi3 ... 35 3.0
emb|AW933203|AW933203 EST359046 tomato fruit mature green, TAMU ... 35 3.0

	emb Z46869 KLEXG1 K.lactis gene for exo-1,3-beta-glucanase/1,3-b...	35	3.0
	emb AA415065 AA415065 Mg0012 RCW Lambda Zap Express Library Pyri...	35	3.0
	emb AL122012 LMFL8342 Leishmania major Friedlin chromosome 23 co...	35	4.2
	emb AW257203 AW257203 EST305340 KV2 Medicago truncatula cDNA clo...	35	4.2
5	emb AC005504 AC005504 Plasmodium falciparum chromosome 12, *** S...	35	4.2
	emb AI784905 AI784905 1268 PtIFG2 Pinus taeda cDNA clone 8876r, ...	35	4.2
	emb AA739776 AA739776 541 PtIFG2 Pinus taeda cDNA clone 8876M 3'...	35	4.2
	emb AI965479 AI965479 sc72e01.y1 Gm-c1018 Glycine max cDNA clone...	35	4.2
	emb AW932343 AW932343 EST358186 tomato fruit mature green, TAMU ...	35	4.2
10	emb AC004710 AC004710 Plasmodium falciparum chromosome 12, *** S...	35	4.2
	emb AC005507 AC005507 Plasmodium falciparum chromosome 12 clone ...	35	4.2
	emb AF236108 AF236108 Glycine max putative purple acid phosphata...	35	4.2
	emb AA739843 AA739843 608 PtIFG2 Pinus taeda cDNA clone 8988M 3'...	35	4.2
	emb AQ849884 AQ849884 LMAJFV1_lm51b04.x1 Leishmania major FV1 ra...	34	5.7
15	emb AV406712 AV406712 AV406712 Lotus japonicus young plants (two...	34	5.7
	emb Z49212 SC9952X S.cerevisiae chromosome XIII cosmid 9952. ...	34	5.7
	emb AW735973 AW735973 EST336741 tomato flower buds 0-3 mm, Corne...	34	5.7
	emb AW668487 AW668487 GA__Ea0014C10 Gossypium arboreum 7-10 dpa ...	34	5.7
	emb AL110295 SPBC106 S.pombe chromosome II cosmid c106. ...	34	5.7
20	gb U08622 SPU08622 Schizosaccharomyces pombe cAMP-dependent prot...	34	5.7
	emb AV411500 AV411500 AV411500 Lotus japonicus young plants (two...	34	5.7
	emb AQ649646 AQ649646 Sheared DNA-16E6.TF Sheared DNA Trypanosom...	34	5.7
	emb AV407948 AV407948 AV407948 Lotus japonicus young plants (two...	34	5.7
	dbj D23667 YSPPKA1 Fission yeast pkal gene for catalytic subunit...	34	5.7
25	emb AW719775 AW719775 LjNEST9G5r Lotus japonicus nodule library ...	34	5.7
	gb BE052571 BE052571 GA__Ea0035M21f Gossypium arboreum 7-10 dpa ...	32	6.1
	emb AQ852061 AQ852061 LMAJFV1_lm60f08.y1 Leishmania major FV1 ra...	34	6.4
	emb AL132675 SPAC144 S.pombe chromosome I cosmid c144. ...	34	7.8
	emb AJ223818 LEAJ3818 Lycopersicon esculentum cv Red River unkno...	34	7.8
30	gb B07277 B07277 G267T3 MVAT4 sheared genomic library Trypanosom...	34	7.8
	emb AW982385 AW982385 HVSMEg0003C03f Hordeum vulgare pre-anthesi...	34	7.8
	emb AW442327 AW442327 EST311723 tomato fruit red ripe, TAMU Lyco...	34	7.8
	emb X13486 CHCMPSBA C. moewusii chloroplast psbA gene for photos...	34	7.8
	emb X15601 CMCHPSBA C.moewusii chloroplast psbA gene. ...	34	7.8
35	Query= AF071527.44_at 19247_at /id_source genbank /description		
	gb aad11587.1 aad11587 (af071527) hypothetical protein [arabidopsis		
	thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link		
	http://www3.ncbi.nlm.nih.gov/htbin-		
40	post/entrez/query?db=n&form=6&dopt=g&uid=gb af071527 /ncgi		
	http://www.ncgr.org/cgi-bin/ff?af071527		
	(1926 letters)		
	Database: plantfungal		
45	661,018 sequences; 426,114,510 total letters		
	Searching.....done		
	Score	E	
50	Sequences producing significant alignments:	(bits)	Value
	emb AI894928 AI894928 EST264371 tomato callus, TAMU Lycopersicon...	58	2e-07
	gb BE033853 BE033853 MG01B02 MG Mesembryanthemum crystallinum cD...	55	2e-06
	emb AW621748 AW621748 EST312546 tomato root during/after fruit s...	53	8e-06
55	emb AI729861 AI729861 BNLGHi5428 Six-day Cotton fiber Gossypium ...	52	2e-05
	emb AW035961 AW035961 EST282820 tomato callus, TAMU Lycopersicon...	51	3e-05
	emb AV420300 AV420300 AV420300 Lotus japonicus young plants (two...	49	1e-04
	emb AZ124241 AZ124241 T223105b Medicago truncatula BAC library M...	49	1e-04
	emb AW694103 AW694103 NF072D04ST1F1041 Developing stem Medicago ...	48	3e-04
60	emb AI896054 AI896054 EST265497 tomato callus, TAMU Lycopersicon...	47	4e-04
	emb AI729969 AI729969 BNLGHi5823 Six-day Cotton fiber Gossypium ...	34	0.002

	emb AZ124239 AZ124239 T223103b Medicago truncatula BAC library M...	43	0.003
	emb AV414054 AV414054 AV414054 Lotus japonicus young plants (two...	44	0.004
	emb AI487562 AI487562 EST245884 tomato ovary, TAMU Lycopersicon ...	44	0.005
	emb Z69731 SPAC6C3 S.pombe chromosome I cosmid c6C3.	44	0.005
5	emb AW164678 AW164678 se76b06.y1 Gm-c1023 Glycine max cDNA clone...	43	0.007
	emb AI489135 AI489135 EST247474 tomato ovary, TAMU Lycopersicon ...	43	0.007
	emb AI736949 AI736949 sb35a01.y1 Gm-c1013 Glycine max cDNA clone...	42	0.017
	emb AW736367 AW736367 EST332286 KV3 Medicago truncatula cDNA clo...	42	0.017
	emb AI164848 AI164848 A069p65u Hybrid aspen plasmid library Popu...	41	0.033
10	emb AQ638202 AQ638202 927P1-9H10.TP 927P1 Trypanosoma brucei gen...	41	0.033
	emb AW040703 AW040703 EST283567 tomato mixed elicitor, BTI Lycop...	41	0.033
	emb AI054990 AI054990 coau0002L09 Cotton Boll Abscission Zone cD...	41	0.033
	emb AI166315 AI166315 xylem.est.16 Poplar xylem Lambda ZAPII lib...	37	0.035
	emb AI055156 AI055156 coau0003D05 Cotton Boll Abscission Zone cD...	40	0.045
15	emb AW256577 AW256577 EST304714 KV2 Medicago truncatula cDNA clo...	30	0.064
	emb AA783893 AA783893 c8g07a1.r1 Aspergillus nidulans 24hr asexu...	30	0.16
	emb AW053754 AW053754 L30-1647T3 Ice plant Lambda Uni-Zap XR exp...	38	0.30
	emb AI054715 AI054715 coau0001M19 Cotton Boll Abscission Zone cD...	37	0.41
	gb BE035556 BE035556 MO09B06 MO Mesembryanthemum crystallinum cD...	29	0.69
20	gb BE036920 BE036920 MP09B06 MP Mesembryanthemum crystallinum cD...	29	0.71
	emb AL033534 SPBC215 S.pombe chromosome II cosmid c215.	36	0.78
	emb AW932897 AW932897 EST358740 tomato fruit mature green, TAMU ...	36	1.1
	emb AW596694 AW596694 sj15e12.y1 Gm-c1032 Glycine max cDNA clone...	35	1.5
	emb X02390 ANTRPC1 Aspergillus nidulans trpC gene.	35	2.0
25	emb X52152 SCIME S. cerevisiae IME1 gene for Ime1, a meiosis ind...	35	2.0
	emb Z49595 SCYJR095W S.cerevisiae chromosome X reading frame ORF...	35	2.0
	gb L47610 PLAEMB4R Picea glauca EMB4 mRNA.	35	2.0
	emb Z49594 SCYJR094C S.cerevisiae chromosome X reading frame ORF...	35	2.0
	emb AI622956 AI622956 TENG0590 T. Cruzi epimastigote normalised ...	35	2.0
30	gb M37188 YSCIME1 S.cerevisiae meiosis-inducing protein (IME1) g...	35	2.0
	gb BE034285 BE034285 MH02G01 MH Mesembryanthemum crystallinum cD...	35	2.8
	emb AW256576 AW256576 EST304713 KV2 Medicago truncatula cDNA clo...	35	2.8
	emb AI167045 AI167045 xylem.est.817 Poplar xylem Lambda ZAPII li...	35	2.8
	emb AW696259 AW696259 NF104F08ST1F1074 Developing stem Medicago ...	29	3.2
35	emb AI974296 AI974296 T110298e KV0 Medicago truncatula cDNA clon...	34	3.8
	emb AI756377 AI756377 EtESTea12b12.y1 Eimeria M5-6 Merozoite sta...	34	3.8
	emb AZ217340 AZ217340 Sheared DNA-117G6.TF Sheared DNA Trypanoso...	34	3.8
	emb AQ988815 AQ988815 11E1D03NE.R1 C. parvum Lambda Zap Express ...	34	3.8
	emb AW565712 AW565712 LG1_348_C03.g1_A002 Light Grown 1 (LG1) So...	34	3.8
40	gb L20566 ASNACDP Aspergillus niger acid phosphatase complete cds.	27	4.0
	emb AW869952 AW869952 NXNV_120_C10_F Nsf Xylem Normal wood Verti...	34	5.3
	emb AW691961 AW691961 NF046B02ST1F1000 Developing stem Medicago ...	34	5.3
	emb AF007946 AF007946 Trautvetteria carolinensis maturase (matK)...	34	5.3
	emb AW185605 AW185605 se79h09.y1 Gm-c1023 Glycine max cDNA clone...	33	7.2
45	emb AQ639089 AQ639089 927P1-ID11.TP 927P1 Trypanosoma brucei gen...	33	7.2
	emb AW731466 AW731466 GA_Ea0030J17 Gossypium arboreum 7-10 dpa ...	33	7.2
	emb AW623353 AW623353 EST321298 tomato flower buds 3-8 mm, Corne...	33	7.2
	emb AI781323 AI781323 EST262202 tomato susceptible, Cornell Lyco...	33	7.2
	emb AZ214634 AZ214634 Sheared DNA-68B12.TR Sheared DNA Trypanoso...	33	7.2
50	emb AQ656501 AQ656501 Sheared DNA-12B14.TF Sheared DNA Trypanoso...	33	7.2
	emb AW932874 AW932874 EST358717 tomato fruit mature green, TAMU ...	33	7.2
	emb AW926434 AW926434 HVSMEg0007D10 Hordeum vulgare pre-anthesis...	33	7.2
	emb AQ945431 AQ945431 Sheared DNA-44E8.TR Sheared DNA Trypanosom...	33	7.2
	emb AQ945478 AQ945478 Sheared DNA-45J6.TF Sheared DNA Trypanosom...	33	7.2
55	emb AL116771 CNS01DFV Botrytis cinerea strain T4 cDNA library un...	33	7.2
	emb AL035476 PFMAL4P3 Plasmodium falciparum chromosome 4 strain ...	33	7.2
	emb AW776850 AW776850 EST335915 DSIL Medicago truncatula cDNA cl...	33	7.2
	emb AZ219905 AZ219905 Sheared DNA-61D10.TF Sheared DNA Trypanoso...	33	7.2
	emb AZ216687 AZ216687 Sheared DNA-84G10.TR Sheared DNA Trypanoso...	33	7.2
60	emb X87941 SCDNAGENS S.cerevisiae CRM1, YML9, PET54, SMI1, PHO81...	28	7.5
	emb AZ124240 AZ124240 T223104b Medicago truncatula BAC library M...	31	7.9

	emb AI213023 AI213023 y6e12a1.fl Aspergillus nidulans 24hr asexu...	33	9.9
	emb AA556848 AA556848 690 Loblolly pine C Pinus taeda cDNA clone...	33	9.9
	emb AA965673 AA965673 m2g10a1.fl Aspergillus nidulans 24hr asexu...	33	9.9
	emb AI212224 AI212224 w9h05a1.fl Aspergillus nidulans 24hr asexu...	33	9.9
5	emb AW924917 AW924917 WS1_73_B03.b1_A002 Water-stressed 1 (WS1) ...	33	9.9
	emb AW127359 AW127359 M110532 DSIL Medicago truncatula cDNA clon...	33	9.9
	emb Y15418 CCY15418 Coprinus cinereus acs-1 gene.	33	9.9
	emb AW694961 AW694961 NF081H09ST1F1079 Developing stem Medicago ...	33	9.9
	emb AW991081 AW991081 SsS0293 Suaeda salsa ZAP cDNA library Suae...	33	9.9
10	emb AW399343 AW399343 EST309843 L. pennellii trichome, Cornell U...	33	9.9
	emb AA784746 AA784746 g2a12a1.fl Aspergillus nidulans 24hr asexu...	33	9.9
	emb Z73017 SCYGR232W S.cerevisiae chromosome VII reading frame O...	28	10.0
Query= AC003028.196_at 19284_at /id_source genbank /description			
15	gb aac27173.1 (ac003028) putative anthocyanidin synthase [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link		
	http://www3.ncbi.nlm.nih.gov/htbin-		
	post/entrez/query?db=n&form=6&dopt=g&uid=gb ac003028 /ncgi		
	http://www.ncgr.org/cgi-bin/ff?ac003028		
20	(1062 letters)		
Database: plantfungal			
	661,018 sequences; 426,114,510 total letters		
25	Searching.....done		
	Score E		
	Sequences producing significant alignments:	(bits)	Value
30	emb AI486803 AI486803 EST245125 tomato ovary, TAMU Lycopersicon ...	358	6e-98
	emb AI486879 AI486879 EST245201 tomato ovary, TAMU Lycopersicon ...	314	8e-85
	emb AW574302 AW574302 EST316893 GVN Medicago truncatula cDNA clo...	255	1e-76
	emb AW459665 AW459665 sh90c10.y1 Gm-cl016 Glycine max cDNA clone...	285	5e-76
	emb AI898341 AI898341 EST267784 tomato ovary, TAMU Lycopersicon ...	282	3e-75
35	gb L42466 PIAEFE Picea glauca ethylene-forming enzyme (EFE) mRNA...	156	4e-75
	emb AW981190 AW981190 EST392384 DSIL Medicago truncatula cDNA cl...	262	2e-73
	emb AI777799 AI777799 EST258678 tomato susceptible, Cornell Lyco...	267	1e-70
	emb AW574101 AW574101 EST316692 GVN Medicago truncatula cDNA clo...	198	2e-67
	emb AW268031 AW268031 EST306309 DSIR Medicago truncatula cDNA cl...	126	6e-65
40	emb AW775553 AW775553 EST334618 DSIL Medicago truncatula cDNA cl...	210	3e-63
	emb AW509400 AW509400 si22f08.y1 Gm-cl029 Glycine max cDNA clone...	237	8e-62
	emb AB003779 AB003779 Perilla frutescens mRNA for leucoanthocyan...	115	5e-59
	emb AW349732 AW349732 GM210006A11F12R Gm-r1021 Glycine max cDNA ...	228	6e-59
	gb U97530 PAU97530 Prunus armeniaca ethylene-forming-enzyme-like...	143	1e-58
45	emb AF082862 AF082862 Pisum sativum unknown mRNA, partial cds.	220	2e-56
	emb Z22543 PHFLASYNA P.hybrida flavonol synthase mRNA.	99	1e-55
	emb X83229 NTRNA1A1C N.tabacum mRNA for 1-aminocyclopropane-1-ca...	176	1e-54
	emb AF184273 AF184273 Daucus carota leucoanthocyanidin dioxygena...	110	9e-54
	emb AW030000 AW030000 EST273255 tomato callus, TAMU Lycopersicon...	186	1e-53
50	emb AF026058 AF026058 Matthiola incana anthocyanidin synthase mR...	116	2e-53
	emb AF184274 AF184274 Daucus carota leucoanthocyanidin dioxygena...	110	2e-53
	emb AF117269 AF117269 Malus domestica anthocyanidin synthase (AN...	114	3e-53
	emb X71360 MSPANTHHY Malus sp. mRNA for anthocyanidin hydroxylase.	114	3e-53
	emb AW686531 AW686531 NF042D05NR1F1000 Nodulated root Medicago t...	166	2e-52
55	gb U54566 NGU54566 Nicotiana glutinosa 1-aminocyclopropane-1-car...	174	2e-52
	emb AF001391 AF001391 Matthiola incana putative flavonol synthas...	118	3e-52
	emb AF119095 AF119095 Malus domestica flavonol synthase (FLS) mR...	91	2e-51
	emb X70786 PHFLV3HDX P.hybrida mRNA for putative flavanone 3-hyd...	112	5e-51
	emb AB012205 AB012205 Lactuca sativa Ls3h1 mRNA for gibberelin 3...	137	9e-51
60	emb AF028602 AF028602 Ipomoea purpurea anthocyanidin synthase (A...	108	1e-50
	emb AB013101 AB013101 Lycopersicon esculentum LE-ACO4 mRNA for 1...	157	2e-50

- emb|AB023786|AB023786 Ipomoea batatas ans I mRNA for anthocyanid... 111 4e-50
 emb|X75966|VVLDOX V. vinifera LDOX mRNA for leucoanthocyanidin di... 105 6e-50
 emb|X04792|LEETHYBR Tomato mRNA expressed during fruit ripening ... 159 1e-49
 emb|AB023787|AB023787 Ipomoea batatas ans II mRNA for anthocyani... 110 1e-49
 5 emb|A35021|A35021 L.esculentum pTOM13. 159 1e-49
 emb|AF053354|AF053354 Phaseolus vulgaris 1-aminocyclopropane-1-c... 159 2e-49
 gb|U06046|VRU06046 Vigna radiata clone pVR-ACO1 1-aminocycloprop... 157 3e-49
 emb|X58885|LEEFEMR L.esculentum mRNA for ethylene-forming enzyme... 157 3e-49
 emb|AB003514|AB003514 Actinidia deliciosa mRNA for 1-aminocyclop... 157 4e-49
 10 gb|U68215|CPU68215 Carica papaya ACC oxidase mRNA, complete cds. 152 5e-49
 emb|AF117270|AF117270 Malus domestica flavanone 3-hydroxylase (F... 100 5e-49
 emb|X69664|MSF3HA Malus sp. mRNA for naringenin,2-oxoglutarate,3... 100 5e-49
 gb|M97961|ACTACCOXI Actinidia deliciosa ACC oxidase homologue pr... 154 7e-49
 emb|AB010991|AB010991 Lycopersicon esculentum Le3OH-1 mRNA for 3... 133 7e-49
 15 emb|AF115262|AF115262 Trifolium repens mature green leaf 1-amino... 158 7e-49
 gb|U19856|PHU19856 Pelargonium hortorum 1-aminocyclopropane-1-ca... 153 1e-48
 gb|U07953|PHU07953 Pelargonium hortorum 1-aminocyclopropane-1-ca... 159 1e-48
 gb|U54565|NGU54565 Nicotiana glutinosa 1-aminocyclopropane-1-car... 156 1e-48
 emb|AW459318|AW459318 sh23e02.y1 Gm-c1016 Glycine max cDNA clone... 165 1e-48
 20 gb|U74081|IPU74081 Ipomoea purpurea flavanone 3-hydroxylase (F3H... 99 2e-48
 emb|AF254125|AF254125 Carica papaya ACC oxidase mRNA, complete cds. 150 2e-48
 emb|AB012857|AB012857 Nicotiana tabacum mRNA for ACC oxidase, co... 155 2e-48
 emb|AB002667|AB002667 Vigna angularis mRNA for ACC-oxidase, comp... 158 2e-48
 emb|AB023789|AB023789 Ipomoea batatas f3h II mRNA for flavanone ... 96 2e-48
 25 emb|AB023790|AB023790 Ipomoea batatas f3h III mRNA for flavanone... 96 2e-48
 gb|U06047|VRU06047 Vigna radiata clone pVR-ACO2 1-aminocycloprop... 157 3e-48
 gb|BE058138|BE058138 sn11h05.y1 Gm-c1016 Glycine max cDNA clone ... 193 3e-48
 emb|Y10749|BPACORNA B.pendula ACO mRNA. 150 3e-48
 gb|U67861|PHU67861 Pelargonium hortorum 1-aminocyclopropane-1-ca... 154 5e-48
 30 emb|X87097|PCPCACO1G P.communis mRNA for 1-aminocyclopropane-1-c... 155 5e-48
 emb|AF115263|AF115263 Trifolium repens senescent leaf 1-aminocyc... 162 5e-48
 emb|AW685998|AW685998 NF032F07NR1F1000 Nodulated root Medicago t... 159 5e-48
 emb|AJ440611|AJ440611 sa68d07.y1 Gm-c1004 Glycine max cDNA clone... 192 5e-48
 emb|AB023788|AB023788 Ipomoea batatas f3h I mRNA for fravanone 3... 95 6e-48
 35 gb|U23066|PAU23066 Persea americana flavanone 3-hydroxylase mRNA... 100 6e-48
 gb|M98357|PEAAMINCAR Pea 1-aminocyclopropane-1-carboxylate oxida... 155 6e-48
 emb|X98493|NTACCO Nicotiana tabacum mRNA for ACC-oxidase (clone ... 154 9e-48
 emb|X81628|BOACCOX1 B.oleracea mRNA for ACC oxidase (ACC0x1). 148 1e-47
 gb|L35152|DINACCA Dianthus caryophyllus amino-cyclopropane carbo... 158 1e-47
 40 emb|AW685110|AW685110 NF025C04NR1F1000 Nodulated root Medicago t... 158 1e-47
 emb|AB032198|AB032198 Nicotiana tabacum mRNA for gibberellin 3be... 135 2e-47
 gb|L37103|DORCAROXI Doritaenopsis sp. 1-aminocyclopropane-1-carb... 125 2e-47
 emb|AB012206|AB012206 Lactuca sativa Ls3h2 mRNA for gibberellin ... 118 2e-47
 dbj|D67038|D67038 Pyrus pyrifolia mRNA for ACC oxidase, complete... 152 2e-47
 45 emb|Y10034|PP1AMCSYN R.palustris mRNA for 1-aminocyclopropane-1-... 159 2e-47
 gb|M62380|DINCARSR Carnation senescence related protein RNA, com... 157 2e-47
 gb|M81794|MAURRP Malus sylvestris ripening-related protein mRNA,. 153 2e-47
 emb|X61390|MDETR M.domestica ethylene-related mRNA. 153 2e-47
 emb|AB011796|AB011796 Citrus unshiu CitFLS mRNA for flavonol syn... 104 3e-47
 50 emb|AJ001646|MDACCOXI2 Malus domestica mRNA for ACC oxidase. 153 3e-47
 dbj|D83041|D83041 Ipomoea nil mRNA for 2-oxogulutarate 3-dioxyge... 95 4e-47
 gb|L29405|HNNACC Helianthus annuus 1-1-aminocyclopropane-1-carbo... 152 4e-47
 emb|AF115261|AF115261 Trifolium repens stolon apex 1-aminocyclop... 156 4e-47
 emb|AF240764|AF240764 Eustoma russellianum flavonol synthase (fl... 100 6e-47
 55 emb|Z46349|NTACCDEAM N.tabacum mRNA for 1-aminocyclopropane-1-ca... 150 8e-47
 gb|L07912|DORACCOXID Moth orchid ACC oxidase mRNA, complete cds. 129 1e-46
 emb|X77232|PPPAO1 P.persica PAO1 mRNA for 1-aminocyclopropane-1-... 156 1e-46
 emb|Z11750|BJEFEMR B.junceae mRNA for ethylene-forming enzyme. 146 1e-46
 emb|AF026793|AF026793 Prunus armeniaca 1-aminocyclopropane-1-car... 156 1e-46
 60 emb|X72594|MIFHT M.incana mRNA for flavanone 3-beta-hydroxylase. 94 2e-46
 gb|M90294|PETEFE Petunia hybrida L. ethylene forming enzyme mRNA... 152 2e-46

emb|AB010992|AB010992 Lycopersicon esculentum Le3OH-2 mRNA for 3... 133 2e-46
emb|X75965|VVF3H V.vinifera F3H mRNA for flavanone 3-hydroxylase. 95 3e-46
emb|AB031027|AB031027 Prunus mume PM-ACO1 mRNA for ACC oxidase, ... 155 4e-46
emb|AW775815|AW775815 EST334880 DSIL Medicago truncatula cDNA cl... 154 4e-46
5 emb|AF041479|AF041479 Rumex palustris 1-aminocyclopropane-1-carb... 154 7e-46
emb|X81629|BOACCOX2 B.oleracea mRNA for ACC oxidase (ACC0x2). 149 7e-46
emb|AW775355|AW775355 EST334420 DSIL Medicago truncatula cDNA cl... 162 8e-46

Query= AL035527.204_at 19762_at /id_source genbank /description
10 emb|cab36812.1| (al035527) peptide transporter-like protein
[arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
/gb_link http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&xuid=gb|al035527|/ncgi
http://www.ncgr.org/cgi-bin/ff?al035527
15 (1731 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

20 Searching.....done

Score E
Sequences producing significant alignments: (bits) Value

25 emb|AF023472|AF023472 Hordeum vulgare peptide transporter (ptr1)... 162 e-119
emb|AW929517|AW929517 EST338305 tomato flower buds 8 mm to pre-a... 162 3e-90
emb|AF016713|AF016713 Lycopersicon esculentum oligopeptide trans... 138 3e-89
emb|AF213936|AF213936 Prunus dulcis amino acid/peptide transport... 132 2e-87
emb|Y13862|NTENRT1 Nicotiana tabacum enr-T1 gene. 173 9e-81
30 emb|X92852|LENIT2 L.esculentum exon 1 of NIT2 gene. 140 1e-80
emb|AW773639|AW773639 EST332625 KV3 Medicago truncatula cDNA clo... 298 9e-80
emb|X92853|LEMIT1 L.esculentum exon 1 of NIT1 gene. 150 9e-74
gb|U17987|BNU17987 Brassica napus RCH2 protein mRNA, complete cds. 80 5e-73
emb|AW929740|AW929740 EST354010 tomato flower buds 8 mm to pre-a... 163 3e-58
35 emb|AW278758|AW278758 sf97b05.y1 Gm-cl019 Glycine max cDNA clone... 127 2e-47
emb|AW186088|AW186088 se63e01.y1 Gm-cl019 Glycine max cDNA clone... 176 4e-43
emb|AQ917114|AQ917114 T233143b Medicago truncatula BAC library M... 112 6e-42
emb|AF080545|AF080545 Nepenthes alata peptide transporter (PTR1)... 111 1e-41
emb|AW677489|AW677489 DG1_8_A08.b1_A002 Dark Grown 1 (DG1) Sorgh... 126 2e-35
40 emb|AW219289|AW219289 EST301771 tomato root during/after fruit s... 144 3e-34
emb|Z69370|CSNITR1 C.sativus mRNA for nitrite transporter. 76 3e-34
emb|AW310175|AW310175 sf32c04.x1 Gm-cl028 Glycine max cDNA clone... 146 5e-34
emb|AW931623|AW931623 EST357466 tomato fruit mature green, TAMU ... 76 8e-34
emb|AW455271|AW455271 EST311931 tomato root during/after fruit s... 144 3e-33
45 emb|AW202366|AW202366 sf14b11.y1 Gm-cl027 Glycine max cDNA clone... 144 3e-33
emb|AW694006|AW694006 NF071D12ST1F1101 Developing stem Medicago ... 79 7e-33
emb|AW691380|AW691380 NF040G02ST1F1000 Developing stem Medicago ... 142 1e-32
emb|AW233936|AW233936 sf32c04.y1 Gm-cl028 Glycine max cDNA clone... 82 4e-32
emb|AW774447|AW774447 EST333598 KV3 Medicago truncatula cDNA clo... 85 8e-32
50 emb|AI488938|AI488938 EST247277 tomato ovary, TAMU Lycopersicon ... 85 2e-31
emb|AF000392|AF000392 Lotus japonicus peptide transporter (LjNOD... 91 7e-31
emb|AW186021|AW186021 se62f04.y1 Gm-cl019 Glycine max cDNA clone... 134 2e-30
emb|AW649721|AW649721 EST328175 tomato germinating seedlings, TA... 109 6e-30
emb|AI485754|AI485754 EST244075 tomato ovary, TAMU Lycopersicon ... 107 9e-30
55 emb|AI812586|AI812586 13F10 Pine Lambda Zap Xylem library Pinus ... 132 1e-29
emb|AW649001|AW649001 EST327455 tomato germinating seedlings, TA... 109 2e-28
emb|AW980440|AW980440 EST391593 GVN Medicago truncatula cDNA clo... 127 3e-28
emb|AW678754|AW678754 WS1_1_E06.b2_A002 Water-stressed 1 (WS1) S... 67 4e-28
emb|AW037664|AW037664 EST279267 tomato mixed elicitor, BTI Lycop... 126 5e-28
60 emb|AW707240|AW707240 sk22e06.y1 Gm-cl028 Glycine max cDNA clone... 111 7e-28
emb|AW694862|AW694862 NF080H12ST1F1103 Developing stem Medicago ... 125 9e-28

- emb|AW688241|AW688241 NF005B02ST1F1000 Developing stem Medicago ... 77 9e-28
emb|AV423709|AV423709 AV423709 Lotus japonicus young plants (two... 83 9e-28
emb|AI899562|AI899562 EST269005 tomato susceptible, Cornell Lyco... 124 2e-27
5 emb|AW201920|AW201920 sf08g07.y1 Gm-c1027 Glycine max cDNA clone... 105 4e-27
emb|A43603|A43603 Sequence 28 from Patent WO9507357. 122 6e-27
emb|AW931044|AW931044 EST356887 tomato fruit mature green, TAMU ... 122 6e-27
emb|AW433292|AW433292 sh55b06.y1 Gm-c1015 Glycine max cDNA clone... 105 7e-27
emb|AW310283|AW310283 sf33g09.x1 Gm-c1028 Glycine max cDNA clone... 121 2e-26
10 emb|AW692300|AW692300 NF054C11ST1F1000 Developing stem Medicago ... 77 1e-25
emb|AW185746|AW185746 se59b06.y1 Gm-c1019 Glycine max cDNA clone... 105 1e-25
emb|AI930829|AI930829 sc47g08.y1 Gm-c1015 Glycine max cDNA clone... 76 1e-25
emb|AW234064|AW234064 sf33g09.y1 Gm-c1028 Glycine max cDNA clone... 93 1e-25
emb|AW758971|AW758971 sl33a12.y1 Gm-c1027 Glycine max cDNA clone... 103 2e-25
emb|AW203699|AW203699 sf37c04.y1 Gm-c1028 Glycine max cDNA clone... 61 2e-25
15 emb|AI736700|AI736700 sb32d07.y1 Gm-c1012 Glycine max cDNA clone... 102 3e-25
emb|AW348589|AW348589 GM210002B22D1R Gm-r1021 Glycine max cDNA 3... 76 4e-25
emb|AW398957|AW398957 EST309457 L. pennellii trichome, Cornell U... 87 5e-25
emb|AW350656|AW350656 GM210008B20D6R Gm-r1021 Glycine max cDNA 3... 116 7e-25
20 emb|AA739757|AA739757 522 PtIFG2 Pinus taeda cDNA clone 8840M 3'... 115 1e-24
emb|AW773596|AW773596 EST332582 KV3 Medicago truncatula cDNA clo... 89 2e-24
emb|AW040857|AW040857 EST283721 tomato mixed elicitor, BTI Lycop... 113 5e-24
emb|AW756588|AW756588 sl24c08.y1 Gm-c1036 Glycine max cDNA clone... 75 5e-24
emb|AW695244|AW695244 NF093A09ST1F1068 Developing stem Medicago ... 111 2e-23
25 emb|AW256423|AW256423 EST304490 KV2 Medicago truncatula cDNA clo... 46 4e-23
emb|AW929518|AW929518 EST338306 tomato flower buds 8 mm to pre-a... 69 4e-23
emb|AI773875|AI773875 EST254975 tomato resistant, Cornell Lycopen... 87 1e-22
emb|AW684249|AW684249 NF014F01NR1F1000 Nodulated root Medicago t... 102 2e-22
emb|AW924370|AW924370 WS1_69_G04.b1_A002 Water-stressed 1 (WS1) ... 86 5e-22
30 emb|AW424380|AW424380 sh64b05.y1 Gm-c1015 Glycine max cDNA clone... 105 8e-22
emb|AW648348|AW648348 EST326802 tomato germinating seedlings, TA... 89 1e-21
emb|AW037585|AW037585 EST279043 tomato mixed elicitor, BTI Lycop... 55 1e-21
emb|AW983508|AW983508 HVSMEg0010N22f Hordeum vulgare pre-anthesi... 57 3e-21
emb|AW929899|AW929899 EST354169 tomato flower buds 8 mm to pre-a... 73 3e-21
35 emb|AW563695|AW563695 LG1_248_G02.g1_A002 Light Grown 1 (LG1) So... 70 6e-21
emb|AW598676|AW598676 sj94d11.y1 Gm-c1023 Glycine max cDNA clone... 71 9e-21
emb|AW696009|AW696009 NF100H07ST1F1063 Developing stem Medicago ... 58 1e-20
emb|AV409553|AV409553 AV409553 Lotus japonicus young plants (two... 100 3e-20
emb|AW219938|AW219938 EST302421 tomato root during/after fruit s... 48 4e-20
40 emb|AW623831|AW623831 EST321776 tomato flower buds 3-8 mm, Corne... 85 4e-20
emb|AW623819|AW623819 EST321764 tomato flower buds 3-8 mm, Corne... 85 4e-20
emb|AV407359|AV407359 AV407359 Lotus japonicus young plants (two... 84 4e-20
gb|BE058256|BE058256 sn13f01.y1 Gm-c1016 Glycine max cDNA clone ... 100 5e-20
emb|AW688046|AW688046 NF003G03ST1F1000 Developing stem Medicago ... 62 8e-20
45 emb|AW257541|AW257541 EST305678 KV2 Medicago truncatula cDNA clo... 58 1e-19
emb|AW040724|AW040724 EST283588 tomato mixed elicitor, BTI Lycop... 84 1e-19
emb|AW623981|AW623981 EST321926 tomato flower buds 3-8 mm, Corne... 84 1e-19
emb|AW219784|AW219784 EST302266 tomato root during/after fruit s... 73 4e-19
emb|AI494943|AI494943 sa92h11.y1 Gm-c1004 Glycine max cDNA clone... 75 5e-19
50 emb|AV418625|AV418625 AV418625 Lotus japonicus young plants (two... 83 5e-19
emb|AI726936|AI726936 BNLGHi6888 Six-day Cotton fiber Gossypium ... 67 7e-19
emb|AW037577|AW037577 EST279035 tomato mixed elicitor, BTI Lycop... 51 7e-19
emb|AW719494|AW719494 LjNEST5b12r Lotus japonicus nodule library... 96 8e-19
emb|AW621680|AW621680 EST312478 tomato root during/after fruit s... 61 1e-18
55 emb|AW219076|AW219076 EST301558 tomato root during/after fruit s... 72 1e-18
emb|AW219778|AW219778 EST302260 tomato root during/after fruit s... 72 1e-18
emb|AI779186|AI779186 EST260065 tomato susceptible, Cornell Lyco... 95 2e-18
emb|AW666093|AW666093 sk32b02.y1 Gm-c1028 Glycine max cDNA clone... 49 2e-18
emb|AW574204|AW574204 EST316795 GVN Medicago truncatula cDNA clo... 93 5e-18
60 emb|AV426308|AV426308 AV426308 Lotus japonicus young plants (two... 76 6e-18
emb|AW458625|AW458625 sh11e08.y1 Gm-c1016 Glycine max cDNA clone... 93 8e-18

emb|AW257391|AW257391 EST305528 KV2 Medicago truncatula cDNA clo... 93 8e-18
emb|AI899409|AI899409 EST268852 tomato ovary, TAMU Lycopersicon ... 48 8e-18
emb|AW720047|AW720047 LjNEST15g6r Lotus japonicus nodule library... 83 9e-18
Query= AC006580.8_at 13381_at /id_source genbank /description
5 gb|aad22369.1|ac006580_1 (ac006580) nam (no apical meristem)-like
protein [arabidopsis thaliana] /blast_score 1.00e-169 /ec_number
/family /chip nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006580|/ncgi
10 http://www.ncgr.org/cgi-bin/ff7ac006580
(828 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters
15 Searching.....done

Score E
Sequences producing significant alignments: (bits) Value
20

emb|AW684737|AW684737 NF021E06NR1F1000 Nodulated root Medicago t... 189 6e-56
emb|AW032396|AW032396 EST275935 tomato callus, TAMU Lycopersicon... 214 5e-55
emb|AW934046|AW934046 EST359889 tomato fruit mature green, TAMU ... 214 5e-55
emb|AW931430|AW931430 EST357273 tomato fruit mature green, TAMU ... 214 5e-55
25 emb|AF011555|AF011555 Lycopersicon esculentum jasmonic acid 2 (L... 214 5e-55
emb|AI896441|AI896441 EST265872 tomato callus, TAMU Lycopersicon... 206 2e-52
emb|AW756289|AW756289 sl18e05.y1 Gm-c1036 Glycine max cDNA clone... 157 8e-52
gb|BE034140|BE034140 MG05E02 MG Mesembryanthemum crystallinum cD... 196 7e-51
emb|AI488099|AI488099 EST246421 tomato ovary, TAMU Lycopersicon ... 200 7e-51
30 emb|AI488758|AI488758 EST247097 tomato ovary, TAMU Lycopersicon ... 200 1e-50
emb|AW220879|AW220879 EST297348 tomato fruit mature green, TAMU ... 200 1e-50
emb|AI487693|AI487693 EST246015 tomato ovary, TAMU Lycopersicon ... 200 1e-50
emb|AW775926|AW775926 EST334991 DSIL Medicago truncatula cDNA cl... 195 1e-50
emb|AW683672|AW683672 NF017D07LF1F1061 Developing leaf Medicago ... 165 4e-50
35 emb|AI487552|AI487552 EST245874 tomato ovary, TAMU Lycopersicon ... 193 5e-50
emb|AI488773|AI488773 EST247112 tomato ovary, TAMU Lycopersicon ... 193 5e-50
emb|AW032532|AW032532 EST276091 tomato callus, TAMU Lycopersicon... 193 5e-50
emb|AI490551|AI490551 EST249105 tomato ovary, TAMU Lycopersicon ... 193 5e-50
emb|AI898058|AI898058 EST267501 tomato ovary, TAMU Lycopersicon ... 193 5e-50
40 emb|AI898890|AI898890 EST268333 tomato ovary, TAMU Lycopersicon ... 193 5e-50
emb|AI488959|AI488959 EST247298 tomato ovary, TAMU Lycopersicon ... 193 5e-50
emb|AW035679|AW035679 EST281698 tomato callus, TAMU Lycopersicon... 191 2e-49
emb|AW443857|AW443857 EST308787 tomato mixed elicitor, BTI Lycop... 192 3e-49
emb|AI488673|AI488673 EST247012 tomato ovary, TAMU Lycopersicon ... 193 4e-49
45 emb|AI899016|AI899016 EST268459 tomato ovary, TAMU Lycopersicon ... 195 4e-49
emb|AW650556|AW650556 EST329010 tomato germinating seedlings, TA... 193 8e-49
gb|BE020071|BE020071 sm38f07.y1 Gm-c1028 Glycine max cDNA clone ... 193 2e-48
emb|AI771859|AI771859 EST252959 tomato ovary, TAMU Lycopersicon ... 193 2e-48
emb|AI487093|AI487093 EST245415 tomato ovary, TAMU Lycopersicon ... 193 2e-48
50 emb|AW032194|AW032194 EST275648 tomato callus, TAMU Lycopersicon... 193 2e-48
emb|AI897442|AI897442 EST266885 tomato ovary, TAMU Lycopersicon ... 193 2e-48
emb|AW035194|AW035194 EST280456 tomato callus, TAMU Lycopersicon... 193 2e-48
emb|AI897257|AI897257 EST266616 tomato ovary, TAMU Lycopersicon ... 193 2e-48
emb|AI490061|AI490061 EST248400 tomato ovary, TAMU Lycopersicon ... 192 2e-48
55 emb|AW040320|AW040320 EST283184 tomato mixed elicitor, BTI Lycop... 191 6e-48
emb|AV410710|AV410710 AV410710 Lotus japonicus young plants (two... 190 1e-47
emb|AW041100|AW041100 EST283964 tomato mixed elicitor, BTI Lycop... 190 1e-47
emb|AI484813|AI484813 EST243074 tomato ovary, TAMU Lycopersicon ... 183 4e-47
emb|AW650475|AW650475 EST328929 tomato germinating seedlings, TA... 187 1e-46
60 emb|AW668121|AW668121 GA_Ea0012N05 Gossypium arboreum 7-10.dpa ... 154 1e-46
emb|AI773440|AI773440 EST254540 tomato resistant, Cornell Lycop... 150 3e-46

	emb AI898263 AI898263 EST267706 tomato ovary, TAMU Lycopersicon ...	185	5e-46
	emb AW696936 AW696936 NF110E07ST1F1054 Developing stem Medicago ...	149	9e-46
	emb AI896058 AI896058 EST265501 tomato callus, TAMU Lycopersicon...	150	1e-45
	emb AI485389 AI485389 EST243710 tomato ovary, TAMU Lycopersicon ...	183	1e-45
5	emb AI895235 AI895235 EST264678 tomato callus, TAMU Lycopersicon...	150	2e-45
	emb AW932278 AW932278 EST358121 tomato fruit mature green, TAMU ...	150	2e-45
	emb AI897596 AI897596 EST267039 tomato ovary, TAMU Lycopersicon ...	183	2e-45
	emb AW034429 AW034429 EST278000 tomato callus, TAMU Lycopersicon...	146	2e-45
	emb AW443468 AW443468 EST308398 tomato mixed elicitor, BTI Lycop...	116	2e-45
10	emb AW442290 AW442290 EST311686 tomato fruit red ripe, TAMU Lyco...	147	3e-45
	emb AW442348 AW442348 EST311744 tomato fruit red ripe, TAMU Lyco...	150	3e-45
	emb AW625882 AW625882 EST319789 tomato radicle, 5 d post-imbibit...	150	3e-45
	emb AW775866 AW775866 EST334931 DSIL Medicago truncatula cDNA cl...	149	4e-45
	emb AW736371 AW736371 EST332290 KV3 Medicago truncatula cDNA clo...	149	4e-45
15	emb AI856667 AI856667 sb42d09.y1 Gm-c1014 Glycine max cDNA clone...	151	4e-45
	emb AW687506 AW687506 NF010C12RT1F1097 Developing root Medicago ...	149	4e-45
	emb AW686733 AW686733 NF041H04NR1F1000 Nodulated root Medicago t...	149	4e-45
	emb AW690801 AW690801 NF035B09ST1F1000 Developing stem Medicago ...	149	4e-45
	gb BE124309 BE124309 EST394434 DSIL Medicago truncatula cDNA clo...	149	5e-45
20	emb AW775409 AW775409 EST334474 DSIL Medicago truncatula cDNA cl...	149	5e-45
	emb AW559397 AW559397 EST314445 DSIR Medicago truncatula cDNA cl...	149	5e-45
	emb AW030038 AW030038 EST273293 tomato callus, TAMU Lycopersicon...	150	6e-45
	emb AW775964 AW775964 EST335029 DSIL Medicago truncatula cDNA cl...	149	1e-44
	emb AW185617 AW185617 se80b05.y1 Gm-c1023 Glycine max cDNA clone...	180	1e-44
25	emb AJ010830 TSP010830 Triticum sp. mRNA for GRAB2 protein.	133	3e-44
	emb A82386 A82386 Sequence 11 from Patent WO9856811.	133	3e-44
	emb AW092910 AW092910 EST286090 tomato mixed elicitor, BTI Lycop...	148	3e-44
	emb AI487779 AI487779 EST246101 tomato ovary, TAMU Lycopersicon ...	148	3e-44
	emb AW442068 AW442068 EST311464 tomato fruit red ripe, TAMU Lyco...	148	3e-44
30	emb AI773092 AI773092 EST254192 tomato resistant, Cornell Lycope...	148	3e-44
	emb AI489361 AI489361 EST247700 tomato ovary, TAMU Lycopersicon ...	148	4e-44
	emb AI488314 AI488314 EST246636 tomato ovary, TAMU Lycopersicon ...	148	5e-44
	emb AI489164 AI489164 EST247503 tomato ovary, TAMU Lycopersicon ...	176	5e-44
	emb AI898478 AI898478 EST267921 tomato ovary, TAMU Lycopersicon ...	176	5e-44
35	emb AW680754 AW680754 WS1_7_A09.b1_A002 Water-stressed 1 (WS1) S...	149	7e-44
	emb AI896316 AI896316 EST265759 tomato callus, TAMU Lycopersicon...	145	7e-44
	gb BE126167 BE126167 DG1_66_F07.b1_A002 Dark Grown 1 (DG1) Sorgh...	149	7e-44
	emb AW931009 AW931009 EST356852 tomato fruit mature green, TAMU ...	147	7e-44
	emb AW035978 AW035978 EST282837 tomato callus, TAMU Lycopersicon...	146	1e-43
40	emb AW932996 AW932996 EST358839 tomato fruit mature green, TAMU ...	146	1e-43
	emb AW278088 AW278088 sf39e10.y1 Gm-c1009 Glycine max cDNA clone...	149	2e-43
	emb AW203537 AW203537 sf35d02.y1 Gm-c1028 Glycine max cDNA clone...	143	2e-43
	emb AW220707 AW220707 EST297176 tomato fruit mature green, TAMU ...	148	3e-43
	emb A82380 A82380 Sequence 5 from Patent WO9856811.	175	4e-43
45	emb AJ010829 TSP010829 Triticum sp. mRNA for GRAB1 protein.	175	4e-43
	emb A82384 A82384 Sequence 9 from Patent WO9856811.	175	4e-43
	emb AW737167 AW737167 EST338594 tomato flower buds, anthesis, Co...	148	4e-43
	emb AW560823 AW560823 EST315871 DSIR Medicago truncatula cDNA cl...	146	6e-43
	emb AI486492 AI486492 EST244813 tomato ovary, TAMU Lycopersicon ...	144	9e-43
50	emb AI486833 AI486833 EST245155 tomato ovary, TAMU Lycopersicon ...	144	9e-43
	emb AW222093 AW222093 EST298904 tomato fruit red ripe, TAMU Lyco...	104	1e-42
	emb AW560904 AW560904 EST315952 DSIR Medicago truncatula cDNA cl...	146	2e-42
	emb AW223963 AW223963 EST300774 tomato fruit red ripe, TAMU Lyco...	147	2e-42
	emb A82382 A82382 Sequence 7 from Patent WO9856811.	131	2e-42
55	emb AW164307 AW164307 se70g05.y1 Gm-c1023 Glycine max cDNA clone...	143	5e-41
	emb AW560434 AW560434 EST315482 DSIR Medicago truncatula cDNA cl...	110	1e-40
	emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon...	146	1e-40
	emb AW306698 AW306698 sf47c01.y1 Gm-c1009 Glycine max cDNA clone...	151	1e-40
60	emb AI729055 AI729055 BNLGHi12472 Six-day Cotton fiber Gossypium...	135	1e-40

Query= AC006218.175_s_at 13818_s_at /id_source genbank /description

gb|aad15433.1| (ac006218) putative aspartate aminotransferase
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link /ncgi
 (1290 letters)

5

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

10

Score E
 Sequences producing significant alignments: (bits) Value

15 gb|BE052217|BE052217 GA_Ea0033E06f Gossypium arboreum 7-10 dpa ... 358 4e-98
 emb|AI941267|AI941267 sb86g03.y1 Gm-c1010 Glycine max cDNA clone... 317 1e-85
 emb|AW472288|AW472288 si23c10.y1 Gm-c1029 Glycine max cDNA clone... 297 2e-79
 emb|AW720283|AW720283 LjNEST20a9r Lotus japonicus nodule library... 295 4e-79
 emb|AW234168|AW234168 sf22a07.y1 Gm-c1028 Glycine max cDNA clone... 288 7e-77
 20 gb|BE021080|BE021080 sm55b08.y1 Gm-c1028 Glycine max cDNA clone ... 282 3e-75
 emb|AW509358|AW509358 si22a10.y1 Gm-c1029 Glycine max cDNA clone... 272 3e-72
 emb|AW622811|AW622811 EST306797 tomato flower buds 3-8 mm, Corne... 252 4e-66
 emb|AV390505|AV390505 AV390505 Chlamydomonas reinhardtii C9 Chla... 147 4e-58
 emb|AW234504|AW234504 sf15a07.y1 Gm-c1028 Glycine max cDNA clone... 225 7e-58
 emb|AI773174|AI773174 EST254274 tomato resistant, Cornell Lycopen... 218 9e-56
 25 emb|AI774300|AI774300 EST255316 tomato resistant, Cornell Lycopen... 210 1e-53
 gb|BE024350|BE024350 894002D06.y1 C. reinhardtii CC-1690, normal... 192 5e-48
 gb|BE056488|BE056488 894009G03.y1 C. reinhardtii CC-1690, normal... 189 3e-47
 emb|AW691828|AW691828 NF044F04ST1F1000 Developing stem Medicago ... 179 2e-44
 emb|AW719571|AW719571 LjNEST6g3r Lotus japonicus nodule library,... 175 6e-43
 30 emb|AW981392|AW981392 EST392545 DSIL Medicago truncatula cDNA cl... 162 4e-39
 emb|AW720570|AW720570 LjNEST8h1 lrc Lotus japonicus nodule librar... 156 4e-37
 gb|L46457|L46457 BNAF1543 Mustard flower buds Brassica rapa cDNA... 152 6e-36
 emb|AT000069|AT000069 AT000069 Apple young fruit cDNA library Ma... 118 9e-36
 emb|AW309618|AW309618 sf22a07.x1 Gm-c1028 Glycine max cDNA clone... 150 2e-35
 35 emb|AW830423|AW830423 sm26e11.y1 Gm-c1028 Glycine max cDNA clone... 140 2e-32
 emb|AW218448|AW218448 EST303631 tomato radicle, 5 d post-imbibit... 133 3e-30
 emb|AW428992|AW428992 EST306532 tomato flower buds 0-3 mm, Corne... 132 5e-30
 emb|AV390398|AV390398 AV390398 Chlamydomonas reinhardtii C9 Chla... 123 2e-27
 emb|AW830756|AW830756 sm29a08.y1 Gm-c1028 Glycine max cDNA clone... 114 2e-24
 40 emb|AV389740|AV389740 AV389740 Chlamydomonas reinhardtii C9 Chla... 113 3e-24
 emb|AV410690|AV410690 AV410690 Lotus japonicus young plants (two... 89 9e-17
 emb|AW217350|AW217350 EST296173 tomato flower buds 0-3 mm, Corne... 62 2e-15
 emb|AW477177|AW477177 ga42h10.y1 Moss EST library PPU Physcomitr... 66 7e-10
 emb|AW559640|AW559640 EST314752 DSIR Medicago truncatula cDNA cl... 60 5e-08
 45 emb|AW691076|AW691076 NF041A07ST1F1000 Developing stem Medicago ... 56 6e-07
 emb|AI773775|AI773775 EST254875 tomato resistant, Cornell Lycopen... 54 3e-06
 emb|AW727211|AW727211 GA_Ea0023N19 Gossypium arboreum 7-10 dpa ... 49 1e-04
 emb|AI729480|AI729480 BNLGHI13474 Six-day Cotton fiber Gossypium... 35 0.001
 emb|AI068927|AI068927 mgae0004dB02f Magnaporthe grisea Appressor... 38 0.003
 50 emb|AW043088|AW043088 ST29B11 Pine TriplEx shoot tip library Pin... 43 0.006
 emb|AL034356|LMFL7610 Leishmania major Friedlin chromosome 4 cos... 41 0.015
 emb|AW568631|AW568631 si60b11.y1 Gm-r1030 Glycine max cDNA clone... 40 0.055
 emb|AW690226|AW690226 NF030F01ST1F1000 Developing stem Medicago ... 32 0.057
 emb|Z12622|ASALLIN A.sativum mRNA encoding precursor alliinase. 39 0.10
 55 gb|S73324|S73324 alliinase [Allium sativum=garlics, bulbs, mRNA,... 39 0.10
 emb|AI068628|AI068628 mgae0003cD03f Magnaporthe grisea Appressor... 38 0.14
 gb|U34986|VRU34986 Vigna radiata 1-aminocyclopropane-1-carboxyli... 38 0.14
 emb|AB018355|AB018355 Vigna radiata gene for 1-aminocyclopropane... 38 0.14
 emb|AB000679|AB000679 Vigna radiata mRNA for 1-aminocyclopropane... 38 0.14
 60 emb|X74106|NTGRPR N.tabacum gene for glycine-rich protein. 26 0.18
 emb|AV414385|AV414385 AV414385 Lotus japonicus young plants (two... 38 0.19

	emb Z73261 SCYLR089C <i>S.cerevisiae</i> chromosome XII reading frame O...	38	0.19
	emb AB021908 AB021908 <i>Musa acuminata</i> MA-ACS3 mRNA for ACC syntha...	38	0.19
	emb AW737762 AW737762 EST339189 tomato flower buds, anthesis, Co...	38	0.19
	gb U53880 YSCL9449 <i>Saccharomyces cerevisiae</i> chromosome XII cosmi...	38	0.19
5	emb AV424265 AV424265 AV424265 <i>Lotus japonicus</i> young plants (two...	38	0.19
	emb AI055499 AI055499 coau0004C15 Cotton Boll Abscission Zone cD...	37	0.27
	emb AI440609 AI440609 sa68d05.y1 Gm-c1004 Glycine max cDNA clone...	37	0.27
	emb AI896625 AI896625 EST266068 tomato callus, TAMU Lycopersicon...	37	0.37
	emb AI896781 AI896781 EST266224 tomato callus, TAMU Lycopersicon...	37	0.37
10	emb AV391798 AV391798 AV391798 <i>Chlamydomonas reinhardtii</i> C9 Chla...	37	0.37
	emb AF119412 AF119412 <i>Lupinus albus</i> 1-aminocyclopropane-1-carbox...	37	0.37
	emb AW033411 AW033411 EST276982 tomato callus, TAMU Lycopersicon...	37	0.37
	emb AI054518 AI054518 coau0001D13 Cotton Boll Abscission Zone cD...	37	0.37
	emb AW032141 AW032141 EST275595 tomato callus, TAMU Lycopersicon...	37	0.37
15	emb Z26322 HVALAAT <i>H.vulgare</i> mRNA for alanine aminotransferase.	37	0.37
	gb BE126096 BE126096 DG1_65_F07.g1_A002 Dark Grown 1 (DG1) Sorgh...	37	0.37
	emb AW934295 AW934295 EST360138 tomato fruit mature green, TAMU ...	36	0.50
	emb AI896469 AI896469 EST265900 tomato callus, TAMU Lycopersicon...	36	0.50
	emb AF007214 AF007214 <i>Phalaenopsis</i> sp. SM9108 ACC synthase 3 (AC...	36	0.50
20	emb AJ277161 CPA277161 <i>Carica papaya</i> partial paccs1B gene for 1-...	35	0.60
	emb Z69909 SPAC19G10 <i>S.pombe</i> chromosome I cosmid c19G10.	36	0.69
	gb U17229 PHU17229 <i>Pelargonium hortorum</i> clone pGAC-1 1-aminocycl...	36	0.69
	emb AL096788 SPBC582 <i>S.pombe</i> chromosome II cosmid c582.	36	0.69
	gb U17228 PHU17228 <i>Pelargonium hortorum</i> clone pGAC-1G 1-aminocyc...	36	0.69
25	emb AW703931 AW703931 sk25h05.y1 Gm-c1028 Glycine max cDNA clone...	36	0.69
	emb AF016460 AF016460 <i>Pisum sativum</i> 1-aminocyclopropane-1-carbox...	36	0.69
	emb AF016458 AF016458 <i>Pisum sativum</i> 1-aminocyclopropane-1-carbox...	36	0.69
	emb AF119414 AF119414 <i>Lupinus albus</i> 1-aminocyclopropane-1-carbox...	35	0.95
	emb AF074929 AF074929 <i>Sinapis arvensis</i> 1-aminocyclopropane-1-car...	35	0.95
30	emb AW685223 AW685223 NF027D03NR1F1000 Nodulated root <i>Medicago t...</i>	35	0.95
	emb AF074931 AF074931 <i>Sinapis arvensis</i> 1-aminocyclopropane-1-car...	35	0.95
	emb Z73199 SCYLR027C <i>S.cerevisiae</i> chromosome XII reading frame O...	35	0.95
	emb AF119410 AF119410 <i>Lupinus albus</i> 1-aminocyclopropane-1-carbox...	35	1.3
	emb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycine max cDNA clone...	35	1.3
35	emb AW033989 AW033989 EST277651 tomato callus, TAMU Lycopersicon...	35	1.3
	emb AF170705 AF170705 <i>Mangifera indica</i> 1-aminocyclopropane-1-car...	35	1.3
	emb AI460900 AI460900 sa70f07.y1 Gm-c1004 Glycine max cDNA clone...	35	1.3
	emb AW032260 AW032260 EST275714 tomato callus, TAMU Lycopersicon...	35	1.3
	emb AF119413 AF119413 <i>Lupinus albus</i> 1-aminocyclopropane-1-carbox...	35	1.8
40	emb X72676 BJMACC <i>B. juncea</i> mRNA for 1-Aminocyclopropane-1-carbo...	35	1.8
	emb AF074930 AF074930 <i>Sinapis arvensis</i> 1-aminocyclopropane-1-car...	35	1.8
	gb L00673 TRBANTA <i>Trypanosoma cruzi</i> antigen tyrosine aminotransf...	31	1.9
	emb AW650504 AW650504 EST328958 tomato germinating seedlings, TA...	34	2.5
	gb U35779 TAU35779 <i>Triticum aestivum</i> 1-aminocyclopropane-1-carbo...	34	2.5
45	emb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheared DNA <i>Trypanosom...</i>	34	2.5
	emb AF119411 AF119411 <i>Lupinus albus</i> 1-aminocyclopropane-1-carbox...	34	2.5
	gb U31975 CRU31975 <i>Chlamydomonas reinhardtii</i> alanine aminotransf...	34	2.5
	emb X87372 LESODCC <i>L.esculentum</i> SodCc;Le;2 gene.	34	3.4
	emb AW651589 AW651589 EST330043 tomato germinating seedlings, TA...	34	3.4
50	emb AW216510 AW216510 EST295224 tomato callus, TAMU Lycopersicon...	34	3.4
	emb Z11562 VRACCSYN <i>V.radiata</i> mRNA for 1-aminocyclopropane-1-car...	34	3.4
	emb Z11613 VRACCSYNM <i>V.radiata</i> mRNA for ACC synthase.	34	3.4

Query= AL049480.183_s_at 13880_s_at /id_source genbank /description
 55 emb|cab39611.1| (al049480) possible apospory-associated like protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link /ncgi
 (990 letters)

60 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	
5	Sequences producing significant alignments:	(bits)	Value	
	emb Z36544 PCAPSPA1 P.ciliare (Higgins) apospory associated mRN...	150	4e-85	
	gb U13148 PCU13148 Pennisetum ciliare possible apospory-associat...	150	4e-85	
	dbj D37938 PENPSBCA Pennisetum ciliare apomixis-associated mRNA.	150	4e-85	
10	emb AW985256 AW985256 NXNV_135_A07_F Nsf Xylem Normal wood Verti...	139	1e-58	
	emb AI731493 AI731493 BNLGHI9967 Six-day Cotton fiber Gossypium ...	167	1e-58	
	emb AI729163 AI729163 BNLGHI12827 Six-day Cotton fiber Gossypium...	170	1e-58	
	emb AW257538 AW257538 EST305675 KV2 Medicago truncatula cDNA clo...	140	4e-58	
	emb AW398709 AW398709 EST309209 L. pennellii trichome, Cornell U...	173	2e-57	
15	emb AW625795 AW625795 EST319702 tomato radicle, 5 d post-imbibit...	171	4e-57	
	emb AW617782 AW617782 EST324181 L. hirsutum trichome, Cornell Un...	172	1e-56	
	emb AW399743 AW399743 EST310243 L. pennellii trichome, Cornell U...	173	1e-56	
	emb AI489136 AI489136 EST247475 tomato ovary, TAMU Lycopersicon ...	133	1e-55	
	emb AW929457 AW929457 EST338245 tomato flower buds 8 mm to pre-a...	171	6e-55	
20	emb AI771804 AI771804 EST252904 tomato ovary, TAMU Lycopersicon ...	133	7e-55	
	emb AW649922 AW649922 EST328376 tomato germinating seedlings, TA...	162	1e-54	
	emb AW257536 AW257536 EST305673 KV2 Medicago truncatula cDNA clo...	138	9e-54	
	emb AV422847 AV422847 AV422847 Lotus japonicus young plants (two...	101	1e-50	
	emb AW289757 AW289757 NXNV005C01F Nsf Xylem Normal wood Vertical...	155	1e-49	
25	emb AI896074 AI896074 EST265517 tomato callus, TAMU Lycopersicon...	171	4e-49	
	emb AW064926 AW064926 ST37E07 Pine TriplEx shoot tip library Pin...	150	6e-48	
	emb AW311433 AW311433 sg39c02.y1 Gm-c1025 Glycine max cDNA clone...	85	1e-47	
	emb AW745200 AW745200 LG1_387_C06.b1_A002 Light Grown 1 (LG1) So...	155	6e-47	
	emb AW011598 AW011598 ST22F11 Pine TriplEx shoot tip library Pin...	153	2e-45	
30	emb AW678250 AW678250 WS1_14_G02.b1_A002 Water-stressed 1 (WS1) ...	155	2e-44	
	emb AV408421 AV408421 AV408421 Lotus japonicus young plants (two...	101	3e-44	
	emb AW216409 AW216409 EST295153 tomato callus, TAMU Lycopersicon...	171	8e-42	
	emb AW290828 AW290828 NXNV047D04F Nsf Xylem Normal wood Vertical...	156	9e-42	
	gb L38079 L38079 BNAF0477E Mustard flower buds Brassica rapa cDN...	116	1e-41	
35	emb AI896567 AI896567 EST266010 tomato callus, TAMU Lycopersicon...	110	2e-41	
	emb AW756192 AW756192 sl17c03.y1 Gm-c1036 Glycine max cDNA clone...	161	8e-39	
	emb AW707185 AW707185 sk10h04.y1 Gm-c1023 Glycine max cDNA clone...	82	9e-38	
	emb AW285821 AW285821 LG1_237_D02.b1_A002 Light Grown 1 (LG1) So...	154	1e-36	
	emb AV422428 AV422428 AV422428 Lotus japonicus young plants (two...	94	1e-36	
40	gb L46551 L46551 BNAF1871 Mustard flower buds Brassica rapa cDNA...	153	2e-36	
	emb AA660918 AA660918 00815 MtRHE Medicago truncatula cDNA 5' si...	92	1e-34	
	emb AW931737 AW931737 EST357580 tomato fruit mature green, TAMU ...	112	1e-34	
	emb AW010913 AW010913 ST12H09 Pine TriplEx shoot tip library Pin...	147	2e-34	
	emb AW306296 AW306296 se48h02.y1 Gm-c1017 Glycine max cDNA clone...	82	2e-32	
45	emb AW226128 AW226128 ST77F07 Pine TriplEx shoot tip library Pin...	136	2e-31	
	emb AI162924 AI162924 A027P14U Hybrid aspen plasmid library Popu...	132	5e-30	
	emb AW692441 AW692441 NF051E02ST1F1000 Developing stem Medicago ...	128	7e-29	
	emb AW266636 AW266636 L0-1345T3 Ice plant Lambda Uni-Zap XR expr...	125	5e-28	
	emb AW730079 AW730079 GA_Ea0027L09 Gossypium arboreum 7-10 dpa ...	112	2e-27	
50	emb AF195243 AF195243 Chlamydomonas reinhardtii apospory-associa...	71	3e-27	
	emb AW038730 AW038730 EST280591 tomato mixed elicitor, BTI Lycop...	72	4e-27	
	emb AW668439 AW668439 GA_Ea0013P01 Gossypium arboreum 7-10 dpa ...	117	1e-25	
	gb BE060242 BE060242 HVSMEg0011K23f Hordeum vulgare pre-anthesis...	69	3e-24	
	emb AV392393 AV392393 AV392393 Chlamydomonas reinhardtii C9 Chla...	59	8e-24	
55	gb H75140 H75140 18 PtIFG1 Pinus taeda cDNA clone 0149e, mRNA se...	106	2e-23	
	emb AW226319 AW226319 ST81A06 Pine TriplEx shoot tip library Pin...	106	3e-22	
	emb AW678374 AW678374 WS1_15_D11.b1_A002 Water-stressed 1 (WS1) ...	70	5e-22	
	emb AW678403 AW678403 WS1_15_D11.g1_A002 Water-stressed 1 (WS1) ...	70	5e-22	
	emb AW678308 AW678308 WS1_14_G02.g1_A002 Water-stressed 1 (WS1) ...	62	3e-21	
60	emb AQ946977 AQ946977 Sheared DNA-47C11.TF Sheared DNA Trypanoso...	92	8e-18	
	emb AW707360 AW707360 832006H03.y1 C. reinhardtii CC-125 nutrien...	71	5e-17	

emb|AW697995|AW697995 NXNV_079_C06_F Nsf Xylem Normal wood Verti... 87 2e-16
 emb|AV386805|AV386805 AV386805 Chlamydomonas reinhardtii C9 Chla... 71 8e-16
 emb|AV427771|AV427771 AV427771 Lotus japonicus young plants (two... 78 8e-14
 5 emb|AW132277|AW132277 sd98h11.y1 Gm-c1013 Glycine max cDNA clone... 73 1e-13
 gb|BE020023|BE020023 sm41b06.y1 Gm-c1028 Glycine max cDNA clone ... 73 1e-13
 emb|AW759481|AW759481 sl42b05.y1 Gm-c1027 Glycine max cDNA clone... 73 1e-13
 gb|BE021423|BE021423 sm48h06.y1 Gm-c1028 Glycine max cDNA clone ... 73 1e-13
 emb|AW776929|AW776929 EST335994 DSIL Medicago truncatula cDNA cl... 77 1e-13
 emb|AU090159|AU090159 AU090159 Hordeum vulgare subsp. vulgare Up... 73 2e-13
 10 emb|AW428681|AW428681 Ljirnp22-758-d3 Ljirnp Lambda HybriZap ... 68 3e-13
 emb|AA556516|AA556516 371 Loblolly pine C Pinus taeda cDNA clone... 76 5e-13
 emb|AW428777|AW428777 Ljirnp23-872-f2 Ljirnp Lambda HybriZap ... 67 1e-12
 emb|AV391480|AV391480 AV391480 Chlamydomonas reinhardtii C9 Chla... 71 2e-12
 emb|AV387347|AV387347 AV387347 Chlamydomonas reinhardtii C9 Chla... 71 2e-12
 15 emb|AV397825|AV397825 AV397825 Chlamydomonas reinhardtii C9 Chla... 71 2e-12
 emb|AW187436|AW187436 BNLGHi5212 Six-day Cotton fiber Gossypium ... 74 2e-12
 emb|AW569198|AW569198 si64a08.y1 Gm-r1030 Glycine max cDNA clone... 68 3e-12
 emb|AV414298|AV414298 AV414298 Lotus japonicus young plants (two... 68 7e-12
 emb|AV389349|AV389349 AV389349 Chlamydomonas reinhardtii C9 Chla... 62 1e-11
 20 emb|AV427840|AV427840 AV427840 Lotus japonicus young plants (two... 71 1e-11
 emb|AV391742|AV391742 AV391742 Chlamydomonas reinhardtii C9 Chla... 55 4e-11
 emb|AW620239|AW620239 si93e10.y1 Gm-c1031 Glycine max cDNA clone... 66 5e-10
 emb|AV424492|AV424492 AV424492 Lotus japonicus young plants (two... 63 3e-09
 emb|AW981390|AW981390 EST392543 DSIL Medicago truncatula cDNA cl... 61 7e-09
 25 emb|AW040546|AW040546 EST283326 tomato mixed elicitor, BTI Lycop... 43 1e-08
 emb|AW624837|AW624837 EST313654 tomato radicle, 5 d post-imbibit... 43 1e-08
 emb|AI491050|AI491050 EST241759 tomato shoot, Cornell Lycopersic... 43 1e-08
 emb|AW096575|AW096575 EST289755 tomato mixed elicitor, BTI Lycop... 43 1e-08
 emb|AW217734|AW217734 EST296448 tomato flower buds 8 mm to pre-a... 43 1e-08
 30 emb|AI778221|AI778221 EST259100 tomato susceptible, Cornell Lyco... 43 1e-08
 emb|AW219376|AW219376 EST301954 tomato root during/after fruit s... 43 1e-08
 emb|AW399557|AW399557 EST310045 L. pennellii trichome, Cornell U... 43 1e-08
 emb|AW755022|AW755022 PC09G01 Pine TriplEx pollen cone library P... 60 2e-08
 emb|AW255147|AW255147 ML144 peppermint glandular trichome Menta... 43 4e-08
 35 emb|AW040573|AW040573 EST283353 tomato mixed elicitor, BTI Lycop... 41 4e-08
 emb|AW933183|AW933183 EST359026 tomato fruit mature green, TAMU ... 59 5e-08
 emb|AW399558|AW399558 EST310046 L. pennellii trichome, Cornell U... 42 7e-08
 emb|AW266367|AW266367 L30-3121T3 Ice plant Lambda Uni-Zap XR exp... 56 6e-07
 emb|AI896247|AI896247 EST265690 tomato callus, TAMU Lycopersicon... 55 1e-06
 40 gb|BE059001|BE059001 sn23g06.y1 Gm-c1016 Glycine max cDNA clone ... 54 2e-06
 emb|AW132969|AW132969 se12g02.y1 Gm-c1013 Glycine max cDNA clone... 53 4e-06
 emb|AW704585|AW704585 sk54a04.y1 Gm-c1019 Glycine max cDNA clone... 52 5e-06
 emb|AV388833|AV388833 AV388833 Chlamydomonas reinhardtii C9 Chla... 52 5e-06
 emb|AW729558|AW729558 GA_Ea0025G01 Gossypium arboreum 7-10 dpa ... 51 2e-05
 45 emb|AW681073|AW681073 WS1_8_H01.b1_A002 Water-stressed 1 (WS1) S... 50 4e-05

Query= AL022373.295_at 14278_at /id_source genbank /description
 emb|caa18503.1| (al022373) hypothetical protein [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link
 50 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022373|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022373|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022373|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?al022373>
 (1518 letters)

55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

60 Score E
 Sequences producing significant alignments: (bits) Value

- gb|BE052481|BE052481 GA__Ea0034B15f *Gossypium arboreum* 7-10 dpa ... 248 8e-65
emb|AW933316|AW933316 EST359159 tomato fruit mature green, TAMU ... 127 2e-28
emb|AI897506|AI897506 EST266949 tomato ovary, TAMU Lycopersicon ... 120 3e-26
5 emb|AI055630|AI055630 coau0004J11 Cotton Boll Abscission Zone cD... 113 4e-24
emb|AW032891|AW032891 EST276450 tomato callus, TAMU Lycopersicon... 103 4e-21
emb|AV427652|AV427652 AV427652 *Lotus japonicus* young plants (two... 88 2e-16
emb|AW307385|AW307385 sf56c11.y1 Gm-c1009 *Glycine max* cDNA clone... 72 1e-11
emb|AW726477|AW726477 GA__Ea0021M14 *Gossypium arboreum* 7-10 dpa ... 60 5e-10
10 emb|AW747181|AW747181 WS1_66_B09.b1_A002 Water-stressed 1 (WS1) ... 59 2e-09
emb|AW091888|AW091888 EST285068 tomato mixed elicitor, BTI Lycop... 53 5e-08
emb|AW306935|AW306935 sf50f05.y1 Gm-c1009 *Glycine max* cDNA clone... 58 1e-07
emb|AW216365|AW216365 EST295109 tomato callus, TAMU Lycopersicon... 58 1e-07
emb|AW306722|AW306722 sf47e06.y1 Gm-c1009 *Glycine max* cDNA clone... 58 1e-07
15 emb|AW221657|AW221657 EST298468 tomato fruit red ripe, TAMU Lyco... 58 2e-07
emb|AW574131|AW574131 EST316722 GVN *Medicago truncatula* cDNA clo... 52 1e-05
emb|AW222358|AW222358 EST299169 tomato fruit red ripe, TAMU Lyco... 43 0.005
emb|AW738043|AW738043 EST339470 tomato flower buds, anthesis, Co... 43 0.005
emb|AW774865|AW774865 EST334016 KV3 *Medicago truncatula* cDNA clo... 43 0.007
20 emb|AW832220|AW832220 sm21a01.y1 Gm-c1027 *Glycine max* cDNA clone... 38 0.011
emb|AW931008|AW931008 EST356851 tomato fruit mature green, TAMU ... 39 0.089
emb|AW396940|AW396940 sg65b05.y1 Gm-c1007 *Glycine max* cDNA clone... 39 0.089
emb|AQ324712|AQ324712 mgxb0019H15r CUGI Rice Blast BAC Library P... 37 0.12
gb|M96818|EUPTBPA *Euplotes crassus* macronuclear 51 kDa telomere-... 39 0.12
25 emb|AV428867|AV428867 AV428867 *Lotus japonicus* young plants (two... 36 0.60
gb|BE122206|BE122206 894018B07.x1 *C. reinhardtii* CC-1690, normal... 36 0.83
emb|AW757802|AW757802 874003G04.x1 *C. reinhardtii* CC-1690, Lambd... 36 0.83
emb|AW720369|AW720369 LjNEST21g3r *Lotus japonicus* nodule library... 36 0.83
emb|Z75009|SCYOR101W *S.cerevisiae* chromosome XV reading frame OR... 35 1.6
30 gb|U32307|SCU32307 *Saccharomyces cerevisiae* oligosaccharyltransf... 35 1.6
emb|X94335|SC130KBXV *S.cerevisiae* 130kb DNA fragment from chromo... 35 1.6
emb|Z75010|SCYOR102W *S.cerevisiae* chromosome XV reading frame OR... 35 1.6
emb|AW573717|AW573717 EST316308 GVN *Medicago truncatula* cDNA clo... 35 2.1
emb|AL049769|SPBC9B6 *S.pombe* chromosome II cosmid c9B6. 34 2.9
35 emb|AW395612|AW395612 sg73b12.y1 Gm-c1007 *Glycine max* cDNA clone... 34 4.0
emb|Z69380|SPAC4H3 *S.pombe* chromosome I cosmid c4H3. 34 4.0
emb|AW688677|AW688677 NF010D01ST1F1000 Developing stem *Medicago* ... 34 4.0
emb|AV425510|AV425510 AV425510 *Lotus japonicus* young plants (two... 33 5.6
emb|AV424161|AV424161 AV424161 *Lotus japonicus* young plants (two... 33 5.6
40 emb|AL354513|LMFL6783 *Leishmania major* Friedlin cosmid L6783, PR... 33 5.6
emb|AQ940380|AQ940380 Sheared DNA-33M12.TF Sheared DNA Trypanoso... 33 5.6
emb|AW703257|AW703257 TgESTzz82h11.y1 TgRH*-Tachyzoite cDNA Toxo... 33 5.6
emb|AC004688|AC004688 *Plasmodium falciparum* chromosome 12 clone ... 33 5.6
emb|AV427411|AV427411 AV427411 *Lotus japonicus* young plants (two... 33 5.6
45 emb|A86068|A86068 Sequence 727 from Patent EP0866129. 33 5.6
emb|AW690594|AW690594 NF031E09ST1F1000 Developing stem *Medicago* ... 33 5.6
emb|AC004709|AC004709 *Plasmodium falciparum* chromosome 12, *** S... 33 5.6
emb|AV423586|AV423586 AV423586 *Lotus japonicus* young plants (two... 33 5.6
emb|AV426453|AV426453 AV426453 *Lotus japonicus* young plants (two... 33 5.6
50 gb|BE055549|BE055549 GA__Ea0034M01f *Gossypium arboreum* 7-10 dpa ... 33 5.6
gb|U16653|YLU16653 *Yarrowia lipolytica* Pay2p (PAY2) gene, comple... 33 5.6
emb|AW719319|AW719319 LjNEST2f7r *Lotus japonicus* nodule library,... 33 5.6
emb|AW696984|AW696984 NF111A10ST1F1072 Developing stem *Medicago* ... 33 7.6
gb|L07391|NEUNIT6X *Neurospora crassa* nitrite reductase (nit-6) g... 33 7.6
55 emb|AQ645907|AQ645907 RPCI93-DpnII-28N21.TV RPCI93-DpnII Trypano... 33 7.6

Query= AC005956.54_at 14320_at /id_source genbank /description
gb|aad23719.1|ac005956_8 (ac005956) putative ring zinc finger protein
[arabidopsis thaliana] /blast_score 1.00e-110 /ec_number /family
60 /chip nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-

post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005956|/ncgi
 http://www.ncgr.org/cgi-bin/ff?ac005956
 (711 letters)

5 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

10	Score	E	
	Sequences producing significant alignments:		(bits) Value
	emb AI895373 AI895373	EST264816	tomato callus, TAMU Lycopersicon... 108 6e-32
	emb AW032769 AW032769	EST276328	tomato callus, TAMU Lycopersicon... 108 6e-32
15	emb AI731540 AI731540	BNLGHi10032	Six-day Cotton fiber Gossypium... 82 2e-21
	emb AW775221 AW775221	EST331943	GVN Medicago truncatula cDNA clo... 72 2e-19
	gb BE124796 BE124796	EST393831	GVN Medicago truncatula cDNA clon... 72 2e-19
	emb AW399006 AW399006	EST309506	L. pennellii trichome, Cornell U... 77 1e-17
	emb AW442210 AW442210	EST311606	tomato fruit red ripe, TAMU Lyco... 75 2e-17
20	emb AW703663 AW703663	sk11g09.y1	Gm-cl023 Glycine max cDNA clone... 69 2e-16
	emb AI727683 AI727683	BNLGHi8604	Six-day Cotton fiber Gossypium ... 79 3e-14
	emb AI729941 AI729941	BNLGHi5757	Six-day Cotton fiber Gossypium ... 79 3e-14
	emb AW329822 AW329822	N201096e	rootphos(-) Medicago truncatula c... 72 5e-14
	emb AI727293 AI727293	BNLGHi7657	Six-day Cotton fiber Gossypium ... 78 5e-14
25	emb AF150724 AF150724	AF150724	Gossypium hirsutum 24 days postan... 78 5e-14
	emb AW219270 AW219270	EST301752	tomato root during/after fruit s... 74 7e-14
	emb AI730749 AI730749	BNLGHi7802	Six-day Cotton fiber Gossypium ... 78 1e-13
	emb AW219137 AW219137	EST301619	tomato root during/after fruit s... 75 1e-13
	gb BE033932 BE033932	MG02C06	MG Mesembryanthemum crystallinum cD... 77 1e-13
30	emb AW508608 AW508608	si34c01.y1	Gm-r1030 Glycine max cDNA clone... 64 2e-13
	emb AW220356 AW220356	EST302839	tomato root during/after fruit s... 77 2e-13
	emb AW267973 AW267973	EST306195	DSIR Medicago truncatula cDNA cl... 75 2e-13
	emb AV413409 AV413409	AV413409	Lotus japonicus young plants (two... 76 3e-13
	emb AW931758 AW931758	EST357601	tomato fruit mature green, TAMU ... 75 5e-13
35	emb AW728679 AW728679	GA_Ea0017M02	Gossypium arboreum 7-10 dpa ... 75 5e-13
	emb AI443724 AI443724	sa45b08.y1	Gm-c1004 Glycine max cDNA clone... 75 5e-13
	emb AI443646 AI443646	sa42f12.y1	Gm-c1004 Glycine max cDNA clone... 75 5e-13
	emb AW682867 AW682867	NF001B05LF1F1044	Developing leaf Medicago ... 75 6e-13
	gb BE059421 BE059421	sn30h03.y1	Gm-c1016 Glycine max cDNA clone ... 75 6e-13
40	emb AW348175 AW348175	GM210001A21E9R	Gm-r1021 Glycine max cDNA 3... 75 6e-13
	emb AW279542 AW279542	sf90h11.y1	Gm-c1019 Glycine max cDNA clone... 75 6e-13
	emb AW277724 AW277724	sf85g08.y1	Gm-c1019 Glycine max cDNA clone... 74 9e-13
	emb AV416001 AV416001	AV416001	Lotus japonicus young plants (two... 74 9e-13
	emb AW223952 AW223952	EST300763	tomato fruit red ripe, TAMU Lyco... 73 2e-12
45	emb AW622165 AW622165	EST312963	tomato root during/after fruit s... 73 2e-12
	emb AW747694 AW747694	WS1_75_E01.g1_A002	Water-stressed 1 (WS1) ... 73 2e-12
	emb AW185181 AW185181	se88a05.y1	Gm-cl023 Glycine max cDNA clone... 73 2e-12
	emb AW223330 AW223330	EST300141	tomato fruit red ripe, TAMU Lyco... 73 2e-12
	emb AW597455 AW597455	sj85c04.y1	Gm-c1034 Glycine max cDNA clone... 69 2e-12
50	emb AZ044879 AZ044879	Gm_UMb001_030_J12R	UMN Soybean BAC Library... 73 3e-12
	emb AW681172 AW681172	WS1_9_C04.g1_A002	Water-stressed 1 (WS1) S... 73 3e-12
	emb AW680957 AW680957	WS1_9_C04.b1_A002	Water-stressed 1 (WS1) S... 73 3e-12
	emb AW622674 AW622674	EST313474	tomato root during/after fruit s... 72 4e-12
	emb AW622457 AW622457	EST313245	tomato root during/after fruit s... 72 4e-12
55	emb AW568305 AW568305	si58a10.y1	Gm-r1030 Glycine max cDNA clone... 72 4e-12
	emb AW443687 AW443687	EST308617	tomato mixed elicitor, BTI Lycop... 72 6e-12
	emb AV412576 AV412576	AV412576	Lotus japonicus young plants (two... 72 6e-12
	emb AW720382 AW720382	LjNEST22a5r	Lotus japonicus nodule library... 72 6e-12
	emb AW351001 AW351001	GM210010B20A4R	Gm-r1021 Glycine max cDNA 3... 72 6e-12
60	emb AW267780 AW267780	EST305908	DSIR Medicago truncatula cDNA cl... 71 8e-12
	emb AV422284 AV422284	AV422284	Lotus japonicus young plants (two... 56 9e-12

- gb|BE052202|BE052202 GA__Ea0034A22f *Gossypium arboreum* 7-10 dpa ... 71 1e-11
 emb|AI782281|AI782281 EST263160 tomato susceptible, Cornell Lyco... 71 1e-11
 gb|BE053763|BE053763 GA__Ea0032N22f *Gossypium arboreum* 7-10 dpa ... 71 1e-11
 emb|AW730444|AW730444 GA__Ea0026G01 *Gossypium arboreum* 7-10 dpa ... 71 1e-11
 5 gb|BE054849|BE054849 GA__Ea0033N22f *Gossypium arboreum* 7-10 dpa ... 71 1e-11
 emb|AA739669|AA739669 434 PUF2 Pinus taeda cDNA clone 8721M 3'... 71 1e-11
 gb|BE052726|BE052726 GA__Ea0007E10f *Gossypium arboreum* 7-10 dpa ... 71 1e-11
 emb|AW728356|AW728356 GA__Ea0016H03 *Gossypium arboreum* 7-10 dpa ... 71 1e-11
 emb|AW727187|AW727187 GA__Ea0023M11 *Gossypium arboreum* 7-10 dpa ... 71 1e-11
 10 emb|AI484163|AI484163 EST248970 tomato resistant, Cornell Lycope... 69 1e-11
 emb|AW981615|AW981615 PC14F10 Pine TriplEx pollen cone library P... 70 2e-11
 emb|AI727213|AI727213 BNLGHi7517 Six-day Cotton fiber *Gossypium* ... 70 2e-11
 emb|AW218481|AW218481 EST303664 tomato radicle, 5 d post-imbibit... 70 2e-11
 gb|BE124891|BE124891 EST393926 GVN *Medicago truncatula* cDNA clon... 70 2e-11
 15 emb|AI731895|AI731895 BNLGHi11234 Six-day Cotton fiber *Gossypium*... 70 2e-11
 emb|AW459552|AW459552 sh44b12.y1 Gm-c1017 *Glycine max* cDNA clone... 70 2e-11
 emb|AI897158|AI897158 EST266601 tomato ovary, TAMU *Lycopersicon* ... 70 2e-11
 emb|AW219915|AW219915 EST302398 tomato root during/after fruit s... 70 2e-11
 emb|AW100926|AW100926 sd63c08.y1 Gm-c1008 *Glycine max* cDNA clone... 70 2e-11
 20 gb|BE055048|BE055048 GA__Ea0001G22f *Gossypium arboreum* 7-10 dpa ... 70 2e-11
 emb|AW667875|AW667875 GA__Ea0011A20 *Gossypium arboreum* 7-10 dpa ... 70 2e-11
 emb|AI442790|AI442790 sa26e11.x1 Gm-c1004 *Glycine max* cDNA clone... 70 2e-11
 emb|AW559695|AW559695 EST314687 DSIR *Medicago truncatula* cDNA cl... 70 2e-11
 emb|AW441213|AW441213 EST310609 tomato fruit red ripe, TAMU Lyco... 70 2e-11
 25 emb|AW219914|AW219914 EST302397 tomato root during/after fruit s... 70 2e-11
 emb|AW108574|AW108574 gate0001G22f *Gossypium arboreum* 7-10 dpa f... 70 2e-11
 emb|AI725540|AI725540 BNLGHi12062 Six-day Cotton fiber *Gossypium*... 70 2e-11
 emb|AI162536|AI162536 A019P13U Hybrid aspen plasmid library Popu... 70 2e-11
 emb|AV422720|AV422720 AV422720 *Lotus japonicus* young plants (two... 69 3e-11
 30 emb|Y14573|HVCH4H *Hordeum vulgare* DNA for chromosome 4H. 69 3e-11
 emb|AW348721|AW348721 GM210003A22A2R Gm-r1021 *Glycine max* cDNA 3... 69 3e-11
 emb|AI900335|AI900335 sc04c07.y1 Gm-c1012 *Glycine max* cDNA clone... 69 3e-11
 emb|AW746279|AW746279 WS1_40_F11.g1_A002 Water-stressed 1 (WS1) ... 69 4e-11
 emb|AW981608|AW981608 PC14F03 Pine TriplEx pollen cone library P... 69 4e-11
 35 emb|AW685535|AW685535 NF028H02NR1F1000 Nodulated root *Medicago t...* 69 4e-11
 emb|AI726225|AI726225 BNLGHi5312 Six-day Cotton fiber *Gossypium* ... 69 4e-11
 emb|AW980916|AW980916 EST392069 GVN *Medicago truncatula* cDNA clo... 68 5e-11
 emb|AI441828|AI441828 sa47h04.y1 Gm-c1004 *Glycine max* cDNA clone... 68 5e-11
 emb|AI897713|AI897713 EST267156 tomato ovary, TAMU *Lycopersicon* ... 68 7e-11
 40 emb|AI485408|AI485408 EST243729 tomato ovary, TAMU *Lycopersicon* ... 68 7e-11
 emb|AI483478|AI483478 EST249299 tomato ovary, TAMU *Lycopersicon* ... 68 7e-11
 emb|AW031045|AW031045 EST274352 tomato callus, TAMU *Lycopersicon*... 68 7e-11
 emb|AI483537|AI483537 EST249386 tomato ovary, TAMU *Lycopersicon* ... 68 7e-11
 gb|BE034706|BE034706 ML03C10 ML *Mesembryanthemum crystallinum* cD... 68 1e-10
 45 emb|AW980667|AW980667 EST391820 GVN *Medicago truncatula* cDNA clo... 67 1e-10
 emb|AW349023|AW349023 GM210003B22B3R Gm-r1021 *Glycine max* cDNA 3... 67 1e-10
 emb|AI794756|AI794756 sb68g04.y1 Gm-c1019 *Glycine max* cDNA clone... 67 1e-10
 emb|AW984973|AW984973 NXNV_118_A01_F Nsf Xylem Normal wood Verti... 66 3e-10
 emb|AW737702|AW737702 EST339129 tomato flower buds, anthesis, Co... 66 3e-10
 50 emb|AW666412|AW666412 sk36c04.y1 Gm-c1028 *Glycine max* cDNA clone... 66 3e-10
 gb|BE034328|BE034328 MH03C07 MH *Mesembryanthemum crystallinum* cD... 66 3e-10

Query= X86958.1_at 14763_at /id_source genbank /description
 emb|caa60521.1| (x86958) protein kinase catalytic domain (fragment)
 55 [arabidopsis thaliana] /blast_score 1.00e-25 /ec_number /family
 kinase /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x86958|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|x86958|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x86958|/ncgi)
[http://www.ncbi.nlm.nih.gov/htbin-](http://www.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x86958|/ncgi)
 60 (168 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments: (bits) Value

	emb AW687233 AW687233 NF007D09RT1F1077 Developing root Medicago ...	114	3e-26
10	emb AW719817 AW719817 LjNEST10E2r Lotus japonicus nodule library...	113	6e-26
	emb AI727531 AI727531 BNLGHi8333 Six-day Cotton fiber Gossypium ...	107	3e-24
	emb AW266829 AW266829 L48-172T3 Ice plant Lambda Uni-Zap XR expr...	102	1e-22
	emb AW756795 AW756795 sl27c08.yl Gm-c1027 Glycine max cDNA clone...	102	2e-22
	emb AI901283 AI901283 sc31d08.yl Gm-c1014 Glycine max cDNA clone...	98	3e-21
15	gb BE021054 BE021054 sm47c02.yl Gm-c1028 Glycine max cDNA clone ...	97	8e-21
	emb AW666857 AW666857 GA__Ea0006D08 Gossypium arboreum 7-10 dpa ...	95	3e-20
	emb AW597214 AW597214 si71g06.yl Gm-c1031 Glycine max cDNA clone...	94	5e-20
	emb AI781266 AI781266 EST262145 tomato susceptible, Cornell Lyco...	92	1e-19
	gb BE058691 BE058691 sn19e05.yl Gm-c1016 Glycine max cDNA clone ...	91	3e-19
20	emb AW279355 AW279355 sf65g10.yl Gm-c1013 Glycine max cDNA clone...	91	5e-19
	emb AI484701 AI484701 EST242962 tomato ovary, TAMU Lycopersicon ...	90	9e-19
	emb AW982539 AW982539 HVSMEg0003I16f Hordeum vulgare pre-anthesi...	89	2e-18
	emb AI728857 AI728857 BNLGHi11808 Six-day Cotton fiber Gossypium...	89	2e-18
	emb AW329840 AW329840 N201116e rootphos(-) Medicago truncatula c...	88	2e-18
25	emb AW509134 AW509134 sh30e11.yl Gm-c1017 Glycine max cDNA clone...	87	6e-18
	emb AW687262 AW687262 NF007G02RT1F1018 Developing root Medicago ...	86	1e-17
	emb AI772117 AI772117 EST253217 tomato resistant, Cornell Lycop...	86	1e-17
	emb AW687777 AW687777 NF013D03RT1F1028 Developing root Medicago ...	86	1e-17
	emb AW667985 AW667985 GA__Ea0012C15 Gossypium arboreum 7-10 dpa ...	85	2e-17
30	emb AW979578 AW979578 EST341174 tomato root deficiency, Cornell ...	85	2e-17
	emb AW223870 AW223870 EST300681 tomato fruit red ripe, TAMU Lyco...	85	3e-17
	emb AW306841 AW306841 sf49d02.yl Gm-c1009 Glycine max cDNA clone...	85	3e-17
	gb BE058485 BE058485 sn16g12.yl Gm-c1016 Glycine max cDNA clone ...	51	6e-17
	emb AW031816 AW031816 EST275270 tomato callus, TAMU Lycopersicon...	59	7e-17
35	emb AW761546 AW761546 sl69a09.yl Gm-c1027 Glycine max cDNA clone...	83	7e-17
	emb AW982145 AW982145 SsS0075 Suaeda salsa ZAP cDNA library Suae...	83	1e-16
	emb AI938653 AI938653 sb56g02.yl Gm-c1018 Glycine max cDNA clone...	82	1e-16
	emb AW132502 AW132502 se04h04.yl Gm-c1013 Glycine max cDNA clone...	82	1e-16
	emb AW092144 AW092144 EST285240 tomato mixed elicitor, BTI Lycop...	81	3e-16
40	emb AW040672 AW040672 EST283536 tomato mixed elicitor, BTI Lycop...	81	3e-16
	emb AW039328 AW039328 EST281585 tomato mixed elicitor, BTI Lycop...	81	3e-16
	emb AW220489 AW220489 EST297042 tomato fruit mature green, TAMU ...	81	4e-16
	emb AW220490 AW220490 EST297043 tomato fruit mature green, TAMU ...	81	4e-16
	emb AW220491 AW220491 EST297044 tomato fruit mature green, TAMU ...	81	4e-16
45	emb AW758828 AW758828 NXNV_091_B05_F Nsf Xylem Normal wood Verti...	52	4e-16
	emb AI896462 AI896462 EST265893 tomato callus, TAMU Lycopersicon...	81	5e-16
	emb AW394569 AW394569 sh32f08.yl Gm-c1017 Glycine max cDNA clone...	81	5e-16
	emb AJ271954 TCA271954 Theobroma cacao microsatellite DNA, clone...	65	6e-16
	emb AW685205 AW685205 NF026F12NR1F1000 Nodulated root Medicago t...	79	1e-15
50	emb AW568064 AW568064 si68a06.yl Gm-r1030 Glycine max cDNA clone...	53	2e-15
	emb AF131222 AF131222 Lophopyrum elongatum protein serine/threon...	78	2e-15
	gb BE060160 BE060160 HVSMEg0011B12f Hordeum vulgare pre-anthesis...	78	3e-15
	emb AW929662 AW929662 EST338450 tomato flower buds 8 mm to pre-a...	78	3e-15
	emb AW684940 AW684940 NF023C12NR1F1000 Nodulated root Medicago t...	77	4e-15
55	emb AW284352 AW284352 LG1_275_D12.g1_A002 Light Grown 1 (LG1) So...	77	4e-15
	emb AI896953 AI896953 EST266396 tomato callus, TAMU Lycopersicon...	57	5e-15
	emb AI727374 AI727374 BNLGHi7892 Six-day Cotton fiber Gossypium ...	77	6e-15
	emb AW926765 AW926765 HVSMEg0008C18 Hordeum vulgare pre-anthesis...	77	6e-15
	emb AW278089 AW278089 sf39e12.yl Gm-c1009 Glycine max cDNA clone...	50	6e-15
60	emb AI794805 AI794805 sb70f02.yl Gm-c1019 Glycine max cDNA clone...	50	7e-15
	emb AW774553 AW774553 EST333704 KV3 Medicago truncatula cDNA clo...	76	8e-15

- emb|AW509847|AW509847 ga66e01.y1 Moss EST library PPU Physcomitr... 76 8e-15
 emb|AI967314|AI967314 Ljirnp00-017 Ljirnp Lambda HybriZap two... 50 1e-14
 emb|AW980333|AW980333 EST391486 GVN Medicago truncatula cDNA clo... 76 1e-14
 emb|AW925036|AW925036 WS1_74_F04.b1_A002 Water-stressed 1 (WS1) ... 76 2e-14
 5 emb|AW437900|AW437900 ST78A08 Pine TriPEX shoot tip library Pin... 76 2e-14
 gb|U59318|LEU59318 Lycopersicon esculentum serine/threonine prot... 51 2e-14
 gb|U13923|LEU13923 Lycopersicon pimpinellifolium serine/threonin... 50 2e-14
 emb|AI960995|AI960995 sc93g03.y1 Gm-c1019 Glycine max cDNA clone... 52 2e-14
 gb|U59317|LPU59317 Lycopersicon pimpinellifolium serine/threonin... 50 4e-14
 10 emb|AW034255|AW034255 EST277826 tomato callus, TAMU Lycopersicon... 74 6e-14
 emb|AW704952|AW704952 sk56f04.y1 Gm-c1019 Glycine max cDNA clone... 74 6e-14
 emb|AI729561|AI729561 BNLGHi13630 Six-day Cotton fiber Gossypium... 67 6e-14
 emb|AW233982|AW233982 sf32g05.y1 Gm-c1028 Glycine max cDNA clone... 73 8e-14
 gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor... 73 8e-14
 15 emb|AW694732|AW694732 NF079D07ST1F1061 Developing stem Medicago ... 73 8e-14
 emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 73 8e-14
 emb|A67797|A67797 Sequence 2 from Patent WO9743427. 73 8e-14
 emb|AW666082|AW666082 sk31h04.y1 Gm-c1028 Glycine max cDNA clone... 73 8e-14
 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 73 8e-14
 20 emb|AW621294|AW621294 EST312092 tomato root during/after fruit s... 73 8e-14
 emb|AW648736|AW648736 EST327106 tomato germinating seedlings, TA... 51 8e-14
 emb|AI896006|AI896006 EST265449 tomato callus, TAMU Lycopersicon... 50 9e-14
 emb|AF220602|AF220602 Lycopersicon pimpinellifolium Rio Grande 7... 50 9e-14
 emb|AF220603|AF220603 Lycopersicon esculentum VFNT Cherry Pto lo... 50 9e-14
 25 gb|T14833|T14833 crs280 lambdaZAPST Ricinus communis cDNA clone ... 47 1e-13
 emb|AI938710|AI938710 sb57g07.y1 Gm-c1018 Glycine max cDNA clone... 49 1e-13
 emb|AI896277|AI896277 EST265720 tomato callus, TAMU Lycopersicon... 73 1e-13
 emb|AW267961|AW267961 EST306183 DSIR Medicago truncatula cDNA cl... 48 1e-13
 emb|AI781597|AI781597 EST262476 tomato susceptible, Cornell Lyco... 72 1e-13
 30 emb|AW201545|AW201545 sf04d10.y1 Gm-c1027 Glycine max cDNA clone... 72 1e-13
 emb|AW621706|AW621706 EST312504 tomato root during/after fruit s... 72 2e-13
 emb|A67796|A67796 Sequence 1 from Patent WO9743427. 72 2e-13
 emb|AW429258|AW429258 EST306714 tomato flower buds 0-3 mm, Corne... 72 2e-13
 emb|AI898120|AI898120 EST267563 tomato ovary, TAMU Lycopersicon ... 48 3e-13
 35 emb|AW617954|AW617954 EST314028 L. pennellii trichome, Cornell U... 71 3e-13
 emb|AW029819|AW029819 EST273074 tomato callus, TAMU Lycopersicon... 48 3e-13
 emb|AI485223|AI485223 EST243527 tomato ovary, TAMU Lycopersicon ... 71 4e-13
 emb|AI897690|AI897690 EST267133 tomato ovary, TAMU Lycopersicon ... 71 4e-13
 emb|AI485585|AI485585 EST243906 tomato ovary, TAMU Lycopersicon ... 71 4e-13
 40 emb|AI489882|AI489882 EST248221 tomato ovary, TAMU Lycopersicon ... 71 4e-13
 emb|AI484547|AI484547 EST242777 tomato ovary, TAMU Lycopersicon ... 71 4e-13
 emb|AI483733|AI483733 EST249604 tomato ovary, TAMU Lycopersicon ... 71 4e-13
 emb|AI484020|AI484020 EST249891 tomato ovary, TAMU Lycopersicon ... 71 4e-13
 emb|AI484550|AI484550 EST242780 tomato ovary, TAMU Lycopersicon ... 71 4e-13
 45 emb|AI487264|AI487264 EST245586 tomato ovary, TAMU Lycopersicon ... 71 4e-13
 emb|AI898374|AI898374 EST267817 tomato ovary, TAMU Lycopersicon ... 71 4e-13
 emb|AI483732|AI483732 EST249603 tomato ovary, TAMU Lycopersicon ... 71 4e-13

50 Query= M96073.6_s_at 14838_s_at /id_source genbank /description
 gb|aaa32835.1| (m96073) phosphoribosylanthranilate transferase
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link /ncgi
 (1602 letters)

55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

60 Score E
 Sequences producing significant alignments: (bits) Value

- emb|AW687938|AW687938 NF001B11ST1F1000 Developing stem Medicago ... 393 e-108
 emb|AW039382|AW039382 EST281639 tomato mixed elicitor, BTI Lycop... 369 e-101
 emb|AW096850|AW096850 EST46F4 potato shoot cDNA library Solanum ... 263 2e-69
 5 emb|AW688778|AW688778 NF011E05ST1F1000 Developing stem Medicago ... 244 1e-65
 emb|AW906002|AW906002 EST342043 potato stolon, Cornell Universit... 234 6e-63
 emb|AI855689|AI855689 sc23a07.y1 Gm-c1013 Glycine max cDNA clone... 191 1e-47
 emb|AW622744|AW622744 EST306881 tomato flower buds 3-8 mm, Come... 171 2e-41
 emb|AW041025|AW041025 EST283889 tomato mixed elicitor, BTI Lycop... 171 2e-41
 10 emb|AL023554|SPBC16G5 *S.pombe* chromosome II cosmid c16G5. 81 1e-31
 gb|BE053060|BE053060 GA__Ea0020N16f *Gossypium arboreum* 7-10 dpa ... 132 7e-30
 gb|BE035432|BE035432 MO05D07 *MO Mesembryanthemum crystallinum* cD... 111 1e-23
 emb|AJ273068|AJ273068 AJ273068 *Metarhizium anisopliae* ARSEF 2575... 54 2e-16
 emb|AV412566|AV412566 AV412566 *Lotus japonicus* young plants (two... 78 2e-16
 15 emb|AV421776|AV421776 AV421776 *Lotus japonicus* young plants (two... 72 4e-13
 gb|U28372|YSCD9476 *Saccharomyces cerevisiae* chromosome IV cosmid... 49 8e-09
 emb|X04273|SCTRP4 Yeast TRP4 gene for anthranilate phosphoribosy... 49 9e-09
 emb|AQ874893|AQ874893 V118C3 mTn-3xHA/lacZ Insertion Library, st... 49 1e-07
 emb|AJ228925|AJ228925 AJ228925 Barley leaf, 8 day old seedling H... 57 4e-07
 20 emb|AW220409|AW220409 EST302892 tomato root during/after fruit s... 53 5e-06
 emb|AW737074|AW737074 CAF50 *Peronospora parasitica* cDNA-AFLP fra... 46 8e-04
 emb|X73297|SCSETRP4 *S.cerevisiae* spacer element. 29 0.002
 gb|U10274|SCU10274 *Saccharomyces cerevisiae* thioredoxin reductas... 44 0.004
 emb|AW933535|AW933535 EST359294 tomato fruit mature green, TAMU ... 38 0.016
 25 emb|AW922212|AW922212 DG1_17_B11.b1_A002 Dark Grown 1 (DG1) Sorg... 41 0.027
 gb|BE125449|BE125449 DG1_25_B11.b1_A002 Dark Grown 1 (DG1) Sorgh... 41 0.027
 emb|AV407038|AV407038 AV407038 *Lotus japonicus* young plants (two... 40 0.037
 emb|AI730383|AI730383 BNLGHi6768 Six-day Cotton fiber *Gossypium* ... 40 0.037
 emb|AW201070|AW201070 se97e05.y1 Gm-c1027 Glycine max cDNA clone... 40 0.050
 30 dbj|E08275|E08275 cDNA encoding cystathionine gamma-lyase. 37 0.46
 dbj|E08276|E08276 gDNA encoding cystathionine gamma-lyase. 37 0.46
 emb|AL113519|CNS01AXJ *Botrytis cinerea* strain T4 cDNA library un... 36 0.88
 emb|Z31724|PCREPELEM *P.chrysosporium* DNA for repetitive element. 36 0.88
 emb|AW695815|AW695815 NF099E03ST1F1021 Developing stem Medicago ... 34 1.4
 35 emb|A46806|A46806 Sequence 3 from Patent EP0684312. 35 1.7
 emb|Z37978|NTCYCMRN *Nicotiana tabacum* mRNA for cyclin B1 (cycB1 ... 35 1.7
 emb|AW729618|AW729618 GA__Ea0025J01 *Gossypium arboreum* 7-10 dpa ... 35 1.7
 emb|A46810|A46810 Sequence 7 from Patent EP0684312. 35 2.3
 emb|AL354572|LMFL5808 *Leishmania major* Friedlin chromosome 19 co... 35 2.3
 40 gb|BE052827|BE052827 GA__Ea0033G24f *Gossypium arboreum* 7-10 dpa ... 29 2.5
 emb|AW661030|AW661030 832009F12.x1 *C. reinhardtii* CC-125 nutrien... 34 3.1
 emb|AQ447557|AQ447557 mgxb0008C17f CUGI Rice Blast BAC Library P... 34 3.1
 emb|AW257438|AW257438 EST305575 KV2 *Medicago truncatula* cDNA clo... 34 3.1
 emb|AW563834|AW563834 LG1_272_A11.b1_A002 Light Grown 1 (LG1) So... 34 3.1
 45 emb|AQ654417|AQ654417 Sheared DNA-20C20.TF Sheared DNA Trypanoso... 34 4.3
 emb|AW756224|AW756224 sl17f04.y1 Gm-c1036 Glycine max cDNA clone... 34 4.3
 emb|X89715|SCAOGENES *S.cerevisiae* AOB567, AOF1001, AOE110, AOE26... 34 4.3
 emb|AF134853|AF134853 *Cuphea hookeriana* acyl-ACP carrier protein... 34 4.3
 emb|Z74896|SCYOL154W *S.cerevisiae* chromosome XV reading frame OR... 34 4.3
 50 gb|U15935|CWKAS3A *Cuphea wrightii* beta-ketoacyl-ACP synthase III... 34 4.3
 gb|BE033595|BE033595 MF04D10 MF *Mesembryanthemum crystallinum* cD... 34 4.3
 emb|AQ952764|AQ952764 Sheared DNA-43G7.TR Sheared DNA Trypanosom... 33 5.9
 emb|X61281|PBPOLII9 *P.berghei* RNA polymerase largest subunit. 33 5.9
 emb|Z36097|SCYBR228W *S.cerevisiae* chromosome II reading frame OR... 33 5.9
 55 emb|AL113095|CNS01ALR *Botrytis cinerea* strain T4 cDNA library un... 33 5.9
 gb|U36470|NCU36470 *Neurospora crassa* vacuolar ATPase 41 kDa subu... 33 5.9
 emb|Z78011|ANAXHA *A.niger* CBS 120.49 axhA gene. 33 5.9
 gb|BE023153|BE023153 sm79a01.y1 Gm-c1015 Glycine max cDNA clone ... 33 5.9
 emb|X71807|ANUAPA *A.nidulans* uapA gene for uric acid-xanthine pe... 33 5.9
 60 emb|AI213031|AI213031 y6f05a1.r1 *Aspergillus nidulans* 24hr asexu... 33 5.9
 emb|AQ874871|AQ874871 V117H8 mTn-3xHA/lacZ Insertion Library, st... 26 6.5

gb|U18839|SCE9747 *Saccharomyces cerevisiae* chromosome V cosmids ... 33 8.1
 emb|AF006304|AF006304 *Saccharomyces cerevisiae* protein tyrosine ... 33 8.1
 gb|U18814|SCE3612 *Saccharomyces cerevisiae* chromosome V lambda c... 33 8.1
 emb|AW719293|AW719293 LjNEST_C6r *Lotus japonicus* nodule library,... 33 8.1
 5 emb|AI441951|AI441951 sa83b07.y1 Gm-c1004 Glycine max cDNA clone... 33 8.1
 emb|AI443684|AI443684 sa50b09.y1 Gm-c1004 Glycine max cDNA clone... 33 8.1
 emb|AW932067|AW932067 EST357910 tomato fruit mature green, TAMU ... 33 8.1
 emb|AW720549|AW720549 LjNEST10b1rc *Lotus japonicus* nodule librar... 33 8.1
 emb|AW706285|AW706285 sj54d11.y1 Gm-c1033 Glycine max cDNA clone... 33 8.1
 10 emb|Z69368|SPAC27F1 *S.pombe* chromosome I cosmid c27F1. 33 8.1
 emb|X55664|SVPEPCA *Sorghum vulgare* mRNA for phosphoenolpyruvate ... 33 8.1
 emb|AW299016|AW299016 EST305690 KV2 *Medicago truncatula* cDNA clo... 33 8.1
 emb|AW171746|AW171746 N100640e rootphos(-) *Medicago truncatula* c... 33 8.1
 emb|AI960269|AI960269 sc81b07.y1 Gm-c1018 Glycine max cDNA clone... 27 9.1
 15 Query= X98676.2_at 15778_at /id_source genbank /description
 emb|caa67234.1| (x98676) zinc finger protein [*arabidopsis thaliana*]
 /blast_score 8.00e-87 /ec_number /family /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|x98676|/ncgi
 20 http://www.ncgr.org/cgi-bin/ff?x98676
 (643 letters)

 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
 25 Searching.....done

	Score	E	
			(bits) Value
30	Sequences producing significant alignments:		
	gb L46574 L46574 BNAF1975 Mustard flower buds <i>Brassica rapa</i> cDNA...	84	2e-29
	emb AB006600 AB006600 <i>Petunia x hybrida</i> mRNA for ZPT2-13, comple...	57	2e-25
	emb AB006599 AB006599 <i>Petunia x hybrida</i> mRNA for ZPT2-12, comple...	57	5e-23
	emb AI485362 AI485362 EST243683 tomato ovary, TAMU <i>Lycopersicon</i> ...	64	4e-22
35	emb AI898309 AI898309 EST267752 tomato ovary, TAMU <i>Lycopersicon</i> ...	63	8e-22
	emb AI483886 AI483886 EST249757 tomato ovary, TAMU <i>Lycopersicon</i> ...	64	2e-21
	emb AB006604 AB006604 <i>Petunia x hybrida</i> mRNA for ZPT2-9, complet...	102	2e-21
	emb AW030869 AW030869 EST274159 tomato callus, TAMU <i>Lycopersicon</i> ...	61	4e-21
	emb AI485555 AI485555 EST243876 tomato ovary, TAMU <i>Lycopersicon</i> ...	55	7e-21
40	emb AB000451 AB000451 <i>Petunia hybrida</i> mRNA for PETHy;ZPT2-5, com...	62	2e-20
	emb AI486627 AI486627 EST244948 tomato ovary, TAMU <i>Lycopersicon</i> ...	55	2e-20
	emb AI486228 AI486228 EST244549 tomato ovary, TAMU <i>Lycopersicon</i> ...	55	2e-20
	emb AI771123 AI771123 EST252223 tomato ovary, TAMU <i>Lycopersicon</i> ...	55	6e-20
	emb AB006601 AB006601 <i>Petunia x hybrida</i> mRNA for ZPT2-14, comple...	62	6e-20
45	emb AI488341 AI488341 EST246663 tomato ovary, TAMU <i>Lycopersicon</i> ...	55	8e-20
	emb AI959966 AI959966 sc35g05.x1 Gm-c1014 Glycine max cDNA clone...	60	1e-19
	emb AI966235 AI966235 sc35g05.y1 Gm-c1014 Glycine max cDNA clone...	60	1e-19
	emb AI897376 AI897376 EST266819 tomato ovary, TAMU <i>Lycopersicon</i> ...	64	2e-19
	emb AB006603 AB006603 <i>Petunia x hybrida</i> mRNA for ZPT2-8, complet...	61	4e-19
50	emb AW033868 AW033868 EST277439 tomato callus, TAMU <i>Lycopersicon</i> ...	62	1e-18
	emb AI894711 AI894711 EST264154 tomato callus, TAMU <i>Lycopersicon</i> ...	61	1e-18
	emb AI485123 AI485123 EST243427 tomato ovary, TAMU <i>Lycopersicon</i> ...	60	2e-18
	emb AI771824 AI771824 EST252924 tomato ovary, TAMU <i>Lycopersicon</i> ...	59	5e-18
	emb AW685937 AW685937 NF031H10NR1F1000 Nodulated root <i>Medicago t...</i>	59	9e-18
55	emb AW216442 AW216442 EST295072 tomato callus, TAMU <i>Lycopersicon</i> ...	57	1e-17
	emb AW684455 AW684455 NF017B06NR1F1000 Nodulated root <i>Medicago t...</i>	62	5e-17
	emb AW687462 AW687462 NF009H03RT1F1031 Developing root <i>Medicago</i> ...	57	8e-17
	emb AV422177 AV422177 AV422177 <i>Lotus japonicus</i> young plants (two...	56	8e-17
	emb AB006602 AB006602 <i>Petunia x hybrida</i> mRNA for ZPT2-7, complet...	60	2e-16
60	dbj D26083 PETZFDB1 <i>Petunia hybrida</i> gene for zinc-finger DNA bin...	56	3e-16
	dbj D26084 PETZFDB2 <i>Petunia</i> mRNA for zinc-finger DNA binding pro...	56	3e-16

- emb|AW680050|AW680050 WS1_3_G12.g1_A002 Water-stressed 1 (WS1) S... 57 1e-15
emb|AW033574|AW033574 EST277145 tomato callus, TAMU Lycopersicon... 53 2e-15
emb|AI487993|AI487993 EST246315 tomato ovary, TAMU Lycopersicon ... 53 2e-15
emb|AW034640|AW034640 EST278324 tomato callus, TAMU Lycopersicon... 53 2e-15
5 emb|AI896031|AI896031 EST265474 tomato callus, TAMU Lycopersicon... 53 3e-15
emb|AW030858|AW030858 EST274148 tomato callus, TAMU Lycopersicon... 53 3e-15
emb|AW033257|AW033257 EST276828 tomato callus, TAMU Lycopersicon... 53 3e-15
emb|AI771191|AI771191 EST252387 tomato ovary, TAMU Lycopersicon ... 53 3e-15
emb|AW032357|AW032357 EST275811 tomato callus, TAMU Lycopersicon... 53 3e-15
10 emb|AI489727|AI489727 EST248066 tomato ovary, TAMU Lycopersicon ... 55 4e-15
emb|AF053077|AF053077 Nicotiana tabacum osmotic stress-induced z... 51 1e-14
emb|AW030876|AW030876 EST274166 tomato callus, TAMU Lycopersicon... 53 4e-14
emb|AI488445|AI488445 EST246784 tomato ovary, TAMU Lycopersicon ... 55 2e-13
emb|AB035133|AB035133 Petunia x hybrida gene for C2H2 zinc-finge... 53 2e-13
15 emb|AB006605|AB006605 Petunia x hybrida mRNA for ZPT3-3, complet... 53 2e-13
dbj|D16415|WHTWZF1A Wheat gene for WZF1, complete cds. 47 3e-13
dbj|D16416|WHTWZF1B Wheat mRNA for WZF1, complete cds. 47 3e-13
emb|AW924420|AW924420 WS1_69_C08.b1_A002 Water-stressed 1 (WS1) ... 48 5e-13
emb|AI778714|AI778714 EST259593 tomato susceptible, Cornell Lyco... 52 7e-13
20 emb|AW037956|AW037956 EST279600 tomato mixed elicitor, BTI Lycop... 52 7e-13
emb|AI485651|AI485651 EST243972 tomato ovary, TAMU Lycopersicon ... 52 9e-13
emb|AI487287|AI487287 EST245609 tomato ovary, TAMU Lycopersicon ... 52 1e-12
emb|AW034622|AW034622 EST278306 tomato callus, TAMU Lycopersicon... 50 2e-12
gb|U76555|BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA... 52 2e-12
25 emb|AW035987|AW035987 EST282846 tomato callus, TAMU Lycopersicon... 53 2e-12
emb|AW153229|AW153229 se37f05.y1 Gm-c1015 Glycine max cDNA clone... 51 3e-12
emb|AW625323|AW625323 EST319146 tomato radicle, 5 d post-imbibit... 52 3e-12
emb|AW924443|AW924443 WS1_69_C08.g1_A002 Water-stressed 1 (WS1) ... 57 3e-12
emb|Y16131|Y16131 Y16131 young root nodules Medicago sativa subs... 49 3e-12
30 emb|AB035132|AB035132 Petunia x hybrida gene for C2H2 zinc-finge... 50 4e-12
emb|AB006597|AB006597 Petunia x hybrida mRNA for ZPT2-10, comple... 50 4e-12
emb|Y18788|MSY18788 Medicago sativa mRNA for putative TFIIIA (or... 49 4e-12
emb|AI988290|AI988290 sc98f10.y1 Gm-c1020 Glycine max cDNA clone... 50 5e-12
emb|AI488218|AI488218 EST246540 tomato ovary, TAMU Lycopersicon ... 52 5e-12
35 emb|AW560934|AW560934 EST315982 DSIR Medicago truncatula cDNA cl... 49 6e-12
emb|AW781249|AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone... 49 6e-12
gb|U68763|GMU68763 Glycine max putative transcription factor SCO... 48 8e-12
emb|AI988657|AI988657 sd06b03.y1 Gm-c1020 Glycine max cDNA clone... 49 8e-12
gb|BE059872|BE059872 sn38c04.y1 Gm-c1016 Glycine max cDNA clone ... 48 8e-12
40 dbj|D26086|PETZFP4 Petunia zinc-finger protein gene. 50 1e-11
emb|AW219517|AW219517 EST301915 tomato root during/after fruit s... 52 1e-11
gb|U76554|BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR... 52 2e-11
emb|AW729218|AW729218 GA_Ea0024G18 Gossypium arboreum 7-10 dpa ... 48 2e-11
emb|AW279005|AW279005 sg04d04.y1 Gm-c1019 Glycine max cDNA clone... 51 2e-11
45 emb|AW164639|AW164639 se74f02.y1 Gm-c1023 Glycine max cDNA clone... 51 2e-11
gb|BE095284|BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two-... 50 2e-11
emb|AW102472|AW102472 sd88f02.y1 Gm-c1009 Glycine max cDNA clone... 54 2e-11
emb|AB000455|AB000455 Petunia hybrida mRNA for PETHy;ZPT4-1, com... 51 4e-11
emb|AW775559|AW775559 EST334624 DSIL Medicago truncatula cDNA cl... 46 4e-11
50 gb|BE123920|BE123920 EST394045 DSIL Medicago truncatula cDNA clo... 46 4e-11
emb|AW278572|AW278572 sf46c03.y1 Gm-c1009 Glycine max cDNA clone... 51 4e-11
emb|AW706944|AW706944 sk08e10.y1 Gm-c1023 Glycine max cDNA clone... 47 4e-11
emb|AW219736|AW219736 EST302218 tomato root during/after fruit s... 52 4e-11
dbj|D26085|PETZFDB3 Petunia zinc-finger DNA binding protein gene. 46 5e-11
55 emb|AW777036|AW777036 M111167e DSIR Medicago truncatula cDNA clo... 59 2e-10
emb|AW032112|AW032112 EST275566 tomato callus, TAMU Lycopersicon... 43 4e-10
emb|AT000773|AT000773 AT000773 Brassica rapa guard cell Brassica... 65 4e-10
emb|AW216968|AW216968 EST295682 tomato callus, TAMU Lycopersicon... 53 4e-09
emb|AW648971|AW648971 EST327425 tomato germinating seedlings, TA... 52 6e-09
60 gb|BE058334|BE058334 sn14g01.y1 Gm-c1016 Glycine max cDNA clone ... 48 1e-08
emb|AI966679|AI966679 sc55a11.y1 Gm-c1015 Glycine max cDNA clone... 54 3e-08

	emb AV426673 AV426673 AV426673 Lotus japonicus young plants (two...	48	4e-08
	gb BE125698 BE125698 DG1_54_B08.g1_A002 Dark Grown 1 (DG1) Sorgh...	57	1e-07
	emb AF119050 AF119050 Datisca glomerata zinc-finger protein 1 (z...	56	3e-07
	emb AW030314 AW030314 EST273569 tomato callus, TAMU Lycopersicon...	53	4e-07
5	emb X60700 PHEPF1 P.hybrida EPF1 gene for DNA-binding protein.	55	7e-07
	emb AW620780 AW620780 sj09e02.y1 Gm-c1032 Glycine max cDNA clone...	54	9e-07
	emb AI960244 AI960244 sc80g07.y1 Gm-c1018 Glycine max cDNA clone...	54	9e-07
	emb AB000452 AB000452 Petunia hybrida mRNA for PETHy;ZPT2-6, com...	54	9e-07
10	Query= X98676.2_g_at 15779_g_at /id_source genbank /description emb caa67234.1 (x98676) zinc finger protein [arabidopsis thaliana] /blast_score 8.00e-87 /ec_number /family /chip nova /gb_link /ncgi (643 letters)		
15	Database: plantfungal 661,018 sequences; 426,114,510 total letters		
	Searching.....done		
20	Score E Sequences producing significant alignments: (bits) Value		
	gb L46574 L46574 BNAF1975 Mustard flower buds Brassica rapa cDNA...	84	2e-29
	emb AB006600 AB006600 Petunia x hybrida mRNA for ZPT2-13, comple...	57	2e-25
25	emb AB006599 AB006599 Petunia x hybrida mRNA for ZPT2-12, comple...	57	5e-23
	emb AI485362 AI485362 EST243683 tomato ovary, TAMU Lycopersicon ...	64	4e-22
	emb AI898309 AI898309 EST267752 tomato ovary, TAMU Lycopersicon ...	63	8e-22
	emb AI483886 AI483886 EST249757 tomato ovary, TAMU Lycopersicon ...	64	2e-21
	emb AB006604 AB006604 Petunia x hybrida mRNA for ZPT2-9, complet...	102	2e-21
30	emb AW030869 AW030869 EST274159 tomato callus, TAMU Lycopersicon...	61	4e-21
	emb AI485555 AI485555 EST243876 tomato ovary, TAMU Lycopersicon ...	55	7e-21
	emb AB000451 AB000451 Petunia hybrida mRNA for PETHy;ZPT2-5, com...	62	2e-20
	emb AI486627 AI486627 EST244948 tomato ovary, TAMU Lycopersicon ...	55	2e-20
	emb AI486228 AI486228 EST244549 tomato ovary, TAMU Lycopersicon ...	55	2e-20
35	emb AI771123 AI771123 EST252223 tomato ovary, TAMU Lycopersicon ...	55	6e-20
	emb AB006601 AB006601 Petunia x hybrida mRNA for ZPT2-14, comple...	62	6e-20
	emb AI488341 AI488341 EST246663 tomato ovary, TAMU Lycopersicon ...	55	8e-20
	emb AI959966 AI959966 sc35g05.x1 Gm-c1014 Glycine max cDNA clone...	60	1e-19
	emb AI966235 AI966235 sc35g05.y1 Gm-c1014 Glycine max cDNA clone...	60	1e-19
40	emb AI897376 AI897376 EST266819 tomato ovary, TAMU Lycopersicon ...	64	2e-19
	emb AB006603 AB006603 Petunia x hybrida mRNA for ZPT2-8, complet...	61	4e-19
	emb AW033868 AW033868 EST277439 tomato callus, TAMU Lycopersicon...	62	1e-18
	emb AI894711 AI894711 EST264154 tomato callus, TAMU Lycopersicon...	61	1e-18
	emb AI485123 AI485123 EST243427 tomato ovary, TAMU Lycopersicon ...	60	2e-18
45	emb AI771824 AI771824 EST252924 tomato ovary, TAMU Lycopersicon ...	59	5e-18
	emb AW685937 AW685937 NF031H10NR1F1000 Nodulated root Medicago t...	59	9e-18
	emb AW216442 AW216442 EST295072 tomato callus, TAMU Lycopersicon...	57	1e-17
	emb AW684455 AW684455 NF017B06NR1F1000 Nodulated root Medicago t...	62	5e-17
	emb AW687462 AW687462 NF009H03RT1F1031 Developing root Medicago ...	57	8e-17
50	emb AV422177 AV422177 AV422177 Lotus japonicus young plants (two...	56	8e-17
	emb AB006602 AB006602 Petunia x hybrida mRNA for ZPT2-7, complet...	60	2e-16
	dbj D26083 PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin...	56	3e-16
	dbj D26084 PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro...	56	3e-16
	emb AW680050 AW680050 WS1_3_G12.g1_A002 Water-stressed 1 (WS1) S...	57	1e-15
55	emb AW033574 AW033574 EST277145 tomato callus, TAMU Lycopersicon...	53	2e-15
	emb AI487993 AI487993 EST246315 tomato ovary, TAMU Lycopersicon ...	53	2e-15
	emb AW034640 AW034640 EST278324 tomato callus, TAMU Lycopersicon...	53	2e-15
	emb AI896031 AI896031 EST265474 tomato callus, TAMU Lycopersicon...	53	3e-15
	emb AW030858 AW030858 EST274148 tomato callus, TAMU Lycopersicon...	53	3e-15
60	emb AW033257 AW033257 EST276828 tomato callus, TAMU Lycopersicon...	53	3e-15
	emb AI771191 AI771191 EST252387 tomato ovary, TAMU Lycopersicon ...	53	3e-15

- emb|AW032357|AW032357 EST275811 tomato callus, TAMU Lycopersicon... 53 3e-15
 emb|AI489727|AI489727 EST248066 tomato ovary, TAMU Lycopersicon ... 55 4e-15
 emb|AF053077|AF053077 *Nicotiana tabacum* osmotic stress-induced z... 51 1e-14
 emb|AW030876|AW030876 EST274166 tomato callus, TAMU Lycopersicon... 53 4e-14
 5 emb|AI488445|AI488445 EST246784 tomato ovary, TAMU Lycopersicon ... 55 2e-13
 emb|AB035133|AB035133 *Petunia x hybrida* gene for C2H2 zinc-finge... 53 2e-13
 emb|AB006605|AB006605 *Petunia x hybrida* mRNA for ZPT3-3, complet... 53 2e-13
 dbj|D16415|WHTWZF1A Wheat gene for WZF1, complete cds. 47 3e-13
 dbj|D16416|WHTWZF1B Wheat mRNA for WZF1, complete cds. 47 3e-13
 10 emb|AW924420|AW924420 WS1_69_C08.b1_A002 Water-stressed 1 (WS1) ... 48 5e-13
 emb|AI778714|AI778714 EST259593 tomato susceptible, Cornell Lyco... 52 7e-13
 emb|AW037956|AW037956 EST279600 tomato mixed elicitor, BTI Lycop... 52 7e-13
 emb|AI485651|AI485651 EST243972 tomato ovary, TAMU Lycopersicon ... 52 9e-13
 emb|AI487287|AI487287 EST245609 tomato ovary, TAMU Lycopersicon ... 52 1e-12
 15 emb|AW034622|AW034622 EST278306 tomato callus, TAMU Lycopersicon... 50 2e-12
 gb|U76555|BRU76555 *Brassica rapa* zinc-finger protein BcZFP1 (BcA... 52 2e-12
 emb|AW035987|AW035987 EST282846 tomato callus, TAMU Lycopersicon... 53 2e-12
 emb|AW153229|AW153229 se37f05.y1 Gm-c1015 Glycine max cDNA clone... 51 3e-12
 emb|AW625323|AW625323 EST319146 tomato radicle, 5 d post-imbibit... 52 3e-12
 20 emb|AW924443|AW924443 WS1_69_C08.g1_A002 Water-stressed 1 (WS1) ... 57 3e-12
 emb|Y16131|Y16131 Y16131 young root nodules *Medicago sativa* subs... 49 3e-12
 emb|AB035132|AB035132 *Petunia x hybrida* gene for C2H2 zinc-finge... 50 4e-12
 emb|AB006597|AB006597 *Petunia x hybrida* mRNA for ZPT2-10, comple... 50 4e-12
 emb|Y18788|MSY18788 *Medicago sativa* mRNA for putative TFIIIA (or... 49 4e-12
 25 emb|AI988290|AI988290 sc98f10.y1 Gm-c1020 Glycine max cDNA clone... 50 5e-12
 emb|AI488218|AI488218 EST246540 tomato ovary, TAMU Lycopersicon ... 52 5e-12
 emb|AW560934|AW560934 EST315982 DSIR *Medicago truncatula* cDNA cl... 49 6e-12
 emb|AW781249|AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone... 49 6e-12
 gb|U68763|GMU68763 Glycine max putative transcription factor SCO... 48 8e-12
 30 emb|AI988657|AI988657 sd06b03.y1 Gm-c1020 Glycine max cDNA clone... 49 8e-12
 gb|BE059872|BE059872 sn38c04.y1 Gm-c1016 Glycine max cDNA clone ... 48 8e-12
 dbj|D26086|PETZFP4 *Petunia* zinc-finger protein gene. 50 1e-11
 emb|AW219517|AW219517 EST301915 tomato root during/after fruit s... 52 1e-11
 gb|U76554|BRU76554 *Brassica rapa* zinc-finger protein-1 (BR42) mR... 52 2e-11
 35 emb|AW729218|AW729218 GA_Ea0024G18 *Gossypium arboreum* 7-10 dpa ... 48 2e-11
 emb|AW279005|AW279005 sg04d04.y1 Gm-c1019 Glycine max cDNA clone... 51 2e-11
 emb|AW164639|AW164639 se74f02.y1 Gm-c1023 Glycine max cDNA clone... 51 2e-11
 gb|BE095284|BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two-... 50 2e-11
 emb|AW102472|AW102472 sd88f02.y1 Gm-c1009 Glycine max cDNA clone... 54 2e-11
 40 emb|AB000455|AB000455 *Petunia hybrida* mRNA for PETHy;ZPT4-1, com... 51 4e-11
 emb|AW775559|AW775559 EST334624 DSIL *Medicago truncatula* cDNA cl... 46 4e-11
 gb|BE123920|BE123920 EST394045 DSIL *Medicago truncatula* cDNA clo... 46 4e-11
 emb|AW278572|AW278572 sf46c03.y1 Gm-c1009 Glycine max cDNA clone... 51 4e-11
 emb|AW706944|AW706944 sk08e10.y1 Gm-c1023 Glycine max cDNA clone... 47 4e-11
 45 emb|AW219736|AW219736 EST302218 tomato root during/after fruit s... 52 4e-11
 dbj|D26085|PETZFDB3 *Petunia* zinc-finger DNA binding protein gene. 46 5e-11
 emb|AW777036|AW777036 M111167e DSIR *Medicago truncatula* cDNA clo... 59 2e-10
 emb|AW032112|AW032112 EST275566 tomato callus, TAMU Lycopersicon... 43 4e-10
 emb|AT000773|AT000773 AT000773 *Brassica rapa* guard cell *Brassica*... 65 4e-10
 50 emb|AW216968|AW216968 EST295682 tomato callus, TAMU Lycopersicon... 53 4e-09
 emb|AW648971|AW648971 EST327425 tomato germinating seedlings, TA... 52 6e-09
 gb|BE058334|BE058334 sn14g01.y1 Gm-c1016 Glycine max cDNA clone ... 48 1e-08
 emb|AI966679|AI966679 sc55a11.y1 Gm-c1015 Glycine max cDNA clone... 54 3e-08
 emb|AV426673|AV426673 AV426673 *Lotus japonicus* young plants (two... 48 4e-08
 55 gb|BE125698|BE125698 DG1_54_B08.g1_A002 Dark Grown 1 (DG1) Sorgh... 57 1e-07
 emb|AF119050|AF119050 *Datisca glomerata* zinc-finger protein 1 (z... 56 3e-07
 emb|AW030314|AW030314 EST273569 tomato callus, TAMU Lycopersicon... 53 4e-07
 emb|X60700|PHEPF1 P.hybrida EPF1 gene for DNA-binding protein. 55 7e-07
 emb|AW620780|AW620780 sj09e02.y1 Gm-c1032 Glycine max cDNA clone... 54 9e-07
 60 emb|AI960244|AI960244 sc80g07.y1 Gm-c1018 Glycine max cDNA clone... 54 9e-07
 emb|AB000452|AB000452 *Petunia hybrida* mRNA for PETHy;ZPT2-6, com... 54 9e-07

Query= AL080252.77_s_at 16232_s_at /id_source genbank /description
emb|cab45796.1| (a1080252) putative protein [arabidopsis thaliana]
/blast_score 1.00e-119 /ec_number /family /chip nova /gb_link /ncgi

5

(639 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

10

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

15

emb|Y11607|MSMP2C M.sativa mRNA for protein phosphatase 2C... 164 7e-70
emb|AJ242803|SST242803 Sporobolus stapfianus partial mRNA for pu... 154 4e-61
emb|AI055336|AI055336 coau0003L08 Cotton Boll Abscission Zone cD... 163 7e-56
emb|AI488711|AI488711 EST247050 tomato ovary, TAMU Lycopersicon ... 158 5e-46
20 emb|AI489841|AI489841 EST248180 tomato ovary, TAMU Lycopersicon ... 173 1e-42
emb|AW832587|AW832587 sm14b05.y1 Gm-cl027 Glycine max cDNA clone... 119 5e-40
emb|AW676724|AW676724 DG1_13_B08.g1_A002 Dark Grown 1 (DG1) Sorg... 152 2e-36
emb|AW423616|AW423616 sh69d07.y1 Gm-cl015 Glycine max cDNA clone... 110 3e-36
emb|AW278110|AW278110 sf39h03.y1 Gm-cl009 Glycine max cDNA clone... 119 2e-35
25 emb|AW698103|AW698103 NXNV_066_C09_F Nsf Xylem Normal wood Verti... 120 2e-33
emb|AI489730|AI489730 EST248069 tomato ovary, TAMU Lycopersicon ... 62 3e-29
emb|AV428740|AV428740 AV428740 Lotus japonicus young plants (two... 59 2e-19
emb|AF092431|AF092431 Lotus japonicus nodule-enhanced protein ph... 64 1e-18
emb|AF092432|AF092432 Lotus japonicus protein phosphatase type 2... 73 8e-18
30 emb|AI731667|AI731667 BNLGHi10427 Six-day Cotton fiber Gossypium... 80 4e-16
emb|AW458317|AW458317 sh86c05.y1 Gm-cl016 Glycine max cDNA clone... 77 7e-16
emb|AW035781|AW035781 EST281935 tomato callus, TAMU Lycopersicon... 84 1e-15
emb|AW647646|AW647646 EST307124 tomato germinating seedlings, TA... 84 1e-15
emb|AW621460|AW621460 EST312258 tomato root during/after fruit s... 84 1e-15
35 emb|AW776573|AW776573 EST335638 DSIL Medicago truncatula cDNA cl... 78 2e-15
emb|AW164504|AW164504 se73e07.y1 Gm-cl023 Glycine max cDNA clone... 76 5e-15
gb|H07534|H07534 cbn054 BNL2 Brassica napus cDNA 5'/3', mRNA seq... 82 5e-15
emb|AJ277743|FSY277743 Fagus sylvatica mRNA for ABA induced prot... 68 6e-15
emb|AW164369|AW164369 se71f04.y1 Gm-cl023 Glycine max cDNA clone... 81 7e-15
40 emb|AW035694|AW035694 EST281848 tomato callus, TAMU Lycopersicon... 81 7e-15
emb|AW683894|AW683894 NF003B07NR1F1000 Nodulated root Medicago t... 71 9e-15
emb|AW201723|AW201723 sf06e04.y1 Gm-cl027 Glycine max cDNA clone... 73 9e-15
emb|AW704555|AW704555 sk38f02.y1 Gm-cl028 Glycine max cDNA clone... 73 9e-15
emb|AI812394|AI812394 1H12 Pine Lambda Zap Xylem library Pinus t... 75 1e-14
45 emb|AI486266|AI486266 EST244587 tomato ovary, TAMU Lycopersicon ... 75 2e-14
emb|AW429253|AW429253 EST306709 tomato flower buds 0-3 mm, Corne... 67 3e-14
emb|AA080599|AA080599 EST054 Sugarcane leaf roll Saccharum sp. c... 74 3e-14
emb|AW328993|AW328993 N200187e rootphos(-) Medicago truncatula c... 78 8e-14
emb|AW926387|AW926387 HVSMEg0007B08 Hordeum vulgare pre-anthesis... 78 8e-14
50 emb|AW560026|AW560026 EST315074 DSIR Medicago truncatula cDNA cl... 77 1e-13
emb|AW981447|AW981447 EST392609 DSIL Medicago truncatula cDNA cl... 77 1e-13
emb|AW775291|AW775291 EST334356 DSIL Medicago truncatula cDNA cl... 77 1e-13
emb|AW223860|AW223860 EST300671 tomato fruit red ripe, TAMU Lyco... 69 1e-13
emb|AW930922|AW930922 EST356765 tomato fruit mature green, TAMU ... 69 1e-13
55 emb|AW126261|AW126261 N100368e rootphos(-) Medicago truncatula c... 71 3e-13
emb|AW217002|AW217002 EST295716 tomato callus, TAMU Lycopersicon... 75 6e-13
emb|AW560025|AW560025 EST315073 DSIR Medicago truncatula cDNA cl... 74 8e-13
emb|AI855433|AI855433 sc16a02.y1 Gm-cl013 Glycine max cDNA clone... 73 1e-12
gb|BE057188|BE057188 sm97g04.y1 Gm-cl015 Glycine max cDNA clone ... 55 3e-12
60 emb|AI898557|AI898557 EST268000 tomato ovary, TAMU Lycopersicon ... 66 6e-12
gb|BE055043|BE055043 GA__Ea0031H07f Gossypium arboreum 7-10 dpa ... 71 1e-11

- emb|AI895824|AI895824 EST265267 tomato callus, TAMU Lycopersicon... 66 1e-11
 emb|AW668385|AW668385 GA_Ea0013M12 Gossypium arboreum 7-10 dpa ... 70 2e-11
 emb|AF075580|AF075580 Mesembryanthemum crystallinum clone Mpc5 p... 47 2e-11
 emb|AW309195|AW309195 sg05e02.y1 Gm-cl019 Glycine max cDNA clone... 62 2e-11
 5 emb|AW934653|AW934653 EST353545 tomato flower buds 0-3 mm, Corne... 69 3e-11
 emb|AW736469|AW736469 EST332483 KV3 Medicago truncatula cDNA clo... 69 3e-11
 emb|AI052979|AI052979 Mpc9 Ice plant seedlings, RT-PCR, pCRII M... 63 3e-11
 gb|BE049699|BE049699 NXNV_142_B11_F Nsf Xylem Normal wood Vertic... 63 3e-11
 emb|AW224147|AW224147 EST300958 tomato fruit red ripe, TAMU Lyco... 69 3e-11
 10 emb|AW623772|AW623772 EST321717 tomato flower buds 3-8 mm, Corne... 68 5e-11
 emb|AW929331|AW929331 EST338119 tomato flower buds 8 mm to pre-a... 68 5e-11
 gb|BE057801|BE057801 sn07d10.y1 Gm-cl016 Glycine max cDNA clone ... 68 5e-11
 emb|AW648269|AW648269 EST326723 tomato germinating seedlings, TA... 68 5e-11
 emb|AW755847|AW755847 sl10a10.y1 Gm-cl036 Glycine max cDNA clone... 68 5e-11
 15 emb|AW290631|AW290631 NXNV044C04F Nsf Xylem Normal wood Vertical... 68 5e-11
 emb|AI489668|AI489668 EST248007 tomato ovary, TAMU Lycopersicon ... 68 7e-11
 emb|AI052978|AI052978 Mpc7 Ice plant seedlings, RT-PCR, pCRII M... 36 1e-10
 emb|AI900423|AI900423 sc05e10.y1 Gm-cl012 Glycine max cDNA clone... 44 2e-10
 emb|AW567769|AW567769 si54f05.y1 Gm-r1030 Glycine max cDNA clone... 44 2e-10
 20 emb|AI489404|AI489404 EST247743 tomato ovary, TAMU Lycopersicon ... 66 2e-10
 emb|AW096523|AW096523 EST289703 tomato mixed elicitor, BTI Lycop... 66 3e-10
 emb|AW442288|AW442288 EST311684 tomato fruit red ripe, TAMU Lyco... 66 3e-10
 emb|AW039555|AW039555 EST281836 tomato mixed elicitor, BTI Lycop... 66 3e-10
 emb|AW094483|AW094483 EST287663 tomato mixed elicitor, BTI Lycop... 66 3e-10
 25 emb|AI167089|AI167089 xylem.est.857 Poplar xylem Lambda ZAPII li... 48 6e-10
 emb|AW279540|AW279540 sf90h08.y1 Gm-cl019 Glycine max cDNA clone... 64 8e-10
 emb|AW101459|AW101459 sd78e02.y1 Gm-cl009 Glycine max cDNA clone... 55 2e-09
 emb|AJ277744|FSY277744 Fagus sylvatica mRNA for ABA and calcium ... 46 3e-09
 emb|AF075579|AF075579 Mesembryanthemum crystallinum clone Mpc2 p... 62 4e-09
 30 emb|AW265949|AW265949 L30-2480T3 Ice plant Lambda Uni-Zap XR exp... 62 4e-09
 emb|AW054059|AW054059 L30-2031T3 Ice plant Lambda Uni-Zap XR exp... 62 4e-09
 emb|AW830157|AW830157 sm23g12.y1 Gm-cl028 Glycine max cDNA clone... 62 6e-09
 emb|AW934014|AW934014 EST359857 tomato fruit mature green, TAMU ... 61 8e-09
 emb|AF211780|AF211780 AF211780 34.1B Nicotiana tabacum cDNA clon... 61 1e-08
 35 emb|AW739238|AW739238 gb39a01.y1 Moss EST library PPN Physcomitr... 59 3e-08
 emb|AW396505|AW396505 sh28f03.y1 Gm-cl016 Glycine max cDNA clone... 44 4e-08
 emb|AI488611|AI488611 EST246950 tomato ovary, TAMU Lycopersicon ... 59 4e-08
 emb|AF079355|AF079355 Mesembryanthemum crystallinum protein phos... 45 5e-08
 emb|AW164418|AW164418 se72c06.y1 Gm-cl023 Glycine max cDNA clone... 47 5e-08
 40 emb|AW687126|AW687126 NF006C06RT1F1049 Developing root Medicago ... 46 7e-08
 emb|AW560258|AW560258 EST315306 DSIR Medicago truncatula cDNA cl... 46 7e-08
 emb|AW923104|AW923104 DG1_49_F11.b1_A002 Dark Grown 1 (DG1) Sorg... 46 7e-08
 emb|AI812431|AI812431 10H3 Pine Lambda Zap Xylem library Pinus t... 57 1e-07
 emb|AW680755|AW680755 WS1_7_A11.b1_A002 Water-stressed 1 (WS1) S... 39 2e-07
 45 emb|AW781533|AW781533 sl81d01.y1 Gm-cl037 Glycine max cDNA clone... 57 2e-07
 emb|AF097667|AF097667 Mesembryanthemum crystallinum protein phos... 38 2e-07
 emb|AI773148|AI773148 EST254248 tomato resistant, Cornell Lycope... 56 3e-07
 emb|AV424435|AV424435 AV424435 Lotus japonicus young plants (two... 40 5e-07
 gb|L33918|USMUAC1A Corn smut fungus uac1 gene, complete cds. 41 5e-07
 50 emb|AW278161|AW278161 sf40e04.y1 Gm-cl009 Glycine max cDNA clone... 55 7e-07
 emb|AI060326|AI060326 Mpc5 Ice plant seedlings, RT-PCR, pCRII M... 37 8e-07
 emb|AW616138|AW616138 EST296905 L. hirsutum trichome, Cornell Un... 54 9e-07
 emb|AW119467|AW119467 sd47d10.y1 Gm-cl016 Glycine max cDNA clone... 54 9e-07
 emb|Z48008|SC8119 S.cerevisiae chromosome IV cosmid 8119. 53 2e-06

55

Query= AC004138.105_at 16257_at /id_source genbank /description
 gb|aac32915.1| (ac004138) putative nucleoside triphosphatase
 [arabidopsis thaliana] /blast_score 0 /ec_number ec_3.6.1.42 /family
 diphosphatase /chip nova /gb_link
 60 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004138|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004138|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004138|/ncgi)

<http://www.ncgr.org/cgi-bin/ff?ac004138>
(1551 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E		(bits)	Value
10	Sequences producing significant alignments:				
	gb U58597 STU58597	Solanum tuberosum ATP-diphosphohydrolase (RRO...	66	1e-31	
	emb Z32743 PSNTPASE	P.sativum (Alaska) NTPase mRNA for nucleosid...	64	1e-30	
	emb AB022319 AB022319	Pisum sativum mRNA for apyrase, complete cds.	64	1e-30	
15	emb AB027616 AB027616	Pisum sativum mRNA for apyrase, partial cd...	64	2e-29	
	emb AW925295 AW925295	HVSMEg0001H23 Hordeum vulgare pre-anthesis...	69	2e-29	
	emb AF156782 AF156782	Medicago sativa nod factor binding lectin-...	66	8e-29	
	emb AW983120 AW983120	HVSMEg0008D22f Hordeum vulgare pre-anthesi...	70	2e-28	
	emb AI771115 AI771115	EST252215 tomato ovary, TAMU Lycopersicon ...	71	4e-28	
20	emb AW934554 AW934554	EST353446 tomato flower buds 0-3 mm, Corne...	71	8e-26	
	emb AW621504 AW621504	EST312302 tomato root during/after fruit s...	62	7e-25	
	emb AF156780 AF156780	Lotus japonicus nod factor binding lectin-...	60	2e-23	
	emb AW618513 AW618513	EST320499 L. pennellii trichome, Cornell U...	67	5e-22	
	emb AF139807 AF139807	Dolichos biflorus nod factor binding lecti...	65	6e-22	
25	emb AW928903 AW928903	EST337691 tomato flower buds 8 mm to pre-a...	71	7e-22	
	emb AB032754 AB032754	Solanum melongena EE45 mRNA, partial cds.	65	2e-21	
	emb AW428956 AW428956	EST306496 tomato flower buds 0-3 mm, Corne...	68	1e-19	
	emb AW201606 AW201606	sf05b09.y1 Gm-c1027 Glycine max cDNA clone...	57	8e-18	
	emb AV421159 AV421159	AV421159 Lotus japonicus young plants (two...	62	8e-18	
30	emb AL121741 SPAC824	S.pombe chromosome I cosmid c824.	53	2e-17	
	emb AL121783 SPCC11E10	S.pombe chromosome III cosmid c11E10.	52	1e-16	
	emb AZ048365 AZ048365	LMAJFV1_lm77d11.x1 Leishmania major FV1 ra...	65	2e-16	
	emb AI900961 AI900961	sc17g01.y1 Gm-c1013 Glycine max cDNA clone...	61	4e-16	
	emb AW233919 AW233919	sf32a09.y1 Gm-c1028 Glycine max cDNA clone...	72	6e-16	
35	emb AI729322 AI729322	BNLGHi13103 Six-day Cotton fiber Gossypium...	56	4e-15	
	gb U18779 SCE8199	Saccharomyces cerevisiae chromosome V cosmid 8...	47	9e-15	
	gb L19560 YSCGUANDIP	Saccharomyces cerevisiae guanosine diphosph...	47	1e-14	
	emb AI855475 AI855475	sc16e11.y1 Gm-c1013 Glycine max cDNA clone...	56	6e-13	
	emb AI488582 AI488582	EST246921 tomato ovary, TAMU Lycopersicon ...	60	8e-13	
40	emb AJ388942 AJ388942	AJ388942 Medicago truncatula R108 Medicago...	63	1e-12	
	emb AW620334 AW620334	sj03g08.y1 Gm-c1032 Glycine max cDNA clone...	61	2e-12	
	emb AF156781 AF156781	Dolichos biflorus apyrase mRNA, complete cds.	62	7e-12	
	emb AA660474 AA660474	00360 MtRHE Medicago truncatula cDNA 5' si...	65	7e-12	
	emb AI441990 AI441990	sa82g03.y1 Gm-c1004 Glycine max cDNA clone...	60	2e-11	
45	emb AW696828 AW696828	NF109D12ST1F1101 Developing stem Medicago ...	57	2e-11	
	gb BE059022 BE059022	sn24b03.y1 Gm-c1016 Glycine max cDNA clone ...	53	4e-11	
	emb AW306606 AW306606	se53a03.y1 Gm-c1017 Glycine max cDNA clone...	56	8e-11	
	emb AI490444 AI490444	EST248770 tomato ovary, TAMU Lycopersicon ...	61	2e-10	
	emb AW564791 AW564791	LG1_301_H10.b1_A002 Light Grown 1 (LG1) So...	51	2e-10	
50	emb AI771846 AI771846	EST252946 tomato ovary, TAMU Lycopersicon ...	61	3e-10	
	emb AI897295 AI897295	EST266654 tomato ovary, TAMU Lycopersicon ...	61	3e-10	
	emb AI485852 AI485852	EST244173 tomato ovary, TAMU Lycopersicon...	61	3e-10	
	emb AI899079 AI899079	EST268522 tomato ovary, TAMU Lycopersicon ...	61	3e-10	
	emb AW922880 AW922880	DG1_47_F10.b1_A002 Dark Grown 1 (DG1) Sorg...	48	4e-10	
55	emb AI490499 AI490499	EST249033 tomato ovary, TAMU Lycopersicon ...	61	5e-10	
	emb AI488302 AI488302	EST246624 tomato ovary, TAMU Lycopersicon ...	60	1e-09	
	emb AV418181 AV418181	AV418181 Lotus japonicus young plants (two...	57	2e-09	
	emb AW924275 AW924275	WS1_52_E03.b1_A002 Water-stressed 1 (WS1) ...	64	3e-09	
	emb AW257004 AW257004	EST305141 KV2 Medicago truncatula cDNA clo...	48	8e-09	
60	emb AI771696 AI771696	EST252796 tomato ovary, TAMU Lycopersicon ...	61	3e-08	
	emb AW623313 AW623313	EST321258 tomato flower buds 3-8 mm, Corne...	58	2e-07	

- emb|AA231755|AA231755 CDO38.R cDNA from oat Avena sativa cDNA cl... 56 7e-07
 emb|AW736308|AW736308 EST332392 KV3 Medicago truncatula cDNA clo... 54 4e-06
 emb|AW563435|AW563435 LG1_214_E12.b1_A002 Light Grown 1 (LG1) So... 38 4e-05
 emb|AB010444|AB010444 Neospora caninum mRNA for NTPase, complete... 41 1e-04
 5 emb|AL160371|LMFLCHR15 Leishmania major Friedlin assembled chrom... 44 0.004
 emb|AF203695|AF203695 Saccharomyces cerevisiae golgi nucleoside ... 43 0.005
 gb|U18778|SCE9537 Saccharomyces cerevisiae chromosome V cosmids ... 43 0.005
 emb|AZ124337|AZ124337 T223080b Medicago truncatula BAC library M... 41 0.026
 emb|AW225681|AW225681 ST70C07 Pine TriplEx shoot tip library Pin... 41 0.026
 10 emb|AW774350|AW774350 EST333501 KV3 Medicago truncatula cDNA clo... 41 0.026
 emb|AI974272|AI974272 T110271e KV0 Medicago truncatula cDNA clon... 40 0.035
 emb|AL049184|PFMAL13P3 Plasmodium falciparum chromosome 13 strai... 39 0.13
 emb|AI728079|AI728079 BNLGHi9928 Six-day Cotton fiber Gossypium ... 29 0.23
 emb|X61608|BNLHCB3A B.napus gene for LHCI Type III chlorophyll ... 37 0.33
 15 emb|AW671082|AW671082 LG1_284_C02.b1_A002 Light Grown 1 (LG1) So... 37 0.33
 emb|AZ124338|AZ124338 T223081b Medicago truncatula BAC library M... 36 0.85
 emb|AF188744|AF188744 Brassica napus high-affinity ammonium tran... 35 1.2
 dbj|D37795|D37795 Ipomoea nil Tpn1 gene. 35 1.2
 dbj|E08493|E08493 gDNA encoding transposable element, Tpn1 which ... 35 1.2
 20 emb|AL356192|NCB24B19 Neurospora crassa DNA linkage group II BAC... 30 1.3
 emb|AF106939|AF106939 Phanerochaete chrysosporium 1,4-benzoquino... 29 1.4
 emb|AL163492|LMFL787 Leishmania major Friedlin chromosome 19 cos... 35 1.5
 emb|AW234282|AW234282 sf23d03.y1 Gm-cl028 Glycine max cDNA clone... 35 1.6
 emb|AL116534|CNS01D9A Botrytis cinerea strain T4 cDNA library un... 35 1.6
 25 emb|AW428880|AW428880 Ljirmp25-999-b7 Ljirmp Lambda HybriZap ... 35 1.6
 gb|N60092|N60092 TgESTzy11d09.r1 TgRH Tachyzoite cDNA Toxoplasma... 35 2.2
 emb|AW056764|AW056764 ST55E11 Pine TriplEx shoot tip library Pin... 35 2.2
 gb|N81562|N81562 TgESTzy59h03.r1 TgRH Tachyzoite cDNA Toxoplasma... 35 2.2
 emb|AW286610|AW286610 LG1_335_A07.g1_A002 Light Grown 1 (LG1) So... 35 2.2
 30 emb|AQ656308|AQ656308 Sheared DNA-27M14.TR Sheared DNA Trypanoso... 35 2.2
 emb|AL162692|SPBP4H10 S.pombe chromosome II P1 clone p4H10. 34 3.0
 emb|AQ652731|AQ652731 Sheared DNA-18C6.TR Sheared DNA Trypanosom... 34 3.0
 emb|AF016222|AF016222 Schizosaccharomyces pombe Rsv1p (rsv1) gen... 34 3.0
 emb|AW350237|AW350237 GM210008A10B2R Gm-r1021 Glycine max cDNA 3... 34 4.1
 35 emb|AQ943814|AQ943814 Sheared DNA-34A9.TF Sheared DNA Trypanosom... 34 4.1
 emb|AW666160|AW666160 sk32h08.y1 Gm-cl028 Glycine max cDNA clone... 34 4.1
 emb|AL109736|SPCC18B5 S.pombe chromosome III cosmid c18B5. 27 4.6
 emb|AW441608|AW441608 EST311004 tomato fruit red ripe, TAMU Lyco... 33 5.7
 emb|AL035476|PFMAL4P3 Plasmodium falciparum chromosome 4 strain ... 33 5.7
 40 emb|AW398001|AW398001 sg71a06.y1 Gm-cl007 Glycine max cDNA clone... 33 5.7
 emb|AW933585|AW933585 EST359428 tomato fruit mature green, TAMU ... 33 5.7
 emb|AI069343|AI069343 mgae0006cG03f Magnaporthe grisea Appressor... 33 5.7
 emb|X62697|NCACU3 N.crassa acu-3 gene for isocitrate lyase. 26 5.7
 emb|AI488866|AI488866 EST247205 tomato ovary, TAMU Lycopersicon ... 31 6.2
 45 emb|Z79690|ANPFA A.niger pfkA gene. 26 7.3
 emb|X13508|HVGHRDSP Barley gene for storage protein gamma-hordein. 28 7.8
 gb|M36378|BLYG1HORDA Barley gamma-1 hordein storage protein gene... 28 7.8
 emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 33 7.8
 emb|AI900865|AI900865 sb95d08.y1 Gm-cl012 Glycine max cDNA clone... 33 7.8
 50 emb|AZ124341|AZ124341 T223084b Medicago truncatula BAC library M... 33 7.8

Query= AL035679.144_at 17653_at /id_source genbank /description

emb|cab38823.1| (al035679) putative protein [arabidopsis thaliana]

/blast_score 0 /ec_number /family /chip nova /gb_link

55 <http://www3.ncbi.nlm.nih.gov/htbin->

post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035679| /ncgi

<http://www.ncgr.org/cgi-bin/ff?al035679>

(1455 letters)

60 Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	
5	Sequences producing significant alignments:	(bits)	Value	
	emb AW091895 AW091895 EST285075 tomato mixed elicitor, BTI Lycop...	306	3e-82	
	emb AW040183 AW040183 EST282682 tomato mixed elicitor, BTI Lycop...	306	3e-82	
	emb AW776130 AW776130 EST335195 DSIL Medicago truncatula cDNA cl...	204	2e-51	
10	emb AI897609 AI897609 EST267052 tomato ovary, TAMU Lycopersicon ...	182	4e-45	
	emb AI055000 AI055000 coau0002L23 Cotton Boll Abscission Zone cD...	90	1e-42	
	emb AI055639 AI055639 coau0004K19 Cotton Boll Abscission Zone cD...	107	2e-22	
	emb AW693198 AW693198 NF061D12ST1F1000 Developing stem Medicago ...	66	6e-10	
	emb AW684256 AW684256 NF014F09NR1F1000 Nodulated root Medicago t...	43	0.007	
15	emb AW667681 AW667681 GA__Ea0010D15 Gossypium arboreum 7-10 dpa ...	43	0.007	
	emb AW736130 AW736130 EST332126 KV3 Medicago truncatula cDNA clo...	39	0.12	
	emb AW683515 AW683515 NF015C12LF1F1097 Developing leaf Medicago ...	36	0.21	
	emb AI781902 AI781902 EST262781 tomato susceptible, Cornell Lyco...	36	0.57	
	gb U12141 SCU12141 Saccharomyces cerevisiae chromosome XIV left ...	35	0.73	
20	emb AW277626 AW277626 sf84e07.y1 Gm-c1019 Glycine max cDNA clone...	36	0.79	
	emb Z71330 SCYNL054W S.cerevisiae chromosome XIV reading frame O...	35	0.80	
	emb AW692595 AW692595 NF057C11ST1F1000 Developing stem Medicago ...	35	1.1	
	emb X54145 ANPECT A.niger gene for pectinesterase.	35	1.5	
	emb A35008 A35008 A.niger PE gene.	35	1.5	
25	emb A34997 A34997 A.niger pectinesterase coding sequence.	35	1.5	
	emb AQ162316 AQ162316 mgxb0012108r CUGI Rice Blast BAC Library P...	34	2.8	
	emb AF132029 AF132029 Hortonia floribunda chloroplast atpB-rbcL ...	34	2.8	
	emb AW567917 AW567917 si67c02.y1 Gm-r1030 Glycine max cDNA clone...	34	2.8	
	emb AQ951657 AQ951657 Sheared DNA-48F5.TR Sheared DNA Trypanosom...	34	2.8	
30	gb U81520 CIU81520 Cichorium intybus sucrose:sucrose 1-fructosyl...	34	3.9	
	emb AZ047925 AZ047925 LMAJFV1_lm68e11.x1 Leishmania major FV1 ra...	34	3.9	
	emb AI730144 AI730144 BNLGHi6313 Six-day Cotton fiber Gossypium ...	34	3.9	
	emb AQ942723 AQ942723 Sheared DNA-42J12.TR Sheared DNA Trypanoso...	34	3.9	
	gb U05812 HMU05812 Herpetomonas muscarum ATCC 30261 kinetoplast ...	34	3.9	
35	emb AW681095 AW681095 WS1_8_B09.g1_A002 Water-stressed 1 (WS1) S...	34	3.9	
	emb AL049180 PFMAL13P1 Plasmodium falciparum chromosome 13 strai...	27	4.9	
	emb AW832107 AW832107 sm30e05.y1 Gm-c1028 Glycine max cDNA clone...	33	5.3	
	gb N82224 N82224 TgESTzy37d01.r1 TgRH Tachyzoite cDNA Toxoplasma...	33	5.3	
	emb A94222 A94222 Sequence 5 from Patent EP0952222.	33	5.3	
40	emb AA741851 AA741851 LmLv39p3/584B Leishmania major promastigot...	33	5.3	
	emb AW728096 AW728096 GA__Ea0029O02 Gossypium arboreum 7-10 dpa ...	33	7.3	
	emb AW278032 AW278032 sf89g07.y1 Gm-c1019 Glycine max cDNA clone...	33	7.3	
	gb N82117 N82117 TgESTzy36b06.r1 TgRH Tachyzoite cDNA Toxoplasma...	33	7.3	
	emb AL355930 NCB208 Neurospora crassa DNA linkage group II BAC c...	32	10.0	
45	emb AW688738 AW688738 NF011A11ST1F1000 Developing stem Medicago ...	32	10.0	
	emb AI781529 AI781529 EST262408 tomato susceptible, Cornell Lyco...	32	10.0	
	emb AI397765 AI397765 NCC5A11T7 Conidial Neurospora crassa cDNA ...	32	10.0	
	emb AF127239 AF127239 Nicotiana tabacum cultivar Burley 21 argin...	32	10.0	
	emb AW180260 AW180260 MgA0351fMgA Library Mycosphaerella gramin...	32	10.0	
50	emb AF127240 AF127240 Nicotiana tabacum cultivar Xanthi arginine...	32	10.0	
	gb BE055666 BE055666 GA__Ea0009H20f Gossypium arboreum 7-10 dpa ...	32	10.0	
	gb BE036548 BE036548 MP01C02 MP Mesembryanthemum crystallinum cD...	32	10.0	
	emb AW038750 AW038750 EST280611 tomato mixed elicitor, BTI Lycop...	32	10.0	
	emb AL133484 LMFL236 Leishmania major Friedlin chromosome 19 cos...	32	10.0	
55	gb BE123936 BE123936 EST394061 DSIL Medicago truncatula cDNA clo...	32	10.0	

Example 4

Immediate Early Transcriptional Responses Controlled by a Salicylic Acid Dependent Local Resistance Pathway

Salicylic Acid (SA) is an important mediator of local and systemic defense responses. In *Arabidopsis*, accumulation of SA is essential for local resistance against many pathogens including *Peronospora parasitica* (*Peronospora*) isolates. Furthermore, numerous defense-related genes can be activated by SA treatment. In addition to local resistance, SA-accumulation is required for systemic acquired resistance (SAR). In the SAR pathway, SA has been shown to act upstream of *NPR1*, which is also essential for SAR. Short application of the SA analog BTH (e.g., 4 hours) to plant tissue appears to simulate local defense responses to *Peronospora parasitica*, whereas sustained SA treatment (e.g., 48 hours) elicits SAR-related plant responses (Maleck et al., 2000).

A previous cDNA microarray study identified a cluster of roughly 30 co-regulated genes that appear to be specifically involved in resistance of the *Arabidopsis* ecotype WS against the *Peronospora* isolate Noco2 (Maleck et al., 2000). These genes are strongly activated in response to infection with Noco2 (incompatible interaction) and 4 hours after BTH treatment. However, these genes were not markedly activated during a compatible interaction with the *Peronospora* isolate Emwa1 or an incompatible interaction with *Pseudomonas syringae* (DC3000 avrRpt2) bacteria. BTH treatment for 48 hours (that simulates SAR) even strongly repressed these genes. Thus, a rapid and transient SA peak may control Noco2 triggered defense genes.

Resistance of the *Arabidopsis* ecotype Col-0 against the *Peronospora* isolate Emoy2 appears to be regulated by a similar pathway that also is dependent on accumulation of SA. Emoy2 resistance in Col-0 is controlled by the resistance gene *RPP4*. To further explore early SA-dependent gene regulatory events and to relate these to *Peronospora*-induced resistance responses, immediate-early target genes of SA were identified using Affymetrix chip experiments with the protein biosynthesis inhibitor cycloheximide (CHX). Genes of this category likely are linked to transcriptional regulators acting closely downstream of SA. Results from these "SA-chip" experiments were combined with those from a set of chip experiments examining expression

profiles triggered in the *Arabidopsis* ecotype Col-0 by the *Peronospora* isolate Emoy2 to identify clusters of co-regulated *RPP4* controlled SA-dependent immediate early genes.

Results

5 To identify genes controlled by the *RPP4* pathway, interactions between the *Peronospora* isolate Emoy2 and Col-0 wild type plants, the defense mutants *ndr1*, *npr1* and *pad4* as well as transgenic NahG plants were examined by chip experiments. The interactions between Emoy2 and Col-0, *ndr1* or *npr1* are incompatible (plant is disease resistant), whereas the interactions involving *pad4* and NahG are compatible (plant is susceptible, i.e., disease develops). For each interaction three different time points were analyzed: 0, 12 and 48 hours post infection with 50,000 Emoy2 spores/ml. Genes that were at one or more time points more strongly expressed in Col-0, *ndr1* and *npr1* as compared to *pad4* and NahG were considered as controlled by the *RPP4* pathway. Genes represented by 271 probe sets showed at least one 2-fold expression difference in comparison between Col-0 and *pad4* or NahG and were selected for further analysis.

To identify immediate early target genes of SA, Col-0 wt seedlings were pretreated with CHX or mock treated 15 minutes before spraying with 2 mM SA or water and harvested 2 hours later (Table 28).

Table 28

<u>Plants</u>	<u>Treatment</u>
Col-0	untreated (mock)
25 Col-0	+ SA
Col-0	+ SA + CHX
Col-0	+ CHX

271 probe sets were found to be upregulated in a *RPP4* pathway-specific manner (SEQ ID NOs: 400-684). Emoy2-induced upregulation of these genes is compromised in *pad4* and *NahG* plants. These *RPP4* controlled genes were further analyzed concerning their responses to SA, CHX and SA + CHX. The 271 probe sets were subcategorized by K-means clustering over the SA/CHX data set. Nine K-means clusters comprised three subgraphs. For each of these subgraphs, the first data point represented the untreated control value, the second data point represented the response to combined SA/CHX treatment, the third

data point represented CHX treatment alone and the fourth data point represented SA treatment alone. K-means clustering defined two categories of RPP4 controlled CHX/SA-responsive genes: immediate early genes (SA-responsive, not CHX affected) and super-induced genes (additive effects of SA and CHX).

Two K-means clusters represent *RPP4*-controlled SA-induced immediate early genes (Table 29; SEQ ID NOs: 150, 159, 117, 126, 208, 428, 426, 436, 430, 434, 478, 641, 609, 615 and 526). *RPP4*-controlled upregulation of these genes is SA dependent and SA induction is not compromised by CHX, which blocks or reduces protein biosynthesis. Thus, all essential regulators that mediate SA-responsiveness of these genes must be already preformed and, hence, are likely to act closely downstream of SA. This set of 15 genes includes seven potential regulator genes that may be involved in the control of secondary response genes (which require protein biosynthesis) or other late responses.

Table 29

12354_g_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase
14978_at	gb AAB64024.1 (AC002333) putative glucosyltransferase
15479_at	emb CAB39671.1 (AL049483) putative protein
15616_s_at	emb CAA08794.1 (AJ009696) wall-associated kinase 1
16061_s_at	gb AAB97145.1 (AF000977) MEK1
16109_s_at	gb AAC05342.1 (AC002521) putative protein kinase
16140_s_at	emb CAB42872.1 (AJ012423) wall-associated kinase 2
16603_s_at	gb AAB58497.1 (U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase
17499_s_at	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel
17930_s_at	emb CAA07352.1 (AJ006960) peroxidase
18966_at	gb AAC95196.1 (AC004561) putative glutathione S-transferase
20429_s_at	emb CAB10219.1 (Z97336) hypothetical protein - weak similarity to NF-kappa-B
20685_at	emb CAB41928.1 (AL049751) short-chain alcohol dehydrogenase like protein
13702_s_at	emb CAA19683.1 (AL024486) putative protein
14704_s_at	gb AAD15461.1 (AC006067) unknown protein

To further subcategorize these genes and to more precisely define a cluster of strictly co-regulated genes, the set of 15 genes was analyzed by K-means clustering over the *RPP4* data set (Emoy2 infections). This allows to use *RPP4* triggered expression timing as an additional criterion for subclustering. Normalized absolute expression levels at 0, 12 and 48 hpi in Emoy2 infected

Col-0 (w.t.), *ndr1*, *npr1*, *pad4* and *NahG* plants are displayed. Genes that share a pronounced almost linear and sustained expression increase were chosen for further analysis. These 5 genes (Table 30, which show a pronounced Emoy2-induced SA-dependent but *npr1*-independent linear expression increase and which encode potential regulators) are upregulated by the *RPP4* pathway, respond to Emoy2 recognition with a steep, sustained, almost linear expression increase. This pronounced “upregulation” is SA dependent and independent of *de novo* protein biosynthesis. Transcription factors that mediate this response must be present when SA is perceived and may act closely downstream of SA.

The mechanism that switches these genes on may involve posttranslational modifications of such preformed transcription factors.

Table 30

12354_g_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase
15616_s_at	emb CAA08794.1 (AJ009696) wall-associated kinase 1
16140_s_at	emb CAB42872.1 (AJ012423) wall-associated kinase 2
17499_s_at	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel
20429_s_at	emb CAB10219.1 (Z97336) hypothetical protein - weak similarity to NF-kappa-B

To identify the potential binding sites of such key transcription factors, the promoters of these five genes were searched for conserved compact sequence motifs (Table 31; SEQ ID NOs: 757-764; SEQ ID NO:765 is a consensus sequence). Using the program “AlignACE”, a strikingly conserved motif was found that is present in all five promoters. This motif resembles the described consensus binding site of WRKY transcription factors, W box. However, the W box core motif, TGAC, is followed by an “A”. The permutation TGACA has never been associated with WRKY binding. In addition to this, four more positions are highly conserved. This motif may be the specific binding site of an unconventional WRKY transcription factor or a factor of a novel so far unknown type. Yeast one hybrid screens can reveal the identity of this factor.

Table 31

W box-like Motif		
MAP Score: 4.4		
ACAGTGACA 0 391 1	(12345)	SEQ ID NO:757
ACAGTGACA 1 236 1	(16140)	SEQ ID NO:758

ACAGTGACA 1 317 1 (16140) SEQ ID NO:759
 ACAGTGACA 2 281 1 (15616) SEQ ID NO:760
 ACAGTAACA 3 84 1 (17498) SEQ ID NO:761
 AAAGTAACA 3 1557 0 (17498) SEQ ID NO:762
 5 AAAGTGACA 4 1840 0 (20429) SEQ ID NO:763
 AAAGTGACA 4 2131 0 (20429) SEQ ID NO:764

ACAGTGACA

SEQ ID NO:765

A

10 Expt. Frequency: 0.02/1kb
 Obs. in SOMc7: 0.06/1kb
 Obs. in this cluster: 0.50/1kb

15 One K-means cluster of the 271 RPP4 controlled probe sets represents
RPP4-controlled SA/CHX super-induced genes (Table 32; SEQ ID NOs: 214,
 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447, and 551).
RPP4-controlled upregulation of these genes is SA-dependent; these genes are
 weakly inducible upon both SA and CHX treatment alone. The response to
 20 combined treatment with SA and CHX is stronger than the response to either
 single treatment. Induction of genes in response to CHX alone has been
 described before and has been attributed to hypothetical proteins that are rapidly
 turned over and either repress transcription of the respective gene or control
 degradation of the respective mRNA. Block of synthesis of such hypothetical
 25 proteins may lead to increased mRNA levels by either increased transcription or
 reduced mRNA degradation. Like the set of immediate early SA responsive
 genes shown before, genes of this set also appear not to require *de novo* protein
 biosynthesis for their response to SA. In contrast to the previous gene set,
 however, the observed CHX-induced up-regulation may point to a de-repression
 30 mechanism.

Table 32

12505_s_at gb|AAC63643.1| (AC005309) putative CONSTANS-like B-box
 zinc finger protein
 35 13656_at gb|AAD22649.1|AC007138_13 (AC007138) predicted protein of
 unknown function
 14116_at gb|AAC26243.1| (AF077407) contains similarity to sugar
 transporters
 14170_at gb|AAF29406.1|AC022354_5 (AC022354) unknown protein
 40 14223_at emb|CAA19683.1| (AL024486) putative protein

14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to
	gb X97864 cytochrome P450
14608_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to
	gb AF038007 FIC1, member of the PF 00122 E1-E2 ATPase
5	family.
14614_at	gb AAC16958.1 (AC004165) putative glucosyltransferase
15646_s_at	gb AAC37474.1 (L42212) serine acetyltransferase
16054_s_at	emb CAA74639.1 (Y14251) glutathione S-transferase
16105_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4
10	16968_at emb CAA17559.1 (AL021961) glucosyltransferase -like protein
	18235_at gb AAB61480.1 (AC000348) T7N9.4
	18567_at gb AAC34217.1 (AC004411) putative alcohol dehydrogenase
	18591_at emb CAA52772.1 (X74756) ATAF2
	19845_g_at emb CAB37510.1 (AL035540) monooxygenase 2 (MO2)
15	20017_at gb AAC16079.1 (AC004521) unknown protein

To further subcategorize these genes based on *RPP4* triggered expression timing, the set of 17 SA/CHX super induced genes was K-means clustered over the *RPP4* (Emoy2) data set (Table 33; SEQ ID NOs: 214, 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447, and 551). A group of five

20 genes was identified that consistently respond quickly ("fast", within 12 hpi) and that have elevated expression ground states in the *npr1* mutant. The fast response is SA dependent (is abolished or attenuated in *pad4* and *NahG*). The elevated expression ground states in *npr1* together with the observed CHX inducibility may point to an *NPR1*-dependent repression mechanism. Since

25 *NPR1* has been shown previously to act closely at the level of transcriptional regulation, a *NPR1* dependent repressor may shut expression of these genes down. Upon CHX treatment this hypothetical repressor is not synthesized anymore and expression of these genes is elevated. This repressor may also participate in *RPP4* triggered activation of these genes and allow Emoy2-

30 induced de-repression.

Table 33

18591_at	emb CAA52772.1 (X74756) ATAF2
14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to
35	gb X97864 cytochrome P450
14614_at	gb AAC16958.1 (AC004165) putative glucosyltransferase
15646_s_at	gb AAC37474.1 (L42212) serine acetyltransferase
16105_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4

To identify binding sites of activating or repressing factors responsible for the co-regulation of this small cluster, the promoters of these genes were searched for conserved compact motifs with "AlignACE" (Table 34; SEQ ID NOs: 766-772, SEQ ID NO:773 is a consensus sequence). One strictly
 5 conserved octameric motif was found, which, however, is absent in one of the promoters. Yeast one hybrid screens can identify factors binding to this motif.

Table 34

Motif 15		
10	MAP Score: 1.23758	
	AATCGAAT 0 40 0	(18591) SEQ ID NO:766
	AATCGAAT 0 1741 1	(18591) SEQ ID NO:767
	AATCGAAT 1 386 1	(PAD3, 14248) SEQ ID NO:768
	AATCGAAT 2 334 1	(14614) SEQ ID NO:769
15	AATCGAAT 2 660 1	(14614) SEQ ID NO:770
	AATCGAAT 2 2105 1	(14614) SEQ ID NO:771
	AATCGAAT 3 1570 1	(15646) SEQ ID NO:772

	AATCGAAT	SEQ ID NO:773
20	expt.: 0.08/kb	
	obs.: 0.70/kb	
	SOMc7: 0.06/kb	
	Random20: 0.00/kb	
25	SOMc3: 0.10/kb	
	SOMc1: 0.10/kb	

As described hereinbelow, sets of genes specifically controlled by the *RPP7* and *RPP8* pathways were defined. Similarly a set of *RPP4* pathway
 30 controlled genes was defined (see Figure 4). Figure 4 shows a "Venn diagram" including only the transcription factor genes of these *RPP4*, *RPP7* and *RPP8* controlled genes. Three transcription factor genes were found to be specifically upregulated by each of the three *Peronospora* defense pathways: AtERF1, HSF4, ATAF2. Furthermore, ERF transcription factors appear to play an
 35 important role in controlling defense responses directed against *Peronospora* in general. Table 35 gives four potential target genes of ERF transcription factors. These genes contain ERF binding motifs in their promoters.

Table 35

40 Genes with potential ERF binding sites (GCCGCC or GCCGAC):

thioredoxin (13189) RPP7/RPP8 and (weakly) RPP4 controlled
 C2H2 zinc finger (15665) RPP7/RPP4 and (weakly) RPP8 controlled
 SigA binding protein (14148) RPP7/RPP4 controlled
 HSP70 (13284) RPP7/RPP8 controlled

5

These genes are specifically controlled by at least two different *Peronospora* defense pathways and show an almost linear increase of transcript levels during incompatible Hiks1 interactions (K-means clusters 3+5).

6 potential ERF binding sites in K-means cluster 3+5: 0.5 motifs /

10 1kbExpected: 0.1 motif / 1kb; Enrichment in K-means cluster 3+5: 5-fold

SEQ ID NO:789

MPTSATAVAPSTGSGVQKKDQDWRAILSPEQFRVLREKGTENRGKGEYT
 KLFDDGIYSCAGCATPLYKSTTKFDSGCGWPSFFDAIPGAIKQTDMFGSN
 15 AADGSIVTSGLDYILISINEKLKAYT

SEQ ID NO:790

1 tgcattcttt tgaggggttt aattttctgc atagctttgt ctaatctctt agagctcaat
 61 aagagaagat ggatgtcca cggccagctt tcaaattgtt tgatgacgat ggccggctta
 20 121 aacgttcagg gacggtttgg accgcgagtg cgcatatcat aaccgccgtg attggatctg
 181 gtgttctatc gcttgcgtgg gctataggtc aactcgggtg gatcgcaggt cctacagtga
 241 tgttgtgtt ctctttgtc acttactact ctccacgct tcttagcgac tgctacagaa
 301 ccggagatcc tgtctctggg aagagaaact atacttacat ggacgctgtc cgatcaatcc
 361 taggtggctt taggttcaag atttgtgggc tgattcagta tttgaatctg tttggtatca
 25 421 cggtcgggta cacaatcgca gcatctataa giatgatggc gatcaagagg tccaactgtt
 481 tccacgagag cggagggaaa aaccgctgtc acatgtcgag caatccatac atgatcatgt
 541 ttggtgtgac cgagatcttg ctctctcaga tcaaagattt tgaccagatt tgggtggctct
 601 ccattgtcgc tgctatcatg tcttccacat actctgcaat cggtttagct ctcggaatca
 661 ttcaagtcgc ggcaaatgga gttgtcaagg gaagtctcac cggaattagc atcggcgcag
 30 721 tgactcagac caaaaaata tggagaacct ttcaagcact tggagacatt gcctttgctt
 781 attcatactc tgttgttctt attgaaattc aggacactgt aagatctcca ccagcagaat
 841 caaaaacgat gaagatcgcc acaagaatca gcatcgctgt tacaacgaca ttttcatgc
 901 tatgtggttg tatgggctat gcggccttcg gagataaagc accgggaaac ctcttaaccg
 961 gttttggtt ctacaatccg tttggctcc ttgacgtggc taacgctgcc atagttatcc
 35 1021 acctttagg agcttatcaa gtctttgctc agcccatctt cgcctttatt gagaaacaac
 1081 tggccgctag gtttcccgac agtgacttgg tgaccaagga atacgaaatc cgaatccctg
 1141 gttttaggtc accgtacaaa gtcaacgtt tcagagcagt ttaccgaagc gggtttgg
 1201 tttgaccac tgtgatatcc atgcttatgc cgttttcaa cgacgtcgta gggattttag
 1261 gtgcgttagg gtttggcct ttgacggtt actttccggt ggagatgtat ataagacaga
 40 1321 ggaagggtga gagatggagt atgaagtggg tttgtctgca gatgttgagc tgtggttgtt
 1381 tgatgatcac gttggtcgcc ggagttggct ccacgcggg agtaatgcta gaccttaagg
 1441 ttacaagcc gttcaagact acttactaaa caaacatga tgatagatga agaagaagaa
 1501 ggtggtggag aaaaaaaca aaagatataa attttaatga tgattttcat tggggaaatg
 1561 tgaataatgt aaaagttctt cgtttcgtat aattttatc ttgcgtaatt tatatacat

45

SEQ ID NO:791

MVKNLKVDP LAKVTASTTSMVILSSLFITDDSYVLVSAKENKNQSEAE
 PSYYETLETYQGLPCPYGGYYGYYPGLDGSVGEAKDNGYYGYGTEVQ
 YPVMQGENGSVIYLMPGFQSYDASQTYMPINPVGVSSQALHSPMYAAQ
 GYYQNQFGYADVSSPTYLWDPVGDYVYGVASYTPPLKQNISSSSHNH
 5 NNYYSKSKNSFTGHGMGDRPKTPRKASQNSYAPPPLL NQEKGR IAYPM
 DPVKKKSGALNRDETEKAKARTKENGTS MNDLANGQDHITNGECESCS
 LDAEGNERSNGVGSVIRRDQYNLPSFQTKYEEAIFV IKSYS EDDIHKSIK
 YNVWSSTLNGNKKLDSAYQESQKKAADKSGKCPVFLFFSVNASGQFCG
 VAEMIGRVDYEKSMEFWQQDKWTGYFPVKWHI I KDVPNPQLRHI LEN
 10 NENKPV TNSRDTQE VRLPQGNEVLNIFKNYA AKTSILDDFD FYENREKV
 MVQKKLRFP PVLKKKEEDLVADFKT MEMSNTVEEGNTELTGTVS

SEQ ID NO:792

1 cgatcacgga tctggcttgg ttcatacaaa accgccgttg ccgcggcacg ggcctacgat.
 15 61 accgctgtgt ttacttacg tggctcttcg gcgagactca attccctga agaggtcttt
 121 aaggatggaa acggcgggtga aggcttagga ggagatatgt ctccgacgtt gatacggaaag
 181 aaggcggctg aggtgggagc tagagtcgac gcagagttgc ggtagagaa taggatggtt
 241 gagaacttag acatgaataa gttgccggag gcatatggat tgaatttat agtttggtag
 301 ttataggtt ggagattgcc cggagacaga gtcaaacaga ggttctctga ctcatatgag
 20 361 gcataatata gtaatatag taattttgt ttgagcata gtaattatgt cataacc

SEQ ID NO:793

1 gggcaatgat tattcgttcg ccggaaccag aagtcaaaat ttggtagat agggatccca
 61 taaaaacttc ttgcaggaa tgggctaaac ccggtcattt ctcaagaaca atagctaagg
 25 121 gacctgatac taccacttgg atctggaacc tacatgctga tgctcacgat ttgatagtc
 181 ataccagtga ttggaggaa atctctcgaa aagtatttag tggccatttc ggccaactct
 241 ctatcatctt tcttggctg agtggcatgt attccatgg tgctcgttt tccaattatg
 301 aagcatggct gattgacct actcacattg gacctagtgc tcaggtgggt tggccaatag
 361 tgggccaaga aatcctgaat ggagtagtgg gcggaggctt ccgaggaata caaataacct
 30 421 caggctttt tcagatttgg cgagcatccg gaataactag tgaattacaa ctttattgta
 481 ccgcaattgg cgcattggc ttcgcagcct taatgcttt tgctgggtgg ttccattatc
 541 acaaagcagc tccaaaattg gcttgggtcc aagatgtaga atctatgtt aatcaccatt
 601 tagcagggt actaggactt gggtccttt ctgggcagg acatcaagta catgtatctt
 661 atccgattaa ccaatttcta aacgtggag tagatcctaa agaaataccg ctctcatg
 35 721 aatttatct gaatcgggat ctttggctc aactttatcc aagtittgct gaaggagcaa
 781 ctccctttt tacctaaat tggtaaaat actcggaatt tcttacttt cgtggcggat
 841 tagatccagt gactgggggt ctatggttaa ccgatatagc acatcatcat ttacgtatcg
 901 caattcttt tctaatecgc ggtcatatgt ataggaccaa ctgggggtatt ggtcatggtg
 961 taaaagatat ttagaggct cataaaggct catttacagg ccaaggccat aaaggcctat
 40 1021 atgaaattct aacaacatca ttgccc

SEQ ID NO:794

MEGSSSSSLISKSDAELEEM LDRMLTRLALCDDSKLES LVS NLLPLTISS
 LSSQSPVVRNKAMCVDFIFQVLEILSHVNKR VKHQHEIGLPLLALWKLY
 45 TDPA AAPMVRNFAIVYVEMAFERAPAKVIGECHASKISDDVSAKYRSLIT
 SQDKDLFLDFCLHMLLYQPSSQGGGSSPGLSVFQVNRIIGKQALKGDTLT
 RRKLPSNTFLTKNYHFLKINQFLKQLGILNVIGNMDLPGESVYPLYIAAS
 VDRVGM DLLVKIHSSQEPVAKRGEELLKKIASGTNLDDPKLINRLFLFN
 GTTG TENVAPEHNVAPGNISLKMKLMSGFCRSIAAANSFPATLQCIFGC
 50 MYDILFLLNLTFREKTEMAVRLFDALKLETQSLRSTIQEAIVSLAAAYKD

SPENILRDLEVLLLANSLAEQNEARFCALRWATSLYNSSHHCPSLYICMLS
 AADPKLDIREIALEGLFLKEEGRSIVSNHDKYPKFIEMLEYILKQQPKLL
 DSSEMRSQKLLFPSQVYLVMIKFLVKCFELEMEESENTQAVGTEFLDSAQ
 KMCSLLEHSLAFEGSAELHACASKALVSVGSYLPENVELYFSRKIVWLR
 5 SLLSHTDLSTRESVSRLLGMAASCALSDAESCSLLSELISSISQPQKLRFEAQ
 HGGLCAVGFVSAHCLHRIPTVSKAVTQNAV KYLVEVVNLETAPLASVA
 MEALGHIGICGALPFLVNDSSPGTQVLEILQERLSKLLSGDDIKSVQKIAL
 SLGHICSNETSSSHLKIALDLLFSLRSKAEELFAAGEALSFLWGGVPVT
 ADMILKTNYTSLSTDSNFLMKEVKSLSDVKTDTEEDSRTTTRETITGKLF
 10 DTTYSSRKEERCAGTVWMLSLTMYCGQQPSIQLMLPKIQEAFSHLLGD
 QNELTQELASQGMSEIYELGDASMKKSLVDALVNTLTGTSKRKRAIKLV
 EESEVFQEGTIGESPSGGKISTYKELCNLANEMGQPDLYKFMDLANHQA
 SLNSKRGAAFGFSKIAKQAGDALRPHLRLLIPRLIRYQYDPDKNVQDAM
 AHIWKALIQDPKKA VDEHLNHIFDDLLVQCGSRLWRSREASCLALADIQ
 15 GRKFDQVKEHLKKLWIAAFRAMDDIKETVRNAGDKLCRAVTSLTIRICD
 VTLTELADAKQAMDIVLPFLLSEGIMSKVNSVRKASIGVVMKLAKFYSK
 HEINQFELLASFGELNVLLGNIYDPLSDFVLFVTVLCRLHAANIGIETEKLE
 NLRISISKGSPMWETL DLCINIVDIESLEQLPRLTQLVRGGVGLNTRVGV
 ASFISLLVQKVGSEIKPFTGMLLRLLFPVAKEEKSSAAKRAFSSACGIVLK
 20 YSSPSQAQSLIEETAALHSGDRSSQIACASLFKSFSSTAADIMSSHQSAIVP
 AIFISRFEDKQISSLFEEVWEDITSGERVTLQLFLQEIVNHICESITSSSRFK
 LSFSLGKDALLDALGALSVACHEAITKEDPTTPTTILSLICSACKKKLKKY
 RESAFSCLEKVIIAFGDPKFFHAVFPMLYEMCNTASIKTNTQVQAASDAV
 KTESENGEDGHVPLEKIMECVKSCIQVATIDDILSAKADLIHVLIISLSPGF
 25 LWTVKMSGISCVGKLCSRFP SLWTD SMDDLSPSDATK FVHEL FHS LVPK
 LLECIHTVKIAQFHVAASQC LLELI ELYSTISSLHPVEVDFKA EVVSLLELE
 KSEEAKSLLRKSRDALANLPSLN

SEQ ID NO:795

30 MDKETEILSRLAANHLHLAQFEPLKATLLALRVNPDALALTILQTIVSNA
 GRFDNVLWSRSCPSPLLSFLSTIELLRFENPTSPWGFDSETLSLRADFL
 MVQVLIDRVTERIKEDEESEDENSGLGNCLRVLQGVLELGVERLK FVVD
 TSSSEGSNKIEEDAVVSLRSIVLDYSDVFDALCCNIQRQLAGCESYGTCL
 VEEVQGEEQRKEMNEATCIGSPELDNINVFALIQRNVQLAQLDAMKTKL
 35 DEGDERGAADRIRYLHLDYGVKENYHAVLKALLSRVMEKKDEYGDS
 WHMVRQNLLFMYKEALSSNCGDLVQMIQGIQDDMLLPHSQLHLSLDNE
 QIPLPLECFRRYLVDLKTERNIEDKSSPMSRAINSCLRDMYHYARISGSHV
 LECVMCAALSSVKKEKLQEANDVLTLPRLRPLVASMGWDLLPGKTAT
 RRKLMRLLWTSDSQALRLEESSLYGNQTDELELASFAACVNSGKSWTP
 40 KASFLMHGNVSSAHDDAEVDPFVENLVLERLSAQSPLRVLFDVVPGIKF
 QDAISLISMQPIASTAEAWKRIEDIELMHMRYALEAIVLALGAMEEAMK
 DETDASHRVVFYHLKDLTNHLEAIKNVPRKIMMVNIVISLLHIDDIRLSST
 QSASSACFSEKSNTPGLDPGDLGTEGEKEIVISFTKQLLDVLRRLPSHPIE
 QECQLDGNYSTDGRQALEWRVSMAKRFIEDCEWRLSVMQHLLPLSERQ
 45 WGLKEVLSILRAAPEKLLNLCMQRAKYDIGEEAVNRFALSAEDKATLEL
 AEWVDNAFKGTLVEDVMSRTAEGAAAVQDLDFHSLGSQLSPLAMVLLF
 AQSQVMLSEIYPGGAPKVGFTYWDQVHEVAIISVLRRLILKRLQEFLEQDD
 PQILQASFSGDTIISCTESHRRQGQKDRALAMLHQMIEDAHRGKRQFLSG
 KLHNLARALADEKPEVDVLKGDGSDMAVEKDGVGLGLKYTKQSPGS
 50 ANRAVDGNPVSHETEDKGKKSFGPLSNKTSTYLSQFILYTAAGDIVDGT

DTTHDFNFFSLVYEWPKDLLTRLVFDRSSTDAAAKVAEVMSADVFHEVI
 SACVPPVYPPRSGHGWACIPVIPTTPCSHSEGKVLSPSIEAKPNCYVRSSA
 TPGVPLYPLQLDVIRHLVKISPVRAVLACVFGGSILYNGSDSISSSLNDEF
 PSSPDADRLFYEFSLDQSERYP T LNRWIQMOTNLHRVSEFVVTPKQKPD
 5 DTRIKPDERTGIKRLLEHDSDESDETEETFSKNNIQPALTDGSARDGGSFE
 NGVCRTDPTVFLSFDWENEVPYEKA VNRLIDEGKLMDALALSDRFLRN
 GASDWLLQLLIKSREENPSTSGRSQGYGGQSNWSWQYCLRLKDKQLAAT
 LALKCCIGDKLCRSTATYFRQMIAIAGKRLSFFLLFEIMFGSWYARCVTL
 KNLNGKQVEAECKEDPEGLALRLAGKGAVSAALEVAESAGLSIDLRREL
 10 QGRQLVKLLTTDPLNGGGPAEASRFLSSLQDSADALPVVMGAMQLLPD
 LRSKQLLILKEFPALRDNNVIMAYAAKAISVTIIPPPREPRITVSASRLRQK
 SRAGPAVKASFTSSLSNFQREARRAFSWAPRNAENRTTSKDVYRKRNKS
 GLGASERAAWEAMTGIQEDQGSSYSADGQDRLPSVSIAEEWMLTGDKT
 KDEGVRASHKYESTPDILFKALLSLCDELVSARSAMDLCISQMKNVLS
 15 SKQLSEGASVETIGRAYHATEAFVQGLSYAKSLLRKLLGTTESTNNNGE
 RSRDVDDISSDAGSSSVGSQSTDEPSDVLSTELWLGRAELLQSLGSGIS
 TSLDDIADQLSSECLRDRLISDERYSMAVYMCKKCKIDVFPVWKA WGL
 ALLRMERYAQARVKFKQAFQLKGEDIPDVIQEINTIEGGPPVDVSIVRS
 MYDHLAKSAPTILDDSLSADSYLNVLHMPSTFPRRSERSRRSLESEKNSSV
 20 PGSDFEDGPRSNLDTRYSECTNYLQEHARQNLLGFMFRHGHFKDACM
 LFFPQSGLPPLQTSSVGAVSTSSSPQRTDPLATEYGTIESLCEFCVGYGAI
 SSLEEVITERLESAKNQDQAINQYIAGALTRICAFFEINRHFNYLYKFLVL
 KKDYVTSGYCCIQLFMNSTTQEDAVRHLEHAKKYWSLTILGVQAHFEE
 ALTARHRGSDSKKLVTKGVRGKSAAEKLSEETLVKLSSRVKMQIDVVK
 25 SFSDSEGAPWKHSLFGNPNDSETSRRRCEIVETLVEKNFDLAYSVIYEFK
 LSAVDIYAGVATSLADRKKGSQ L TELFKNIKG TI QDDDDWDQVLNIADTG
 KARSVWLIFCEMLQVLGAAINIYANKHKERPDR L IDMLTSSHRKVLACV
 VCGRLKSAFQIASKSGSVADVQYVAHQALHANSHTVLD MCKQWLAKY
 M

30

References

- Aarts et al., Proc Natl Acad Sci 95:10306 (1998).
 Allison et al., (1986).
 Altschul et al., J. Mol. Biol. 215:403 (1990).
 35 Altschul et al., Nucleic Acids Res. 25:3389 (1997).
 An et al., EMBO J. 4:277 (1985).
 Aoyama T. et al., N-H Plant Journal, 11:605 (1997).
 Bailey and Elkan In: Proceedings of the second international Conference on
 Intelligent Systems for Molecular Biology (Altman, R., ed), pp 28-36, AAAI
 40 press (1994).
 Ballas et al., Nucleic Acids Res. 17:7891 (1989).
 Bansal et al., Proc. Natl. Acad. Sci. USA, 89:3654 (1992).
 Batzer et al., Nucleic Acid Res., 19:5081 (1991).

- Beals et al., Plant Cell, 9:1527 (1997).
- Belanger et al., Genetics, 129:863 (1991).
- Bevan et al., Nature, 304:184 (1983).
- Blochinger & Diggelmann, Mol Cell Biol, 4:2929.
- 5 Bourouis et al., EMBO J., 2:1099 (1983).
- Boyes et al., Proc Natl Acad Sci USA, 95:15849 (1998).
- Byrne et al. Plant Cell Tissue and Organ Culture, 8:3 (1987).
- Campbell and Gowri, Plant Physiol., 92:1 (1990).
- Cao et al., Plant Cell, 6:1583 (1994).
- 10 Cao et al., Cell, 88:57 (1997).
- Century et al., Science, 278:1963 (1997).
- Chandler et al., Plant Cell, 1:1175 (1989).
- Christou et al., Biotechnology, 9:957 (1991).
- Christou et al., Plant Physiol., 87:671 (1988).
- 15 Cordero et al., Plant J., 6:141 (1994).
- Corpet et al., Nucleic Acids Res. 16:10881 (1988).
- Crameri et al., Nature Biotech., 15:436 (1997).
- Crameri et al., Nature, 391:288 (1998).
- Creelman et al., Annu Rev Plant Physiol Plant Mol Biol 48:355 (1997).
- 20 Crossway et al., BioTechniques, 4:320 (1986).
- Czako et al., Mol. Gen. Genet. 235 (1), 33-40 (1992).
- Datta et al., Bio/Technology, 8, 736 (1990).
- Dayhoff et al., Atlas of Protein Sequence and Structure, Natl. Biomed. Res. Found., Washington, C.D. (1978).
- 25 De Blaere et al., Meth. Enzymol. 143:277 (1987).
- de Framond, FEBS, 290:103 (1991).
- Delaney et al., Proc. Natl. Acad. Sci. USA 92:6602 (1995).
- Della-Cioppa et al., Plant Physiology, 84:965 (1987).
- Dennis et al., Nucleic Acids Res., 12:3983 (1984).
- 30 Dong et al., Curr Opin Plant Biol 1:316 (1998).
- Dzelkalns et al., Plant Cell, 5:855 (1993).
- Eisen et al., Proc. Natl. Acad. Sci. USA, 95:14863 (1996)
- Eisen et al., Trends in Plant Sci. 95:14863 (2000).
- Ellis and Jones, Curr Opin Plant Bio 1:288 (1998).

- Elroy-Stein et al., PNAS USA, 86:6126 (1989).
- English, et al., Plant Cell 8:179 (1996).
- Eulgem et al., Trends in Plant Sci. 5:199 (2000).
- Falk et al., Proc Natl Acad Sci USA 96:3292 (1999).
- 5 Feys et al., Plant Cell 6:751 (1994).
- Franken et al., EMBO J., 10:2605 (1991).
- Fromm et al., Bio/Technology 8:833 (1990).
- Gallie et al., Molecular Biology of RNA, 237 (1989).
- Gallie et al., Nucl. Acids Res., 15:8693 (1987).
- 10 Gan et al., Science (1995), 270 (5244), 1986-8).
- Gatz Current Opinion in Biotechnology, 7:168 (1996).
- Gatz, C., Annu. Rev. Plant Physiol. Plant Mol. Biol., 48:89 (1997).
- Gelfand, eds., PCR Strategies (Academic Press, New York (1995)).
- Glazebrook et al., Genetics 143:973 (1996).
- 15 Glazebrook et al., Proc. Natl. Acad. Sci. USA 91:8955 (1994).
- Gordon-Kamm et al., Plant Cell, 2, 603 (1990).
- Graham et al., Biochem. Biophys. Res. Comm., 101:1164 (1981).
- Graham et al., J. Biol. Chem., 260:6555 (1985).
- Graham et al., J. Biol. Chem., 260:6561 (1985).
- 20 Guerineau et al., Mol. Gen. Genet. 262:141 (1991).
- Hammond-Kosack and Jones, Ann. Rev. Plant Physiol. Plant Mol. Biol., 48:575 (1997).
- Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA, 89:10915 (1989).
- Hiei et al., Plant J. 6:271 (1994).
- 25 Higgins et al., Gene 73:237 (1988).
- Higgins et al., CABIOS 5:151 (1989).
- Hinchee et al., Biotechnology, 6:915 (1988).
- Hoekema, In: The Binary Plant Vector System. Offset-drukkerij Kanters B.V.
- 30 Huang et al., CABIOS 8:155 (1992).
- Hudspeth & Grula, Plant Molec. Biol., 12:579 (1989).
- Huffman et al., J. Cell. Biochem., 17B: Abstract.
- Hunt et al., Mol. Plant-Microbe Int. 9:261 (1997).
- Ingelbrecht et al., Plant Cell, 1:671 (1989).

- Innis et al., eds., PCR Protocols: A Guide to Methods and Applications (Academic Press, New York (1995).
- Innis and Gelfand, eds., PCR Methods Manual (Academic Press, New York) (1999).
- 5 Jobling et al., Nature, 325:622 (1987).
John et al., Proc. Natl. Acad. Sci. USA 89(13):5769 (1992).
Jones et al., Adv Bot Res 24:89 (1997).
Joshi et al., Nucleic Acid Res. 15:9627 (1987).
Joshi, NAR, 15:6643 (1987).
- 10 Karlin and Altschul, Proc. Natl. Acad. Sci. USA 87:2264 (1990).
Karlin and Altschul, Proc. Natl. Acad. Sci. USA 90:5873 (1993).
Keller et al., Genes Dev., 3:1639 (1989).
Kirsh et al., Plant J. 26:217 (2001).
Klein et al., Bio/Technology, 6:559 (1988).
- 15 Klein et al., Nature (London) 327:70 (1987).
Klein et al., Plant Physiol., 91:440 (1988).
Klein et al., Proc. Natl. Acad. Sci. USA, 85:4305 (1988).
Kohler et al., Plant Mol. Biol., 29:1293 (1995).
Knauf, et al., Genetic Analysis of Host Range Expression by *Agrobacterium*
- 20 In: Molecular Genetics of the Bacteria-Plant Interaction, Puhler, A. ed., Springer-Verlag, New York, 245 (1983).
Koziel et al., Biotechnology, 11:194 (1993).
Kridl et al., Seed Science Research, 1:209 (1991).
Kriz et al., Mol. Gen. Genet., 207:90 (1987).
- 25 Kunkel, Proc. Natl. Acad. Sci. USA, 82:488 (1985).
Kunkel et al., Methods in Enzymol., 154:367 (1987).
Langridge et al., Cell, 34:1015 (1983).
Lindstrom et al., Dev. Genet., 11:160 (1990).
Lommel et al., Virology, 81:382 (1991).
- 30 Lorz et al. Mol. Gen. Genet. 199:178 (1985).
Macejak et al., Nature, 353:90 (1991).
Maleck et al., Nature Genetics, 26:403 (2000).
Mansson et al., Gen. Genet., 200:356 (1985).
Martin and Paz-Ares, Trends in Genetics 13:67 (1997).

- Martinez et al., J. Mol. Biol., 208:551 (1989).
- McBride et al., Proc. Natl. Acad. Sci. USA, 91:7301 (1994).
- McCabe et al., Bio/Technology, 6:923 (1988).
- McDowell et al., Plant J. 22:523 (2000).
- 5 McDowell et al., Plant Cell 10:1861 (1998).
- McNellis et al., Plant J. 1998, 14:247-257.
- Meinkoth and Wahl, Anal. Biochem., 138:267 (1984).
- Messing & Vierra, Gene, 19:259 (1982).
- Mogen et al., Plant Cell 2:1261 (1990).
- 10 Moore et al., J. Mol. Biol., 272:336 (1997).
- Munroe et al., Gene 91:151 (1990).
- Murray et al., Nucleic Acids Res., 17:477 (1989).
- Myers and Miller, CABIOS 4:11 (1988).
- Needleman and Wunsch, J. Mol. Biol. 48:443 (1970).
- 15 Odell et al., Nature, 313:810 (1985).
- Odell et al., Nature, 313:810 (1985).
- Ohtsuka et al., J. Biol. Chem., 260:2605 (1985).
- Okamuro et al., Biochemistry of Plants, 15:1 (1989).
- Paszkowski et al., EMBO J., 3:2717 (1984).
- 20 Pacciotti et al. Bio/Technology 3:241 (1985).
- Park et al., J. Plant Biol. 38(4):365 (1985).
- Pearson et al., Meth. Mol. Biol. 24:307 (1994).
- Pearson and Lipman, Proc. Natl. Acad. Sci. 85:2444 (1988).
- Penninck et al., Plant Cell 8:2309 (1996).
- 25 Perlak et al., Proc. Natl. Acad. Sci. USA, 88:3324 (1991).
- Pieterse et al., Plant Cell, 10:1571 (1996).
- Pieterse et al., Plant Cell, 8:1225 (1998).
- Potrykus Mol. Gen. Genet. 199:183 (1985).
- Proudfoot, Cell 64:671 (1991).
- 30 Quigley et al., J. Mol. Evol., 29:412 (1989).
- Ralston et al., Genetics, 119:185 (1988).
- Reina et al., Nucleic Acids Res., 18:6425 (1990).
- Reina et al., Nucleic Acids Res., 18:7449 (1990).
- Riggs et al., Proc. Natl. Acad. Sci. USA, 83:5602 (1986).

- Rochester et al., (1986).
- Ronald, Curr Opin Plant Biol 1:294 (1998).
- Rossolini et al., Mol. Cell. Probes, 8:91 (1994).
- Roth et al., Nature Biotechnology, 16:939 (1998).
- 5 Ruiz et al., Plant Cell 10:937 (1998).
- Ryals et al., Plant Cell 8:1809 (1996).
- Ryals et al., Plant Cell 9:425 (1997)
- Sambrook et al., Molecular Cloning: A Laboratory Manual (2d ed., Cold
Spring Harbor Laboratory Press, Plainview, New York) (1989).
- 10 Sanfacon et al., Genes Dev. 5:141 (1991).
- Sanford et al., Particulate Science and Technology, 5:27 (1987).
- Schernthaner et al., EMBO J., 7:1249 (1988).
- Schindler et al., Plant Cell 4:1309 (1992).
- Schwob et al., Plant J., 4:423 (1993).
- 15 Shah et al., Mol. Plant-Microbe Interact. 10:69 (1997).
- Shimamoto et al., Nature, 338:274 (1989).
- Shirasu et al., Plant Cell 9:261 (1997).
- Shulaev et al., Plant Cell 7:1691 (1995).
- Simpson, Plant Mol. Biol., 19:699 (1985).
- 20 Skuzeski et al., Plant Molec. Biol., 15:65 (1990).
- Slater et al., Plant Mol. Biol., 5:137 (1985).
- Smith et al., Adv. Appl. Math. 2:482 (1981).
- Smith et al., Planta 168:94 (1986).
- Spencer et al., Theor Appl Genet, 79:625 (1990).
- 25 Staswick et al., Proc. Natl. Acad. Sci. USA 89:6837 (1992).
- Staub et al., EMBO J., 12:601 (1993).
- Staub et al., Plant Cell, 4:39 (1992).
- Stemmer, Nature, 370:389 (1994).
- Stemmer, Proc. Natl. Acad. Sci. USA, 91:10747 (1994).
- 30 Sukhapinda et al. Plant Mol. Biol. 8:209 (1987).
- Sullivan et al., Mol. Gen. Genet., 215:431 (1989).
- Svab et al., Proc. Natl. Acad. Sci. USA, 87:8526 (1990).
- Svab et al., Proc. Natl. Acad. Sci. USA, 90:913 (1993).

- Tijssen, Laboratory Techniques in Biochemistry and Molecular Biology-
Hybridization with Nucleic Acid Probes, part I chapter 2 "Overview of
principles of hybridization and the strategy of nucleic acid probe assays"
Elsevier, New York (1993).
- 5 Turner et al., Molecular Biotechnology, 3:225 (1995).
VanTunen et al., EMBO J., 7:1257 (1988).
Vasil et al., Biotechnology, 11:1553 (1993).
Vernooij et al., Plant Cell 6:959 (1994).
Vodkin, Prog. Clin. Biol. Res., 138:87 (1983).
- 10 Vogel et al., EMBO J., 11:157 (1992).
Walker and Gastra, eds., Techniques in Molecular Biology, MacMillan
Publishing Company, New York (1983).
Wandelt et al., Nucleic Acids Res., 17:2354 (1989).
Waterman, M.S. Introduction to Computational Biology: Maps, sequences
15 and genomes. Chapman & Hall, London (1995).
Weeks et al., Plant Physiol., 102:1077 (1993).
Weissinger et al., Annual Rev. Genet., 22:421 (1988).
Wenzler et al., Plant Mol. Biol., 13:347 (1989).
Weymann et al., Plant Cell 7:2013 (1995).
- 20 White et al., Nucl Acids Res, 18:1062 (1990).
Willitset al., Mol Plant-Microbe Interact 11:795 (1998).
Xie et al., Science 280:1091 (1998).
Yamamoto et al., Nucleic Acids Res., 18:7449 (1990).
Yang & Klessig, PNAS 93:14972 (2000).
- 25 Yu et al., Proc Natl Acad Sci USA 95:7819 (1998).
Zhang et al., Proc. Natl. Acad. Sci. USA, 94:4504 (1997).
Zhou et al., Plant Cell 10:1021 (1998).
Zhou et al., Plant Cell 8:2235 (1996).
- 30 All publications, patents and patent applications are incorporated herein by
reference. While in the foregoing specification this invention has been described
in relation to certain preferred embodiments thereof, and many details have been
set forth for purposes of illustration, it will be apparent to those skilled in the art
that the invention is susceptible to additional embodiments and that certain of the

details described herein may be varied considerably without departing from the basic principles of the invention.

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a plant or fungal nucleotide sequence encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795 or the complement of the open reading frame, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
2. An isolated polynucleotide comprising a plant or fungal nucleotide sequence which is substantially similar to an *Arabidopsis* nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
3. An isolated polynucleotide comprising a plant or fungal nucleotide sequence which hybridizes under high stringency conditions to the complement of a nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
4. The isolated polynucleotide of claim 1, 2, or 3 which is DNA.
5. The isolated polynucleotide of claim 1, 2, or 3 which is RNA.
6. The isolated polynucleotide of claim 1 wherein the nucleotide sequence encodes a polypeptide having at least 90% amino acid sequence identity to the *Arabidopsis* polypeptide encoded by the open reading frame.
7. The isolated polynucleotide of claim 1 wherein the nucleotide sequence is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat sequence.

8. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a dicot.
9. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a monocot.
10. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a cereal plant.
11. An isolated polypeptide encoded by the polynucleotide of claim 1, 2, or 3.
12. An expression cassette comprising the polynucleotide of claim 1, 2, or 3 operably linked to suitable regulatory sequences.
13. The expression cassette of claim 12 wherein the polynucleotide is linked to a promoter for expression in a plant.
14. A recombinant vector comprising the polynucleotide of claim 1, 2, or 3.
15. A host cell comprising the expression cassette of claim 12.
16. A host cell comprising the polynucleotide of claim 1, 2, or 3.
17. The host cell of claim 15 or 16 which is selected from the group consisting of yeast, bacteria and plant.
18. A transformed plant, the genome of which is augmented with the polynucleotide of claim 1, 2, or 3 or a polynucleotide which comprises one of SEQ ID NOs: 1-684 and 789-795 which is expressed in an amount which confers resistance or tolerance to the plant to pathogen infection.

19. A transformed plant, the genome of which is genetically altered so as to inhibit the expression of a gene corresponding to the polynucleotide of claim 1, 2, or 3 or a gene corresponding to one of SEQ ID NOs: 1-684 and 789-795.
20. The plant of claim 19 which is altered by T-DNA insertion, transposon insertion, or targeted DNA insertion.
21. The plant of claim 19 in which expression is inhibited by transcription or post-transcriptional mechanisms.
22. The plant of claim 18 or 19 which is a monocot.
23. The plant of claim 18 or 19 which is a dicot.
24. The plant of claim 18 or 19 which is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat plant.
25. A method of expressing a polynucleotide in a cell, comprising:
introducing the polynucleotide of claim 1, 2, or 3 into a cell so as to express the open reading frame.
26. The method of claim 25 wherein the cell is a plant cell.
27. The method of claim 25 wherein the cell is a monocot cell.
28. The method of claim 25 wherein the cell is a dicot cell.
29. A composition comprising the polynucleotide of claim 1, 2, or 3 or comprising the polypeptide of claim 11.

30. A method to identify an open reading frame in the genome of a plant cell, the expression of which is altered by oomycete infection of the cell, comprising:
- a) contacting a plurality of isolated nucleic acid samples on a solid substrate with a probe comprising plant nucleic acid corresponding to RNA isolated from plant cells infected with an oomycete, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
 - b) comparing complex formation in a) to complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising plant nucleic acid corresponding to RNA from uninfected plant cells or from mutant plant cells which have a response to pathogen infection that is different than the plant cells in a), so as to identify which samples corresponding to genes having an open reading frame, the expression of which is altered in response to oomycete infection, wherein the genes comprise orthologs of *Arabidopsis* genes comprising one of SEQ ID NOs: 1-684 and 789-795.
31. The method of claim 30 further comprising identifying an open reading frame in the gene, the expression of which is induced in response to infection.
32. The method of claim 30 further comprising identifying an open reading frame in the gene, the expression of which is decreased in response to infection.
33. The method of claim 30 wherein the probe comprises nucleic acid from a dicot.
34. The method of claim 30 wherein the probe comprises nucleic acid from a monocot.

35. An isolated polynucleotide comprising an open reading frame of a gene identified by the method of claim 30.
36. A method to confer resistance or tolerance to a plant to a pathogen, comprising:
 - a) contacting plant cells with an expression cassette comprising a polynucleotide encoding a polypeptide that is substantially similar to a polypeptide encoded by a nucleic acid sequence comprising an open reading frame comprising one of SEQ ID NOs: 1-684 and 789-795 so as to yield transformed plant cells; and
 - b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the polynucleotide in the cells of the plant in an amount effective to confer resistance or tolerance to the plant to the pathogen relative to a corresponding plant which does not comprise the expression cassette.
37. The method of claim 36 wherein the polynucleotide hybridizes under moderate hybridization conditions to the complement of one of SEQ ID NOs: 1-684 and 789-795.
38. The method of claim 36 wherein the polynucleotide hybridizes under stringent hybridization conditions to the complement of one of SEQ ID NOs: 1-684 and 789-795.
39. A transformed plant prepared by the method of claim 36.
40. A seed of the plant of claim 39.
41. A progeny plant of the plant of claim 39.
42. A method for identifying a plant cell infected with a pathogen, comprising:

- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with at least one oligonucleotide under conditions effective to specifically amplify a nucleotide sequence substantially similar to one or more of SEQ ID NOs:1-184, 301-494 or 500-803, or a portion thereof so as to yield an amplified product; and
 - b) detecting or determining the presence or amount of the amplified product, wherein the presence or amount of the product is indicative of pathogen infection.
43. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection, which plant nucleotide sequence is from a gene encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising at least one of SEQ ID NOs: 685-788.
44. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, which nucleotide sequence hybridizes under high stringency conditions to the complement of at least one of SEQ ID NOs: 685-788 or which nucleotide sequence hybridizes under very high stringency conditions to the complement of at least one of SEQ ID NOs: 685-788.
45. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, wherein the plant nucleotide sequence comprises SEQ ID NO: 710, SEQ ID NO: 711, SEQ ID NO: 714, SEQ ID NO: 715, SEQ ID NO: 764 or SEQ ID NO: 773.
46. The isolated polynucleotide of claim 43, 44, 45 or 46 wherein the nucleotide sequence which directs transcription is 25 to 2000 nucleotides in length.

47. A recombinant vector comprising the polynucleotide of claim 43, 44, 45 or 46.
48. The vector of claim 47 which is a plasmid.
49. An expression cassette comprising the polynucleotide of claim 43, 44, 45 or 46 operatively linked to an open reading frame.
50. The expression cassette of claim 49 operably linked to other suitable regulatory sequences.
51. A host cell comprising the expression cassette of claim 49.
52. A transformed plant, the genome of which is augmented with the expression cassette of claim 49.
53. A plant cell containing the expression cassette of claim 49.
54. A transformed plant comprising transformed plant cells, the transformed plant cells containing the expression cassette of claim 49.
55. The transformed plant of claim 54 wherein the plant is a dicot.
56. The cell of claim 53 which is a dicot cell.
57. The transformed plant of claim 54 wherein the plant is a monocot.
58. The cell of claim 53 which is a monocot cell.
59. The transformed plant of claim 54 which is a cereal plant.
60. A method of augmenting a plant genome, comprising:
 - a) contacting plant cells with the expression cassette of claim 49 so as to yield transformed plant cells; and

- b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the open reading frame in the cells of the plant.

61. A transformed plant prepared by the method of claim 60.
62. A seed of the plant of claim 61.
63. A progeny plant of the plant of claim 61.
64. A method of using a plant promoter, comprising: introducing the expression cassette of claim 49 to a plant cell and detecting the expression of the product of the open reading frame.
65. A recombinant vector comprising the expression cassette of claim 49.
66. A plant cell comprising the vector of claim 65.
67. A transformed plant, the cells of which comprise the vector of claim 65.
68. The plant of claim 52, 54, 61 or 67 which is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat plant.
69. The expression cassette of claim 49 wherein the open reading frame is in an antisense orientation.
70. The expression cassette of claim 49 wherein the open reading frame is in a sense orientation.
71. A transformed plant, the genome of which is augmented with a polynucleotide which is substantially similar to any one of SEQ ID NOs:

1-684 and 789-795 and which is expressed in an amount which inhibits or prevents pathogen infection.

72. A transformed plant, the genome of which is genetically altered so as to inhibit the expression of a gene comprising a polynucleotide substantially similar to any one of SEQ ID NOs: 1-684 and 789-795.
73. The plant of claim 71 or 72 wherein the polynucleotide is substantially similar to SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 32, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 792, SEQ ID NO: 57, SEQ ID NO: 68, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 102, SEQ ID NO: 111, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 682, SEQ ID NO: 129, SEQ ID NO: 137, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 157, SEQ ID NO: 161, SEQ ID NO: 165, SEQ ID NO: 170, SEQ ID NO: 174, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 184, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 197, SEQ ID NO: 208 or SEQ ID NO: 211.
74. The method of claim 36 wherein the polynucleotide is substantially similar to SEQ ID NO: 308, SEQ ID NO: 300, SEQ ID NO: 272, SEQ ID NO: 362, SEQ ID NO: 265, SEQ ID NO: 241, SEQ ID NO: 261, SEQ ID NO: 380, SEQ ID NO: 228, SEQ ID NO: 658, SEQ ID NO: 243, SEQ ID NO: 254, SEQ ID NO: 216, SEQ ID NO: 225, or one of SEQ ID NOs: 400-684.
75. The expression cassette of claim 12 wherein the polynucleotide is in antisense orientation.
76. The expression cassette of claim 12 wherein the polynucleotide is in sense orientation.

77. A method for identifying a plant cell infected with a pathogen, comprising:
- a) contacting a sample comprising polypeptides obtained from a plant cell suspected of being infected with a pathogen with an agent that specifically binds to a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by an open reading comprising sequences selected from the group consisting of SEQ ID NOs: 1-684 and 789-795 so as to form a complex; and
 - b) detecting or determining the presence or amount of the complex, wherein the presence or amount of the complex is indicative of pathogen infection.
78. A method for identifying a plant cell infected with a pathogen, comprising:
- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with a probe comprising at least a portion of a polynucleotide that is substantially similar to any one of SEQ ID NOs: 1-684 and 789-795 under conditions effective to form a specific complex between the probe and the nucleic acid; and
 - b) detecting and determining the presence or amount of complex formation wherein the presence or amount of complex formation is indicative of pathogen infection.
79. A computer-readable medium having stored thereon a data structure comprising:
- a) a nucleic acid molecule that has at least 70% nucleic acid sequence identity to a nucleotide molecule selected from the group consisting of SEQ ID NOs: 1-791 or the complement thereof; and
 - b) a module receiving the nucleic acid molecule which compares the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.

80. The computer readable medium of claim 79 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.
81. A computer-readable medium having stored thereon computer executable instructions for performing a method comprising:
- a) receiving a nucleic acid molecule having at least 70% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-791 or the complement thereof; and
 - b) comparing the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.
82. The computer readable medium of claim 81 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.
83. The method of claim 42, 60, 77 or 78 wherein the cells are dicot cells.
84. The method of claim 42, 60, 77 or 78 wherein the cells are monocot cells.
85. The method of claim 42, 60, 77 or 78 wherein the cells are maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat cells.

1/12

RPP-DEPENDENT DEFENSE PATHWAYS

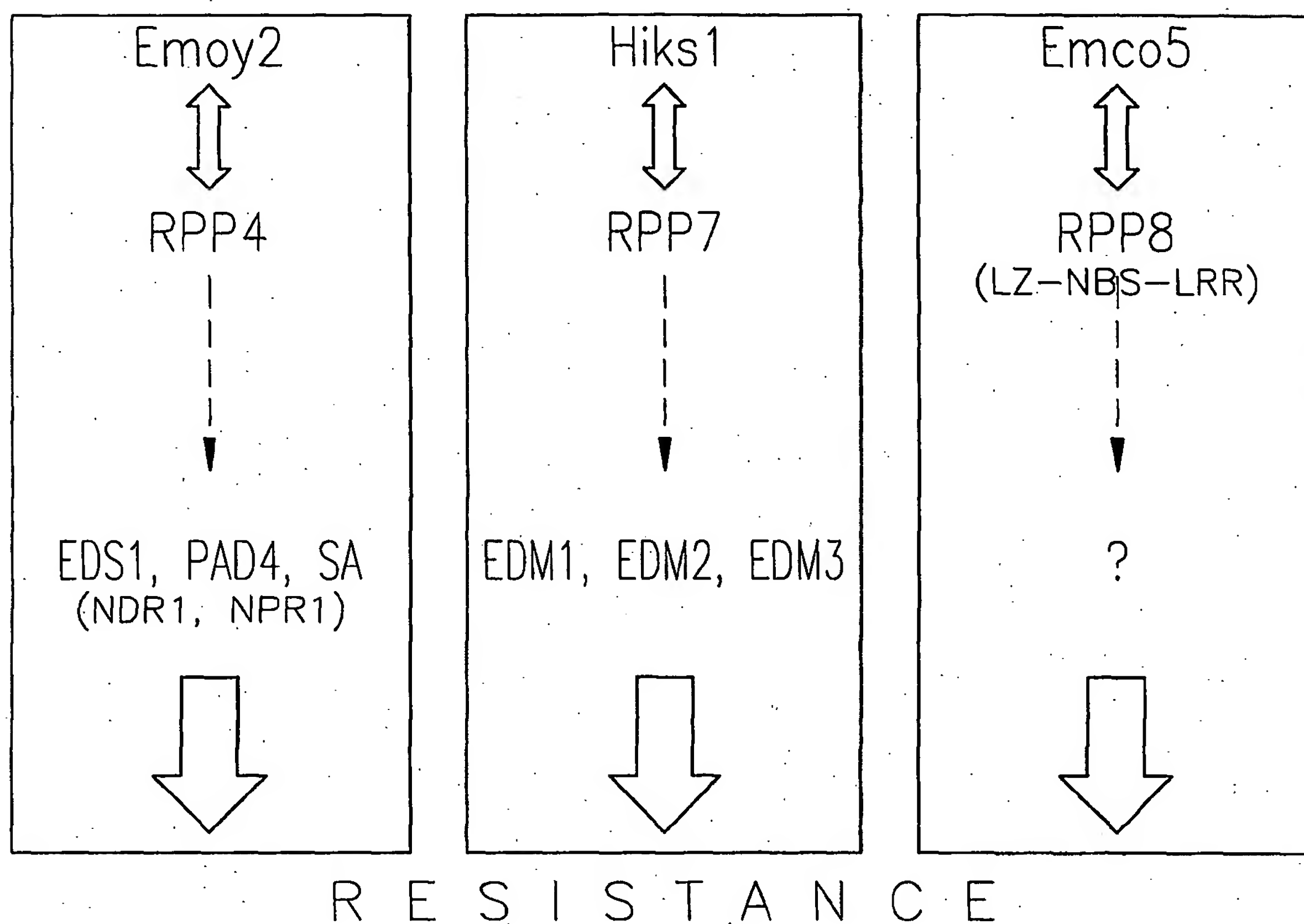


FIG. 1

2/12

motifs:

Motif 1/ MAP Score: 6.87857

CAACAATGAC

TT TT

Motif 2 MAP Score: 2.22382

GATGGGNCNAA

TT A

C

Known stress-responsive cis-elements:

ttgacc, ttgact, ggtcaa and agtcaa W box

ttgaca and tgtcaa

W box-like

tgacg and cgtca

TGA-bZIP binding site

acgt

bZIP binding site core

cacgtg

G Box

gccgcc and ggcggc

GCC box

| Subcluster A
17014 ribonuclease RNS1

SEQ ID NO:
774

tagaattgaaaaagggtaatgtgaaaagggtattctcaacaattattcaagataaaaat
tgtataggtgttaaataataatgtgtaaaagagaagacgatgtgaagtattaaaagaaa
aaaaaaatggatggtgtatataagtaaccattgtagatagtttaagcaagaaaaattga
tgttgcattggaaattaaaaaatttcaataaaattagaaaagcaactctaaatcattac
ttatttttattattttcaagaagttataaagtattaaacaattcgTTGACAaataagttt
gatcgacattgtgtgacaaattttaaacacatcattaataacaacgaggacaaatacag
ttcagatatcgtctactattaaaacacttcttctataggagcaaagaaaaattgtcggc
aacgaactggggaccaataatattccgagtttgagttcaaactgagtaattttattttg
agaaaatttgccaagttaacttataattctggtttACGTgtagtaattttattaagttgt
tataggaaaatgagaaaataactaagacacatccaagaaagtttcacacgaaatttactt
acaaaaagattgtttatttaataacttccgtatatagatatataaatatttaacacatta
attataaagttcaagataattgattatctatctttttttgtcatctgaaattattatcg
ctcaaacgaagtaattctgaggaaagttgtttacaaactagttatttcattattgtcta
cttatataatagaattaaaaaaaattattgcttaatgcaatttagtttttagataaaatc

FIG. 2A

3/12

attaaacttaatagattatataagttagatatcaataattgggcttgcttaaaaacata
aatataaaatattattgggcccgttACGTgcatacaaaaacgaaccttctaacaacaagt
gtgaACGTtacgacttcaaaattaaaaaaacacacacaactatgtccacACGTaattct
catatgattcagattccaaggagaacaaaattaaaaacaaatctcgtaaacatacatat
acttcacataaaaacaaaagggtacagtatataccataaatctccgagattcttttgatgt
atctgtccatttcattattacacaaactaggaaactgatatctctctattcacattcct
ctgattctattttctctttatatatattcacccattaaccatctcaatcttataaccctc
aaaatcacaaatcttctcttacaaaaaactttgaaagatg

14609 putative cytochrome P450

SEQ ID NO:

775

aattatattagctggaaattttaaattttgtacagacacattgtttgttctcatcttcc
tttgctcagccttttggtggtctctaccgcttaggaccacttactgcaaatctagaaaat
taaaatatatgacttagctaaaatgtgaggtatattgagaagtgagttcttaaaactact
tggaacttgcttacttagaatttgagacattataagtacaattgatgttaattctaaaagt
gtagaacattgttaatttcttgaacagctgtagccaacaatgacggacgatacgaatca
ttgatcgaagaggcgattttgtttcacatcgatcagtggatctcttggcgaagtacatg
accaaccaccagatgatcagaagcattcaacacctctctatttatcccaatttgtaagt
acatatatgtatgatagtatgtatgtatgtatatattatgagtacatatatacattagaaa
atactattaactttcaagtcgttatagtaattggacaatattattcgtaattatcaaaag
cgcttttttcattttctatctgaacctaatgcctagcgagttgaaaacatagctacctaa
taggctactactacacaatcttgaagcacaataataacaacgaaACGTcccttgggtat
gagattatttagaagtttcataagattctagtccttattcaattgtgcccatcaagcac
aaagtacggaagcgataggaaggACGTCAcagtcctgttttgataatctaataatgatcgta
gaaagcGTTGGGtgcttttaagttttttctttcgccctaaatatttttaaggtcttttgtc
aggaatagaaatatagataaagtctattgagtttgtaagacctatgtatattgggtccgg
atgcaatgcttttttactcatgcgcatcattcaatagaagaatttggttatcagtgaacgagt
acaaTGTCAAatataatttaacaaattattttaaaaccttttaaatatgtgcatagttttt
ttcgtactcggatagaaattaataataacaaaaattactgatttgataaaaatgaatttc
gctttgtaaataaattatatataattcaaaatcctcatcgtcgaaaacaatttttaaaat
aaaacaaccaagatattttccacaaattaaattaatttttagttttgaattcagatatata
taacaaacaatgatataagaatatttcattaaataaaaagatattcttaactgaat
ttatttattaatttggaatatacttattaccgaaataaaggattgtttatttcttacaac
tcgtcttattagtggtgcatagcataacaagggtgaaagagaaaacatg

16649 putative S-adenosyl-L-methionine:trans-caffeoyl-
Coenzyme A 3-O-methyltransferase (function:disease resistance) (promoter up to next ORF) SEQ ID NO: 776

catgtctcttgagtctcgtgggttggtgcaaatgttcgttggttataaacgagagatgt
atgtcaatatataattggcttctggtcaaactaattgagctactaataagacccaaat
taaggactaacacaccaattgatcttatccatgacttttcaaccatgggactagaaaat
caattatctagacagtacttgatgcgaatatattaacgtttatgtttcttaaggatttt

FIG. 2B

4/12

ttttctctcttaagggttgcatacaaatggttgaaatgcaagcaggcgaacagtttgca
atgtagtttttattgactaatataaatttggtatgtgagattttaaatagcaaaaaaagta
tatagtatagaattatttaaagaatatatcaaattgaagggtactaaaaaacggatttg
aattcgaatgctaacaataacgaataaccagcataaatctccaaagatgattcaaattttg
cagtttcaatccctcaatccgcttcaacggatgaaacaataataattcaacatgttc
taacaatttttcaagtatgcatgaagaaatcacttaaaaaattccaagatatgtattta
aagtttagtgaatcatcaaagcgcaaaaattcacaactaagtaagaagggtgtcgataa
aaagcaaaaacaaaagttacagaatgtcttgaggagaggattcctcaaacctcctaaga
aaagatcttttgggtttttgtaatctgtcattgttaagtaagcaagtttggtgaataa
gtgttccagagatatgataagttgaccttttggattgtctaactctggaatcttttagtt
tatgggtgaactctcaccccaagctcaatgtgatgtccatgtaactaatcttaggcaaca
tgatgtggcataggagattgggcatcctcatcatcaagatccctaaatgacgaaatgat
tttaaataataattcctaagatttcacatccttaaaccttattaagtcctaacattc
gaaaatacacacattcatttgatttaatttaaatttttatattaacttctctattttc
attaaaaattgtaaaatatttttttattgtcgtaaaatgttttacttttctatttccat
taaagttgtaaatatgttttattaacgtcgtaaaatgttatttttttaataaaaaatat
ctgttgggccaaga

17653 (similarity to DNA damage inducible)
(promoter up to next ORF)

SEQ ID NO:
777

acaataatttccataattcaaattgctttcagaaaggatttctcaatacagggttaaaaat
atcaatctaattctttgcaaactcattaaactaatttagttactttccttaactttaaga
aaacaaatctcaaattttgtggctataaccaccattttcattgaaactaactactcaatt
aacggtctgaaagaggacaaaaagattttcacaagtgtacaccaataaaaagaaaatcgt
tttttcccttataaaaatgacaaaaattaccaagaaattaaatggaacataacttacga
cgaaatttacctgacgatttttttttcttactgaaaattaccaagaaatcgcggtggaag
tcggaaatgttacatacttttctttgtaactacactgcgaaagcaaaaaaaaaaacat
aaagtcaaccttttgggaaaattgtcgtctttgacatcagaagagattcaaactaaaat
gaatgagtacgttacttgcggttatgggttggttttcttttttaatttttagaaacttttc
ttacttatattttgaatcaacagttgataacacaagtataaattatttttgcgccatc
acactggagtcaagctcgagagagacttggtttcctaatttaattcataaacttggttcg
acagtgaatatatacatcttcgaagaaataacaccattgacttaaaaccaaataaata
acaatagtcttataattttatattattcacacttaaaattacaataacaagtcttttcaa
agtctttttaattatataaacaatagaagtctttttcattgtctctttttgactaattaa
taaagaccatgaaaagacttgattgttaagttttgagtgtaaatgttaataaattacta
tggttttggttggttttatatttctgccatctaaataattacattatatgataaaataat
taccctagcgacaaatgacagctagaaatgtaataagaacaccaactaaataattatgc
aggttaataatggagcaagtgatgttctttctatatactgtacattttctttttaaaaa
attatgtaatttcgcgagaagagaaaaagaaaaacacgtgggtgattagagagtagtataaa
gatagttgggttggtttctgtttttttctgtatctcgaggcgccaaaaacaacaaaaa
aaaacttcagagcggtgatcagattcaccgatttttctcaaaatg

FIG. 2C

5/12

17008 putative tyrosine aminotransferase

SEQ ID NO:

778

cataggactactacaatcagTTGAGAgagacgacgatctgggttaatggcatggccactg
agtttgatagcttccttgggagatggcatgacgatcatagaaaccttttagtcTGTCAAa
tatttcttgtaccactgattcggttcctatcgatatacctcaccacaattctctgccc
ctagagccactcctaaaaatttcaacacaaaaataaataataaataagtaaataaaaaaag
attgatcataattaacgatgcaaattttataaattaaaatcatatgtaagaagatgacta
tgggagccccaagttcttaagatggtgtatattgttaaagagatcaatacctgggtataa
ggataagactctcctcactaactagcttcgTGACGaaatcaaaatcatttttgatatta
ttcaacattgatgTGTCAGcttcaactgtaaaataaatacgtttaagctaatacatttat
tattataagcaaaatatggagcatccaatagcaaaaaaaaaatctagaaaaccaagaatc
caagaaaaagaattaaagtaccataaataagaacaagattcggttttcttgggacaaa
agagacaaggaatatccttgagcctctcacatgaaagctcgACGTtgcggtctcatggct
ttgatcttcttctcgaagaactctttaggtgttttctccaatatatcaggaagtgttc
ctatcaaaatccataaataatctcacattatttagagaacccaaaacttatagcttacgat
gatagtgagagattacaaacctggagaataaatagaaggctgtggagttaaatacaagaaa
atcctctattgcttgaactacctgttggtgaacgaaaggcccatatattagttagaatc
ttcttaattggtgcggtaatcttattttaagtaaaaactatagtgtttagaagTGACTg
accctgtagatacaaagataaccattaggatcgttcatggcgatccagccaactctcca
gcctgggTGACCcatcctttggatatggatccgagcgtgatcaccggagctattgatg
caaacttccccatgggaataaaaaggcttgtctccatatacaacatgatcatataacttcg
tcggatattatcattataccgagttttctagccatctccgcgacctaaagattagtcga
tatattaccaaaaaACGTtagttgttttacacttcaaaaaaacttatattacattaaat

15042 cinnamyl alcohol dehydrogenase-like
protein (promoter up to BAC end)

SEQ ID NO:

779

cattttttgatgattctttcttctttcttatcttgatctgctgctttcacgcttttgct
gtttatgtgtgtgtattactatatatatatagagaaagttggaaacgtaacgtatgc
gtatgtgtgatgaaataattgggtgtttctgcatagcacacatttgatggctataattga
gtgtaaatttggtgtatattattgacaaaatttagtcaaaaagcttaaaaatcttttttagtc
gttgaaagatccttctagaaaaagacattttttttcttcttctttcatacgtatggctc
atggctgtgtagtttattagaatttttaggtgaaaaaaatattagaagccaacaaaactt
aaatgaaatttatttgcattcataattcattttaccagtttataacaacaacgtaatcc
aaaaagtaaaatgagaaagaatggaatttgtgtactttgaaaggaagaaaaaccactat
tgacgtggacacgtcggctaaaggagggtccacgggggttggtgaacaaacaatgtggg
gtctaatacgtgtgttttgctttggtttaaaatcatggttgccacgtgttgattcttgac
ctctctctgacatgaaactgtagcattgacggcccagatcagctgogagaatacttccc
acaaccttggaattttacggcccagatcaacaaagaatcgatttgctctttactattt
cgaagaacaaagagtgcagttatgaataatagaaaagaaggacaaagagtgtgtgaat
ggcttcacattaaaacaaaagcccattatgaatgaccattcacatttcacaccagtt
tgaaaaatcgaccgtccaattaagtaaacattcaaaaacccaaaagataaacctctaatt
cacgaatcacacagcagcatgagccgtttcatcacgacgttatctcagagtttcttgg
aaataatttggtgtagcggacttgtggctgtaaatggggccaatgcttaaatttacttg
tctcgtctcttctacacgtcttctcttccgaccacacccttcattcaattcaacgtctc

FIG. 2D

SUBSTITUTE SHEET (RULE 26)

6/12

12778 Lipase/Acylhydrolase with GDSL-motif family
(promoter up to next ORF)

SEQ ID NO:
780

catcatttagagagagggagaaacagaactgtgaaaagagaagaagattgcttttgtgc
cttagctcgtagaccgattcgttatatttatattgcaagtactacaatttggcaatgaa
aataatagttcattttactatacaataataacgtgtagcgcgagggttcattttactat
acacctatttaacgcactagcaaacgattatcgatcaattatattatagttcgctta
atcacgtctgacgcattactggtttctcttctactttatttttaattctcaacaaaata
tctattgttactacgagtaccaagaaagatcgtgcttttttttttttgggttcaacaaca
acttacaattacacaagagtctgaatacacataagctttaacccaatccggcaatatag
aatacaatttgggatcataattcagaaaagaaagagattccctagcaattctatctgcc
acacaattcccttctcatcgggtaaaagtcactttaacctcttcgaagtgtgaaaaga
tcgtgcatttagaggcaagaagtagaattaaacatacaaatcctcacggaaatatagggt
gtaaatggtaacactaaaccagattcagtaatttctgcagtaaccatttgcataaaact
aaattttgctgactagccaaattcaacaaaaaaatttcaacaccaacatatagtagat
atgtttatttctgctaaaacttttgggataatttacgagtagacacaactcgaattaaaata
tttttaatatcaaaatacatatcaaatagatatattttaaataagtcagattatactgat
acgatatatgaataatatagatacataaaatatcactaccagaatagacaagagacgaa
tatgttcgggataattatagataatttgggataataattttaataacgtttagataactta
aatcaattattaaaattttgcaaaaacaactcacacctatgctaagatatcttttaaaa
gataaattatagtaatttccttaatcatcctcatcatattattgattaaattacttgaa
aacaattaaaaaaaacaattaacaattctatatattttatcatcatgttaatttttgaaatt
attttcttaatagtgttttgacaaagattttcggttaattatttacatatattttaatagt
tcaaatttaataaagaagaataactcaattttgcggttgacacaattcttaatagtatag

|| Subcluster B

20245 glutathione-conjugate transporter
AtMRP4

SEQ ID NO:
781

atttttctaataagacttttcttattctcatagactcttcttattcatctttcttaatc
aattcgaccaactcagtggagacaaaatctcacacgaccctttccactttttggtaact
ttattattaatttattagtagtggtgtagttcctttctttcttctgctgatctTGTC AAC
aaaataactaaatttttcttaagcggctgtttatatattattaacaaagggtttccgcgtg
tctcttggttaactagtagactaaaaacaaatcgtaaaactcgatttttctcaaccaaatt
tagaagatactacggcatgtaattagctaatgataaaagattcgaattttcgttccaat
ggatttgtcttttcttttgcccaaaaaccaagaatttgtcttctcttggcagtagtttagc
tagacaacgcataatagctatatattttgtgtacactGGTCAAggtcgtggatACGTCA
taataatattatttccaataagtcctattaaaacattaaacaactttgagtttttaaac
aaacttagtgtaagaaaaataaaaaatagcagacagtttacgggtaagactagatgacca
tatatgattgagtgcataaaacatcttttttcttttcttttttgaaaaagcgaaactaa
aagattattagttggttggaatcagcttagcgtaatcttcgagaaaaatgactctaattgc
taaaatactgatttaataatcaattttctaatggtTTGACCCAACagactttttttttttt
ctatcctctaataatatataatcatatagtagtaattatttagtagataatatgattaa
cACGTgaatagcaaagtttctatcatttttattcaaaaaaagattcataagtaataaaa
tgatAGTCAActtttcttttttctttttgtgtttggccttttgtTGACGCGTCAttgttg

FIG. 2E

SUBSTITUTE SHEET (RULE 26)

7/12

tacaccaccagtcacactattgtgggatgtgataatcggtaccttttaatgtcaggagc
ttctttcttacattttccacttcaaacaaccgataattcagaggaattttctcttcct
ctctctctctcttttttatattttttcactgggaaaaatg

17051 CTF2B involved in hydroxylation
and oxidation of an aromatic ring

SEQ ID NO:
782

catagccgcgttccaagaggaGGTCAAgaggattcacttttctataatcaatattaaat
tgtagtcacaaaattcaagaaacttatatagaccttatttttatttttgaacatcaatag
ttgtcgttgaaaagtatcttggggatatttagatttagcatatgAGTCAATGTTGgggc
cttaagagttgaggctacaaatttataactcagaaaaagtgtatatgccctttaatttt
tggcctattgggtcttttatggCGTCAactccaatttcagtttgaaaagaaaTGTCAAta
actaacaatggttctttTGACTttgaaatcttagaagtttcgacttaccattttctac
aagtgttaaatagcactgttattcaaaatcttatatttggttaattgtgcttaatatatt
ttaaatttaaataacttcattaaaatccaatgttattcaaaactaaattacttttgaaa
tatgtgtatatgaagtcattttgaaatgaaatctcataaagtttcataagtaaattatta
gaataaaaacccaaggtaattgtatagattttgaaatccacacaataatatcgaattgt
aaaatctagagaattcaattttcaattcatgaaggagtgttaatcaatcatggatttttaa
agttagttgattgaatataaaaagtaggaaagatgtgggattcatgtgggtgggtttggccc
atctccatgatctctagtgaatttcagctTGACGcaactttcgtttaagatcttacttca
ttgtgtgttggtgttgagcctcactggattgggtgtgtcggttttttagttcactcagag
ttaagagtcttcgagtaagactctatcactatttaaataattaatgtaattgagttatg
ataattcaaattggatctccttcattccatagttgcatTTGACAtttttatataaaactt
gctgattatctaagtcacaaatttgagtccttggttaataattcagtttcaatcatcaggag
atgtctaatagattaaaaattaaagatagaaatgtctaattggattgaaatatataaagt
gactcagccaaaaacatgttaactgaaaatcttgtataaaatggagattctctgataac

19640 putative glutathione S-transferase

SEQ ID NO:
783

aatgtagttttttctgggtttgtggagttaatcactaccttttagcttggatttatagc
cttatgggtgttgatgggtcttgtgataaaacgacgacgaactttgccgttttatatgggc
ggcagtgtgatgtaaattgcaagagtctagaaggaaacagatgTTGACTttacaacata
tttataACGTtccctttataatttttttttatctcttttttagtaagtggagatgtgtc
ctaattcctaacccttgcccttatccctggagcatgtgtaccTTGACTtgatccattcatt
ttctgaagacaaccccatgcttCGTCAagaatttcttctgcttccccaattataacccat
cactttatcgtgggttcttcataattgatccattttgtctgtgtatgaaacatcaacagc
tttaaaaccattttgtcattctcgtttgttatattgacgcccaagaaaacaaacaactct
atagtctgagctataaaaaaagaatttagtactaatctgttatttgatgttccttttggc
atatattaaaaatgttggtgttatataataggcgttggtttttccgtttctccatctacga
acttggttgctgaattttccttccaacaatggtataaagtatcggtgaattttctatgg
ttacaagactcaccacctcacgataactaaaaatataactaaagaaatttggttatattgtg
ccgcaacaatatagaccacatgtccgttggtactttcctctgtttacacaacttcttACG
TgtcgaaatacatgttcacatttaatacatagttgtgggttttattaagaaggatgggtTTG

FIG. 2F

8/12

ACTaaattatagctttttatctactttttctttcatatgaaaactccagggtttatgaacca
atttcttatgatttgtaagaaattgaatactactacattttaaagtgtttataataatta
aTTGACAttagaatttagtaaaaacactaattgttcatacaaatgtttcattttattgtt
catacaaaactattataacaagattacacaaacatatagttaacatctactgatcgaaga
gtatcattgttgtctcttaggctgatttgattctttctacaactttcttcatatg

14248 PAD3_at member of the PF|00067
Cytochrome P450 family

SEQ ID NO:
784

gttctggtcgaaggatttgtcccgaatgccaatggcgattgctagtgtggaactagca
ttgatgaatttgctttattattttgattggagtatgcctgatgggactaaagggtgaaga
cattgatatggaagaagctggtaatatctctatTGTCAAgaaaatacctcttcaacttg
tgctgttcaACGTtattgatgagcaataatataagctcgataacatggaaagtgtatg
aagcaaaaaacataagattcttttagattttgttgtgttatataagaaagaaatgttcca
ataataaatcaagaaagaataacttttgttcatttacttaaaaactagatcataatcaa
cacggattaagatcttttttcttcaacaaaattctaaattttgtttttttaagtaaaaa
atgttatagcataaatgttcagatttttatgtcgtatttatattgaattaaatataggac
aaagaaaaataagatacagaacaaagagaaattttgatccaaaaaaaaaagaaagaga
aataagatctagaacaaaaacgatacattcagattgattattgaaatcaaataatcgaa
tttataattgaatttgatggaatttataatgtattttttgtcatggaaataataaagtt
tgtaatatagtaggcacgatcgaatctggagcttcaattttttttaactaattgtta
tggaagatgctggaatgatctcttttttacaagaaagctcctctcattcttgttccggtt
aaacaccattaatgacatcggcacacaaaaattcaaacaccgttgaagattgtttgcta
tactttatttttatcaataataagttgcggtacttggttaactgtatACGTacttctat
ttcttatagttgtgcgataattaccacaagtccaaaaaagtaaaaatatgaatttgataa
agcagtgtaaacctgagattttcaagatttggggcctaaacccattagagaatgctACGT
agagaaccattggggcccataaacttattttattcccgcaaagcctgagtggaattcgaa
cactaccacaaaaagtaagagtttgggttattttgatttttaattcattcactttgaattat
tatagacaccggacagtgacttatgataaagagatttttaacctttaaaactaaaacac
taaaatacataatccaaagaagacggaacaaaaaaacaaaaacagagccaggaataatg

17500 athcallga_s_at calmodulin-like protein
(promoter up to next ORF)

SEQ ID NO:
785

catcaaactaattttggttattcttgagattaggaatgtgtgttcacctaaaagctagta
attgattactaaaatgtaatgcatgcaacaagaagagtcaatcgaatttttatagagata
agtcataataaaatgattaattatcgctagaggaagctgcgatgaaattttcttacagctt
ttgtctttttaccatctaatcatttaattctctgagcctacgccatcacacatatctaaa
agcaccttcttcgaaattcccttggaggacaaaacatggacctcttttttgttctacttg
gattttctcggaataatgacttgcattgtcttcttactatattttatgtatcccttcattc
tatactttttcgaaattctaatttaactctacataataatccactcccaccagctaaag
tttagacatgacaagtattttatcaaatgctccttcaattcaaactactgaatattgtt
tggaataagtactttttggagacgtaagctatattttccaatccgaaatgaatgaaccaa
atgtccatagttctgtttttttttcctcctaaagtgaatatattaagagacactaaatt
ctagaaaatatgtttaaaataataataatcagtaattgtccaaaaaatgtgaataactta

FIG. 2G

9/12

aatcaaaatcaggatacgttgtcacaagaacaaactttcctagataatgtatatatttt
 atattattatcatattatgtatgcacttaagacatctccatccatgagaaacctacaaa
 gtttttcaaacaaaaaaatattaatattatattataatttgattattttttattaaaaa
 agtattttttgttaaaaaaattaaaccaatagtaagatgagaattgtcatgatgggttgta
 caaagtatctcagagtatctcagagtttctcacttgagaaactttctacactctctctc
 cttcattttttattattttttatttttttaattgtgagaaattcttatgagatacccacaa
 tagagatgggtcttataaatttatcaacatgggtgaatctctcatgttatatatagaggtg
 atttaaaggctaaatagaataacacactacagcatataaactcaatgatatg

18928 putative endochitinase (promoter up to next repeat region) SEQ ID NO: 786

cattttgtgtatggagggtgttgtgtgaagaaatgaagaagggtgtgttgatgtattttat
 agtgtaaatttgggtctattcaaattgaaatattgatcagtggttagacatctttcacgat
 tattgattggctttttctgagtc aaagtcaatgccactttgtaccacttaacaaaagtc
 aatgacacagttttttctcttgctgttatgagaaattccatgtcgggtcatagatcagat
 caaaaacgaatatgtaatcaaaatttttaagagccaagttacttggatgaaaatcattc
 tcataaaaacttgattgagataatcaagtttagattagttcaaacgtttgagatttttc
 tattgaatagttccaagtttttggttaattagctcaaacgatattgttagctaatatagc
 attttttttgggtcaactaatatagcatttagaacgttctttttaagtccttactttgatt
 ttttaacaaaaattgtatggaattgtgagaaaaatgactagtgaagccaaaatgtttcta
 tttataaatcaaaatcaacccaaaattagaaaaatccaactcaattattgcaatttccaa
 atagtcatgcgtcaaaattaaaccagcatatcaataaaaagcggtttagtcttaccac
 cctgggtctagagactctagaaccatcggagctcaagtgaaaaacgacgcggttaagctg
 catctttcaagatagataaaaactttttgtcgatcgcttcacacagagtttcgggc
 tcctccggtgtgttttcaggacgacgcaaaggggaaaaaaaattgaattctttctctcca
 agcgaaactagggtttcgaaagtctctgtctcatcaaagcttcgaaaaggtagattttat
 ggtttcttactctcctttctctatgatattccaatttcttgcgagcttgctcagtggtc
 ttaccttatatttaccgaaccagtgccctttatattctatcacattcgaagttattgggtt
 tctgggttacttatattgcttattgttctatgactacgatataattatcccaaagatttg
 ttctttttctccgaatttggattagaaatggatataactcaaattctgaacatgcccagaa
 gaatcct

14614 putative glucosyltransferase (promoter up to next repeat region) SEQ ID NO: 787

ttaatttatccacacctcaacgaaaatttccggttggtgcgctaacgaattcaggctgtg
 aagttaaaagaaaaataaacaataattatagcttcacataagcgatcgatcttcaaactct
 acacatgacagaagcaaataactaaattaaatagcgtaaatTTTgtaataatactagaa
 aacctaataaaccaaatgtaaaaaaccttatgggaaaaaatgtgataaagcacctaaacc
 atagaataacttaaaatttcaatttcccaatcaagggtatgatataaaaacccatggaaaa
 caaattctcagccatatttctatctgaccgagtccttttcaaaataatatatagacggt
 agagtcttatatagtaaaaaacatttttttaaaactaatttatcttctcatatgaaaatg
 aatgcaataaaaaatgaccatatatgctgtaatgatattcaaggaagagatatcacaac
 aaggtcgaagaaatatacaatatctgaaagtcgactatatgggtccactttccaaattag

FIG. 2H

10/12

agatggaaagaagaacgattatgcagcaaaccattgatcggacgaagaagaataaa
tatggaggccattactatagtagtatttggccttgaaatattttgggtccgagaaataataa
ataaacagttatggcttttcggatttgggtgctttcaattttctcaaagtgttggacaa
gtgttattacactcacctaaaacaggatcattccaatttcttgggctcagagtctgtac
tttcttcttctttaaaccaaggtcttataagtattctctaaaccaagtcactaaacaat
aattgggtcttgggtctgggtcaaacttggatcaatgttgccacatagccattagccaca
caaaacaaaaattgtcttgcctttatatggaatgaagaaaaatcgaattttgtaaccat
ttttgacttttaaagtcacactcgccgtatacggcacaccaaatgaccaaaaacatttga
ccaccaactttgctttaatgttaaaaactttttttttgcatcccactactctcttcttca
cctcctcaagtcacagtgaccaaaaatcacacacttcacaagaaacaacctatg

||| Additional genes showing early and transient RPP-triggered
expression

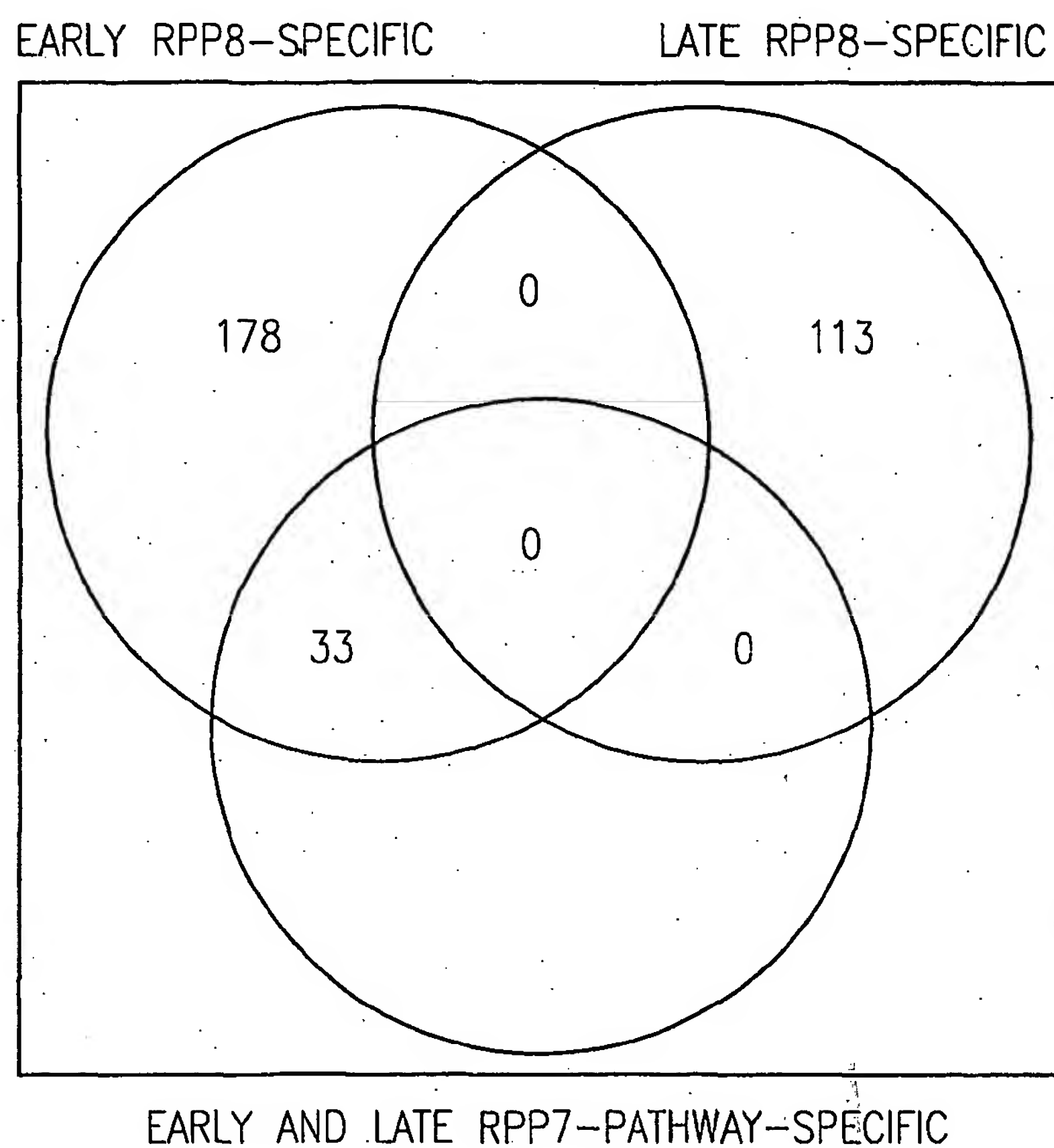
13176 Contains Myb DNA-binding domain
repeat signatures

SEQ ID NO:
788

ttccaaaacttaaacctttaaaccttaaatgaacttcaatctacaccatataaagagga
agagatataccttcgccatCGTCAttggcccaaagaacaaaatgtacatactttacaag
aggaatcaatattaaagtgtatataaccaatgacaagggtccaataatatcttctttgt
cgtaattggagatcttctgaacatgacagtggaaggtatacaatgggctagttccaata
tcaccaataacaaccccaagtgtctgcaaagcaagtatgagtttctttcctataaccagt
gtcctgaaaaaacacattaccaagttcaacaactcaatcagatcgaaaagtaaacaaca
tgaagaagaagaagaacattcacacacaaatgctaacctcgatttcgtttttctgagtt
ccaggaatctcaagagcatctacatcgaaagAGTCAAcggcagggctagtgccaatcaa
acgctgctccacattgtcatcctcctcatcggaatccatttccgggtgattatgctcat
catatccatcatcgtcgtaatcttcattaacctcataatcatctttctcatcgaacacc
catcgcgacaaTGACGTcggttgaaatcgctctccgccaaactcctcatcaatctcagaccc
atcgctccactgcttttcttcttccACGTgaaacatcaatcacggttggaacactga
agatctcgagattgtgattcagattcgatctctgatccaaggaaacaggattggaatt
gggtgtttttgagagattgagagatggaagagagagattgatctacatacactggagagg
acctggcacgaatgagaaagaagcttacACGTgtccaatcatgattggattcgagactc
acggtttaaggaaaaaacaaccagaccaaattaggcttaaccgctaaaaaacgggttc
tcgttttgaaagattgagagagacgatctacaaaggaggacaggacccggcacgaatga
gaagaagcttacACGTgtccaatcaggattgaacgatttaataagcttaaccgtatgt
aaaccggatttttagctgggtccacaagtAGTCAAatatagattttttaatAGTCAAata
attttcatagggggcgaagttcaagatgagttactacactcatcaaagctcacaaaaaga
gaagagaagagacgaggatcaatcaccattctcatg

11/12

26 *Peronospora* (Hiks1 and Emco5) induced
RPP7, EDM1,2,3 and RPP8-Dependent genes

**FIG. 3**

RPP4-pathway, RPP7-pathway and
RPP8-up-regulated transcription factor genes

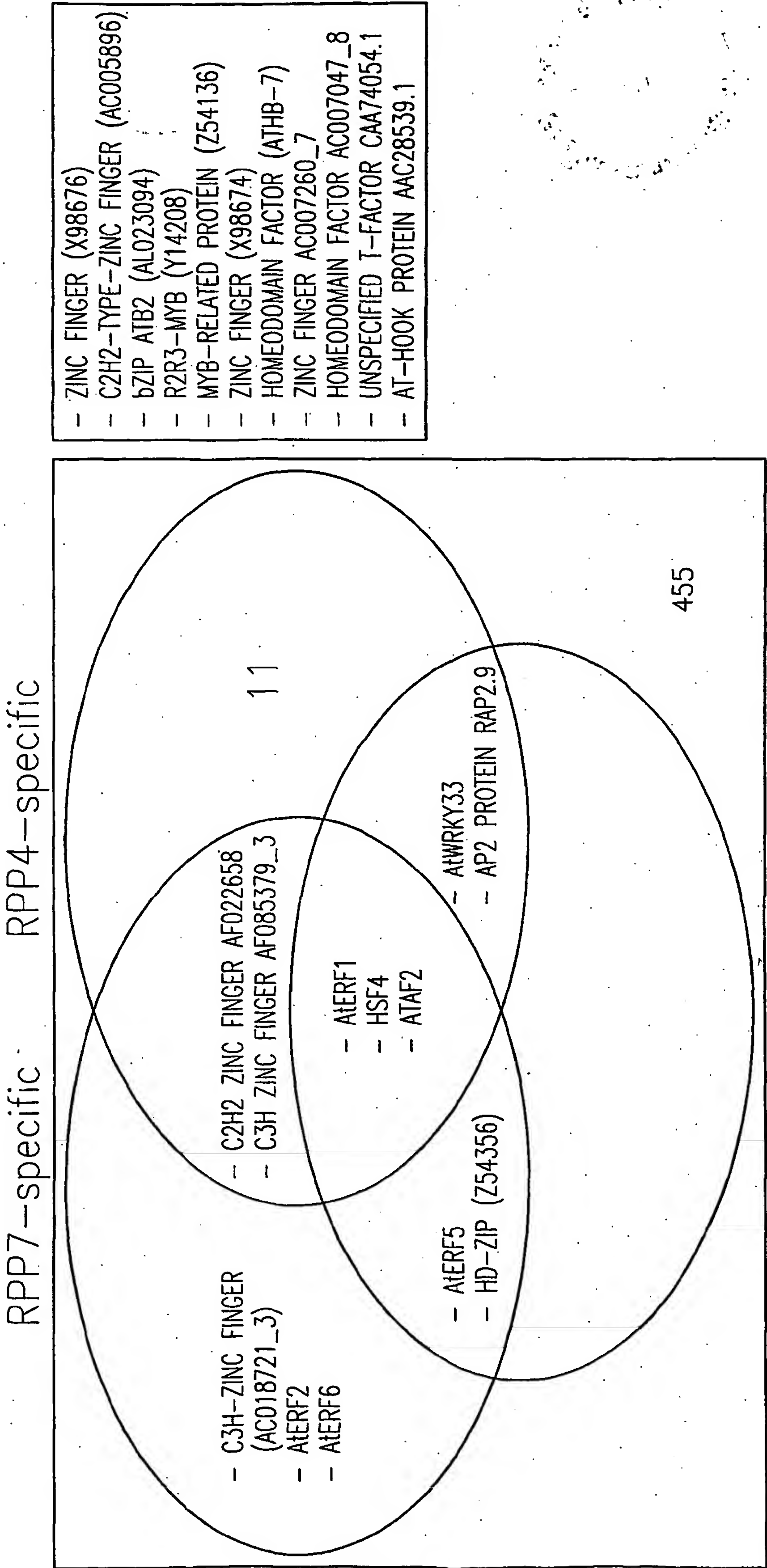


FIG. 4

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record.**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.